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Minimum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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    A_Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
3: geneseqp2000
4: geneseqp2001
5: geneseqp2002
6: geneseqp2003
7: geneseqp2003
8: geneseqp2003
8: geneseqp2003
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538
1 MAADPESTAALPDG
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geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
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geneseqp2004s:*
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(c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                      Gapext 0.5
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1133.996 Million cell update
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Biocceleration Ltd
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                                                                                                                                                                                                                                                                              2443163
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score greater than and is derived by a Pred. No. 18 the number of results predicted by chance to have a r than or equal to the score of the result being printed. ed by analysis of the total score distribution.

## SUMMARIES

24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	<sub>L</sub>	No.	Regult
99	99	104	105	105	105	112.5	123.5	127.5	127.5	128.5	131.5	132	185	266.5	266.5	266.5	423	449	485	531	533	534	534	Score	
18.4	18.4	19.3	19.5	19.5	19.5	20.9	23.0	23.7	23.7	23.9	24.4	24.5	34.4	49.5	49.5	49.5	78.6	83.5	90.1	98.7	99.1	99.3	99.3		Ouerv
1088	1088	539	1041	1041	1040	1080	1067	1185	1185	1035	1065	1091	1103	1063	1054	1052	1059	1061	1045	108	107	1041	1041	Length	
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AAY00892	AAY00891	AAY37205	ADC34773	AAY56782	AAW97216	ADM26293	AAB96257	ABM39522	AAU43003	ABU24074	ADN46385	ABU48588	ABP66334	ADD13268 .	AAG92098	ABU26087	ABU35902	ABU34060	AAW57448	AAY21902	AAW72885	ABU36647	ABU34693	ID	
Aay00892 Isoleucyl	Aay00891 Isoleucyl	Aay37205 Protein i	Adc34773 Chlamydia	-		Adm26293 Hyperther	Aab96257 Putative	Abm39522 Propionib	Aau43003 Propionib	Abu24074 Protein e	Adn46385 Thermococ	_	Abp66334 Bifidobac	ი	Aag92098 C glutami	P	Abu35902 Protein e	Abu34060 Protein e	_	Aay21902 Amino aci	Aaw72885 Mycobacte	Abu36647 Protein e	Abu34693 Protein e	Description	

WPI; 2003-029926/02. N-PSDB; ACA38563.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 62617; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
78.5	78.5	79	80.5	80.5	80.5	80.5	82.5	82.5	82.5	82.5	86	87	89	93	96	96	97	97	97.5	98
14.6	14.6	14.7	15.0	15.0	15.0	15.0	15.3	15.3	15.3	15.3	16.0	16.2	16.5	17.3	17.8	17.8	18.0	18.0	18.1	18.2
1077	329	375	348	348	348	348	11096	9477	7068	659	1232	1038	1363	1042	1072	1072	1085	1026	1036	1088
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ABJ26121	ABU34127	ADI37312	ADV80926	ADV83074	ADV89673	ABP26034	AAB10129	AAE10144	AAE10142	ADS29586	ABM95065	ABU25711	ABU08100	ABU19362	ADK62202	ABR52806	ABU20747	ADS08184	ABU27203	ABP73361
Abj26121	Abu34127	Adi37312	Adv80926	Adv83074	Adv89673	Abp26034	Aae10129	Aae10144	Aae10142	Ads29586	Abm95065	Abu25711	Abu08100	Abu19362	Adk62202	Abr52806	Abu20747	Ads08184	Abu27203	Abp73361
Aspergill	Protein e	M. tuberc	Streptoco	Streptoco	Streptoco	Streptoco	Streptomy	Streptomy	Streptomy	Bacterial	M. xanthu	Protein e	Human kin	Protein e	Disease t	Protein s	Protein e	Staphyloc	Protein e	Candida a

## ALIGNMENTS

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RESULT 1
ABU34693
Wang L, Wall D,
                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                   03-OCT-2002.
                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                              Mycobacterium bovis.
                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #20220.
                                                                                                                                                                                                                                                                                        19-JUN-2003
                                                                                                                                                                                                                                                                                                       ABU34693;
                                                                                                                                                                                                                                                                                                                    ABU34693 standard; protein; 1041 AA.
                                                                                                                                            (ELIT-)
                                                                                                                                           BLITRA PHARM
                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                     Malone
, Carr G
                                                                                                                                            INC.
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                                                                                                                     Haselbeck R, Yamamoto R,
                                                                                                                      Ohlsen
Forsyth
                                                                                                                      3 2
                                                                                                                       Zyskind JW;
Xu HH;
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RESULT 2
ABU36647
ID ABU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 107; Conserv
                                                          Wang
Wall
                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-0094893.

25-OCT-2001; 2001US-034293P.

08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #22174.
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                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU36647 standard; protein; 1041 AA
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2003-029926/02
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                                                                                                                                                    ELITRA PHARM INC.
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                                                          Zamudio C,
Trawick JD,
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99.1%;
                                                          Malone
Carr G
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Pred. No. 1.7e-54;
                                                          Haselbeck R, Yamamoto R,
                                                          Ohlsen
Forsyth
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                                                             Zyskind JW;
Xu HH;
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs
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Claim 25; SEQ ID NO 64571; 1766pp; English.

cc encoding a polypeptide whose expression is inhibited by the antisense cnucleic acid; (2) a host cell containing the vector; (3) an isolated copolypeptide or its fragment whose expression is inhibited by the activity of a gene in an operon required for the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular coproliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibite cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of solateration. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required correctly programs. or for screening homologous nucleic acids acids. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this Sequence 1041 AA; patent did not form part of the printed spi in electronic format directly from WIPO at the 6213 antisense sequences given in the specification where of the nucleic acid inhibits proliferation of a cell. Also inc ftp.wipo.int/pub/published\_pct\_sequences (1) a vector comprising a promoter operably linked to the nucleic acid invention relates to an isolated nucleic acid specification, but comprising any one of Also included are:

S 밁 Matches 107; Query Match Best Local Similarity 934 VAADPESTAALPDGAGLVVLDGTVTABLBAEGWAKDRIRBLQBLRKSTGLDVSDRIRVVM 1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM Conservative 99.3%; 1; Score 534; DB 6; Length 1041; Pred. No. 1.7e-54; Mismatches 0 Indels 0 Gaps 60 993

RESULT 3
AAW72885
ID AAW7 밁 AAW72885 standard; protein; 107 B

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61 SVPASREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT

AAW72885;

21-JAN-1999 (first entry)

Mycobacterium tuberculosis antigen CFP9

Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen; infection.

Mycobacterium tuberculosis

WO9844119-A1

08-OCT-1998

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Best Local &
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                       10-NOV-1997;
05-JAN-1998;
01-APR-1998;
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18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                              Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CEP7A; CEP3OA; CFP7B; CFP19; CFP27; CFP3OA; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
                                                                                                                                                                                                                                                                  06-SEP-1999
                                                                                                                                                                                                                                                                                                                AAY21902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                       08-OCT-1998;
                                                                                              20-MAY-1999
                                                                                                                      WO9924577-A1
                                                                                                                                            Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 125; 163pp; English
 (STAT-) STATENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or vaccination against tuberculosis caused by M. tuberculosis, ricanum or M. bovis
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                                                                                                                                                                                                                                          acid
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                                                                                                                                                                                                                                         sequence of antigen CFP9
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Florio |
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                                                                                                                                              tuberculosis.
                       97DK-00001277.
98US-0070488P.
98WO-DK000132.
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97US-0044624P.
97DK-00001277.
98US-0070488P.
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  SERUM INST
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                                                                                                                                                                                                                                                                                                              protein; 108
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Pred. No. 1.1e-55;
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RESULT 5
AAW57448
ID AAW5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC to the tuberculosis complex. The invention provides a (1) fusion of the comprising at least one polypeptide fragment (1) and at least cone fusion partner; (2) a fusion polypeptide fragment (2) and at least cone fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cepitope from M. tuberculosis protein ESAT-6, or MPT59 and a second conferent amino acid sequence from M. tuberculosis, and/or including a conference which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment cut that encodes the above polypeptides. The polypeptides and mucleic acid concentration against TB caused by Mycobacterium tuberculosis, africanum or convisor. The polypeptides are also useful for diagnosis, africanum or convisor. The polypeptides are also useful for diagnosing ongoing or cut tuberculosis complex. The invention also describes the use of CPP7A or convisor. The invention also describes the use of CPP7A or convisor in a mammal in the induction of a strong immune convisor in a mammal by performing a DTH type skin convisor of for the preparation of an immunological composition; and convert the propagation of a subunit vaccine of convisor the preparation of a subunit vaccine converted to the preparation of a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2004
12-AUG-1998
                                                                                                                                                                                                                                                          Isoleucyl-tRNA
antimicrobial;
                                                                                                                                                                                                                                                                                                                           M. tuberculosis isoleucyl-tRNA synthetase (IleRSs) enzyme.
                                                                                                                                                                                         Mycobacterium 
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57448 standard; protein; 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging
                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic fragment of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Fig 4; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVPAERGDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAADPESTAALPDGAGLVVLDGTVTABLEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                 tuberculosis
                                                                                                                                                                                                                                                          tester strain;
                                                                                                                                                                                                                                                                                    synthetase; IleRSs; Mycobacterium tuberculosis;
/note= "if the first GTG codon at position 640 is used for initiation of translation, the GTG codon at position 670 would be translated as Valine at this position to yield a 1045 amino acid protein; if the GTG codon at position 670 is used for initiation, it would be
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 531; DB 2;
Pred. No. 1.9e-55;
0; Mismatches 1
                                                                                                                                                                                                                                                            leprosy; tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
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ABU34060
ID ABU3
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AC ABU3
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AC ABU3
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AC Prot
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AC Anti
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                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This represents a Mycobacterium tuberculosis isoleucyl-tRNA synthetase (IlleRSs). Mycobacterial strains are responsible for leprosy (M. leprae) and tuberculosis (M. tuberculosis). RSs's are mycobacterial enzyme that are generally responsible for the reaction: aaRS+aa+ATP => aaRSaa-AMP+PPI -AMP+CHNA => aa-CRNA+aaRS+ANP, where aa is an amino acid. IleRSs is the enzyme specific for Isoleucine, with each amino acid having its own specific enzyme. These enzymes are essential for protein production. As more and more mycobacteria become resistant to drugs and antibiotics, tester strains comprising host cells containing a recombinant mycobacterial isoleucyl-tRNA synthetase gene, can be used to rapidly assess the antimicrobial effect and specificity of isoleucyl-tRNA synthetase inhibitors. The recombinant enzymes are also useful for biochemical studies of the enzyme in elucidation of further treatment strategies. The cloning and recombinant production of the enzyme has not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding mycobacterial isoleucyl-tRNA synthetase - and corresponding vectors, recombinant hosts and tester strains for recombinant production of the enzyme used in assays to identify inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5756327-A
                                Protein encoded by Prokaryotic essential gene #19587.
                                                                                            ABU34060;
                                                                                                                         ABU34060 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schimmel PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1998
                                                              19-JUN-2003
                                                                                                                                                                                                 1004
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DB; AAV32142.
                                                                                                                                                                                                                                                                                                                                                                                                                                        previously possible
                                                                                                                                                                                                                                                           944
                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                       1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                        SVPAEREDWARTHROLIAGEILATDFEFADLADGVAIGD
                                                                                                                                                                                                                                                           SVPAEREDWARTHROLIAGEILATDFEFADLADGVAIGD 1042
                                                                                                                                                                                                                                                                                                                                                                                 1045
prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5A-0; 62pp;
                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translated as Met at this position yielding a protein 1035 amino acids (residues 12 to 1045 of AAW57448) 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by STG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= Leu,
                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                 90.1%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                         1061
                                                                                                                                                                                                                                                                                                                                   Score 485; DB 2;
Pred. No. 1.3e-48;
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    drug
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61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK 107

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                                                                                                                                                            CC the 6213 antisense sequences given in the specification where expression cc (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: (2) a vector comprising a promoter operably linked to the nucleic acid ce encoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (4) a host cell containing the vector; (3) an isolated copypeptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding copypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway copying a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent compound that inhibits cellular proliferation of compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the compound that inhibits are useful for compound that inhibits the compound that inhibits are useful caids required for proliferation to isolate candidate molecules for rational compound that caids such as a com
                                                                              Query Match
Best Local S
Matches 92
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Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                          Sequence 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 61984; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium avium
                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolate candidate molecules for rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-)
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ACA37930.
                                                                                                  Similarity
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Trawick JD,
                                                                                Conservative
                                                                                                                                                              B
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Carr GJ,
                                                                                                83.5%;
                                                                              Score 449; DB 6;
Pred. No. 2.8e-44;
4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen
Forsyth
                                                                                  11;
                                                                                                                   Length 1061;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising
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Xu HH;
                                                                                  <u>.</u>
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                                                                                Gaps
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1014
SVPAGRAEWAHTHRDLIAGEILATRFEFGEPADPVAIGDGVRVSISK 1060
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Protein encoded by Prokaryotic essential gene #21429
                                                   19-JUN-2003
                                                                                                   ABU35902
                                                                                                                                               ABU35902 standard; protein; 1059 AA
                                                   (first entry
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Mycobacterium leprae. Antisense; prokaryotic essential gene; cell proliferation; drug design

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 06-SEP-2001; 25-OCT-2001; 06-MAR-2002; 08-FEB-2002; ; 2001US-00815242. ; 2001US-00948993. ; 2001US-0342923P. ; 2002US-00072851. ; 2002US-0362699P.

(BLIT-) BLITRA PHARM INC.

2003-029926/02 ACA39772 Zamudio Trawick ą, Malone Carr G ရိပ္ ရ Haselbeck R, Yamamoto R, Ohlsen Forsyth ដ្ឋ Zyskind JW; Xu HH;

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 63826; 1766pp; English.

ABUSULT 7
ABUSSON 7
ABUSSO CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated color, polypeptide or its fragment whose expression is inhibited by the containing the vector; (3) an isolated color, containing the vector; (3) an isolated color, containing the vector; (3) an isolated color, containing the polypeptide; (5) producing the polypeptide; (6) inhibited by the continent of the polypeptide; (5) producing the polypeptide; (6) inhibited by the continent color, containing cellular color, containing cellular color, containing cellular proliferation of the gene product or that has an activity against a biological pathway of the gene required for cellular proliferation or the biological pathway in which hat test compound that inhibits gene product lies cor a gene on which the test compound that inhibits gene product lies cor agene on which the test compound that inhibits proliferation of an compound; sactivity; (11) a culture comprising strains in which the gene compound; sactivity; (11) a culture comprising strains in which the gene compound; sactivity; (11) a culture comprising strains in which the gene compound; overexpressed or underexpressed; (12) determining the extent compound; overexpressed or compound that inhibits the gene compound; overexpressed or sompound; that inhibits the gene compound; overexpressed or sompound; (12) determining the extent compound; overexpressed or sompound; (12) determining the extent compound; (13) identifying the target of a compound that inhibits the contained; or contained; or for screening for homologous nucleic acids required for goileration to isolate candidate molecules for rational contained; (12) determining the extent contained; (13) determining the extent contained; (14) profileration of contained; (15) determining the extent contained; (15) determining the extent contained; (15) determining the extent the 6213 antisense sequences given in the specification where expresof the nucleic acid inhibits proliferation of a cell. Also included invention relates to an isolated nucleic acid comprising any one expression are:

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Best Local
                                                                                                                                                                                                          Wang L,
Wall D,
                                                                                                                                                                                   WPI; 2003-029926/02.
N-PSDB; ACA29957.
                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                  03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                 Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                 Antisense;
                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #11614.
                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 ABU26087;
                                                                                                                                                                                                                                                                                                                                                                                                                                ABU26087 standard; protein; 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1059 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   (BLIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 VAANPEFTAELPDGSGLVVLDDTVTPELEAEGWAKDRIRELQBLRKLIGLDVSDRIRVLM 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                  BLITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVPAERADWARVHRDFIAREILATSFEFGEPADSVAIGDGVRVSLLK 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK
                                                                                                                                                                                                                                                                                                                                                                prokaryotic essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                           Malone
Carr G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 423; DB 6;
Pred. No. 3.7e-41;
                                                                                                                                                                                                           Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                 gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                           Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1059;
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                                                                                                                                                                                                           Zyskind JW;
Xu HH;
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New antisense nucleic a for homologous nucleic isolate candidate molec molecules acids, useful for identifying proteins or scruc acids required for cellular proliferation to scrules for rational drug discovery programs.

Claim 25; SEQ ID NO 54011; 1766pp; English

The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense cC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibited by the cC the polypeptide; (5) producing the polypeptide; (6) inhibited polypeptide; (7) identifying a compound that influences the activity of a green product or that has an activity against a biological pathway crequired for proliferation, or that inhibite cellular proliferation; (8) contentifying a gene required for cellular proliferation or the biological pathway in which a proliferation—required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an

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RESULT 9
AAG92098
ID AAG92098
XX AAG9
XX AAG9
XX AAG9
XX COT,
XX COT,
XX COT,
XX COT,
XX COT,
XX COT,
XX II 6-
PR 03-
XX II 6-
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Best Local S
Matches 57
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   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum are useful for identifying the mutation point of a gene derived fi
                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                        Claim 17; SEQ ID NO 5852; 246pp +
                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 VVPEEKKEWALRHTDMIAGEVLATSPE-----VVTGEPABHDIVAGVTATVQK 105:
                                                                                                                                                                                                                                                                                                        2001-376931/40.
DB; AAH67317.
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Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid synthesis; vitamin; saccharide;
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Pred. No. 2.2e-22;
8; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                               S, Hayashi M,
Ozaki A;
                                                                                                                           Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Ochiai K,
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      erium glutamicum.
gene derived from
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from

New nucleic acid encoding variant forms of proteins required genetic stability and proper protein folding, useful for procfine chemicals, specifically lysine, in microorganisms.

Claim 1; SEQ ID NO 76; 265pp; German

This invention describes novel polynucleotides and polypeptides involved in genetic stability (DNA repair and recombination, transposition of genetic material), gene expression and folding of proteins in

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RESULT 10
ADD13268
ID ADD13
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                                                                                                                                                                                                                                                                                                                                                                                                                             genetic scattery; with the production; gene expression; protein folding; fine chemical production; lysine production; nucleotide production; nucleotide production; nucleotide production; lipid production; diol production; carbohydrate production; aromatic compound production; vitamin production; co-factor production; food; animal feed; cosmetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                  WPI; 2003-505062/47.
N-PSDB; ADD13267.
                                                                                                                                                                                                                                                                    31-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic stability; DNA repair; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. glutamicum stability and
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                                                                                                                                                                         Haberhauer
                                                                                                                                                                                       Zelder O,
                                                                                                                                                                                                                                          05-NOV-2001; 2001DE-01054180
                                                                                                                                                                                                                                                                                               15-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
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                                                                                                                                                                        Pompejus
G;
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                                                                                                                                                                                                                                                                                                                                                                                                       glutamicum.
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /note= "Optionally substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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                                                                                                                                                                                      Schroeder H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              folding associated protein RXA02726.
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Pred. No. 2.2e-22;
5; Mismatches 33
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                                                                                                                                                                                       Kroeger
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RESULT 11
ABP66334
ID ABP66
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Best Local !
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The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequences given in ABQ81843. Also described is a polynucleotide (II) encoding fusion protein, comprising a sequence selected from 1097 sequences giver in ABPG6258 to ABBG6354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum. Polynucleotides are isolated from a nucleic acid library of C. glutamicum then mutated at the specified positions, cloned and expressed by standard methods. Cells containing vectors that express the polynucleotides are used for production of fine chemicals, preferably amino acids and specifically lysine, but more generally nucleotides, nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic compounds, vitamins, co-factors and enzymes. These are useful in the food, animal feed, cosmetics and pharmaceutical industries. The polynucleotides, optionally as primers and probes, can also be used for identification of metabolic activity. Cells that contain the polynucleotides of the invention may produce fine chemicals in better yields, with higher productivity and/or more efficiently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antidiarrheic; antibacterial; inhibitor of Salmonella; detect identification; lactic acid bacterium; diarrhoea; pathogenic rotavirus; food composition; pharmaceutical composition.
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                                                                                                                                                                                                                                                             Claim
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T
                                                                                                                                                                                                                                                                                                                                      polynucleotide comprising Bifidobacterium genome sequence useful
be or primer for detecting and/or identifying Bifidobacterium lon
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                                                                                                                                                                                                                                                                                                                  sample.
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Pred. No. 2.3e-22;
"Midmatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                       given
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be used

28

an

inhibitor of Salmonella.

(which

Claim 25;

SEQ

ID NO

76512; 1766pp; English

N-PSDB;

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC a probe) is useful for the detection and/or identification of CC Bifidobacterium longum in a biological sample. A carrier containing the CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be CC used for preventing and/or treating diarrhoea brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented CC products, ice-creams, fermented cereal based products, milk based CC powders, infant formula, pet food or a pharmaceutical composition CC selected from tablets, liquid bacterial suspensions, dried oral CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. CC (I) is useful in DNA arrays or chips to carry out analysis of the CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent CC Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented CC in the printed specification but is based on sequence information CC supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                  Wang L, wall D,
                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #34115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU48588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU48588 standard; protein; 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1103 AA;
                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2.
                                                                                                                                                                                                  (BLIT-)
                                                                                                      2003-029926/02.
)B; ACA52458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAERE 67
                                                                                                                                                                                                  BLITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKVEQFRDLIAHETLATSFE---VKEGAELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAALPTG-GFVILDTALDADLLAEGYARDVÍRSVÓDARKAADLDIADRÍSLVLTVPÁVDV 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DWARTHROLIAGEILATDFEFADLADGVAIG
                                                                                                                                                                                                                                                                                                                                                                                                                  pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                               prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.4%;
                                                                                                                                                    Malone
Carr G
                                                                                                                                                    5,2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185; DB 5;
Pred. No. 1.4e-12;
                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                  Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                      3,5
                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 13
ADN46385
ID ADN46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1091 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                             30-AUG-2002; 2002JP-00319011
                                                                                                                                                                                                                                                                                                                                                                                    WO2004022736-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococcus kodakaraensis KOD1 protein sequence SeqID263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN46385 standard; protein; 1065 AA.
                                                                                                                                                                                     29-AUG-2003; 2003WO-IB003597
                                                                                                                                                                                                                                                                                       18-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermococcus kodakaraensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forensic
(NISC-) JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 DIVCARKAY-DLHRSYIVGETLAAHVQWARVRDGASAVYVKSDAVLWEVSIDK 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 -VPAEREDWARTHRDLIAGEILATDFEFADLADGVAI----GDGV--RVSIEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          science;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESLKAINEGTL/TVALDTTL/TEDL/LEGAIRDL/VRGVQNL/RKERGFSL/VDRICLR/VFSSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESTAALPDGAGLVVLDGTVTABLBAEGWAKDRIRELQELRKSTGLDVSDRI--RVVMS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 132; DB 6;
Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inspection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biology; immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                               I arbitrary region in the sequence, providing a vector that contains a CC sequence homologous with the selected region and a marker gene, cc transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly contemporate some in the genome of a for targeting the cc disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the cdisruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein concoded by the genome of Thermoscocus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in which interestly from WIPO at
                                                                                                                                                                        Matches
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least
                                                                                                                                                                                                                                                         Sequence 1065 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Imanaka
                                                                                                                                                                                            Local
1019 DENRELLQENLDYİMRETRAVEVRFEBAKGYVVEWPEVQAKIGIEK
                                                                                   959
                                                                                                              11 LPD-----GAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; SEQ ID NO 263; 598pp; Japanese.
                                      64 AEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGV--RVSIEK 107
                                                                                                                                                                      37;
                                                                                                                                                                                          Similarity
                                                                                   LPDFFVAEEFDGGRVFVDKTLTRELLAEGLAREFVRRIQEMRKRLDLDVNDRIVVTIETT 1018
                                                                                                                                                                        Conservative
                                                                                                                                                                                          24.4%;
                                                                                                                                                                      16;
                                                                                                                                                                      Score 131.5; DB 8
Pred. No. 3.6e-06;
6; Mismatches 44
                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                        44;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                 Length 1065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    be achieved
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21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                 03-OCT-2002
                                                                                                                                      Clostridium acetobutylicum
                                                                                                                                                                                                                                       ABU24074 standard;
                                                                            21-MAR-2002; 2002WO-US009107
                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #9601.
                                                                                                                                                                                                 19-JUN-2003
                                                                                                                                                                                                                    ABU24074;
                                                                                                                    WO200277183-A2
 (BLIT-)
 BLITRA
                                                                                                                                                                                                (first entry)
  PHARM
                                                                                                                                                                                                                                      protein; 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC polypeptide or its fragment whose expression is inhibited by the continuence of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cC proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway cC required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound is activity; (11) a culture comprising strains in which the gene compound is extent to which each of the strains is present in a culture or collection of compound is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene cc identifying proteins or screening for homologous nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational cc drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C kneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this gatent did not form part of the printed specification, but was obtained of in electronic format directly form WIPO at
                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 28
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                          Propionibacterium acnes immunogenic protein #3899
                                                                                                                                                                                            27-PEB-2002
                                                                                                                                                                                                                                                                                                                AAU43003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1035 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid comprising any one of 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio
Trawick
                                                                                                                                                                                                                                                                                                             standard; protein; 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKETLATDIIYSENKEAAIYNINGEBLNVFVKK 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRDLI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGBILATDFBFADLADGVAI---GDGVRVSIBK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 51998; 1766pp; English.
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Pred. No. 7.9e-06;
6; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R, Yamamoto R,
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1035;
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Xu HH;
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Matches
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                                                                                                                                                                                                                                                                                                                                      nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                         Sequence 1185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, gustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides. The proteins and their associated DNA sequences the treatment, prevention and diagnosis of medical conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 4198; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-616774/71.
N-PSDB; AAS59519.
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-2001; 2001WO-US012865
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                                                                                                                                                                                                                                     Local
 1158
                                                                      1098 EITPELARAGQAREVIRFVQDSRKKAGLDVSDRITLAWSASADLATAIEEHAEQISQEVL 115:
                                                                                                                                             1038 AADPEWLASELAIKGSVEMDVPEVEGGKAVVTADDVIVSERPREGWSVVNEQGETVALDL 1097
                                   83
                                                                                                                                                                                 N
                                                                                                                                                                                                                                     Similarity
 ÁVQMSREPRÁDDWÁVEPDLGLAVKVVK 1184
                                                                                                        -----AKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRDLIAGEIL 82
                                                                                                                                                                                 AADPESTAA------LPD---GAGLVVLDGTVTAELEAEGW------
                                   ATDFEFADLADGVAIGD--GVRVSIEK 107
                                                                                                                                                                                                                    Conservative
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2000US-0208841P
2000US-0216747P
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e J, Zhang
                                                                                                                                                                                                                                   23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides and nucleic acids useful diagnosing infections, especially use
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, Jen S, Carter
                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                Score 127.5; DB 4;
Pred. No. 1.3e-05;
8; Mismatches 47;
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538
1 MAADPESTAALPDG
                                                                                                                                                                                      283416 seqs, 96216763 residues
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                                           PIR_80:*
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Listing first
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•				
Result No.	Score	Query Match	Length	80	ID	Description
1	534	99.3	1041	מ	B70760	probable iles prot
N	423	78.6	1059	ผ	E87058	1-trni
w	174.5	32.4	1078	N	<b>E75407</b>	isoleucyl-tRNA syn
4	139.5	25.9	1047	N	T34946	probable isoleucyl
ű	132	٠	1091	N	B71322	isoleucine-tRNA li
6	128.5		1035	N	G97273	isoleucyl-tRNA syn
7	126.5		1066	N	F71100	- 73
8	123.5	23.0	1067	N	H75139	isoleucyl-tRNA syn
9	111	20.6	1044	N	H69049	isoleucine-tRNA li
10	110	20.4	1045	_	SYEXI	isoleucine-tRNA li
11	105	19.5	1036	N	P71565	probable isoleucin
12	104.5		986	N	B90220	isoleucine-tRNA sy
13	101.5	18.9	1064	N	T40751	isoleucyl-trna syn
14	100.5	18.7	1070	N	H84369	isoleucyl-tRNA syn
15	97.5	18.1	1036	N	F81719	isoleucyl-tRNA syn
16	96	17.8	1072	_	SYBYI4	ie-tring
17	95.5	17.8	1064	N	B72729	probable isoleucyl
18	94.5	17.6	1106	N	A97819	isoleucine-tRNA li
19	93		1042	N	H70203	isoleucine-tRNA li
20	89	16.5	1086	N	B71667	isoleucine-tRNA li
21	88	16.4	1018	N	A69329	probable isoleucin
22	86.5		1039	N	C64418	isoleucine-tRNA li
23	Ņ		659	N	D84286	3-hydroxyacyl-CoA
24	82		332	N	AH1994	hypothetical prote
25	80.5		309	Ŋ	G98311	
26	80.5	15.0	309	N	AC2971	hypothetical prote
27	79		375	N	G70966	
28	79	14.7	485	N	T01968	Ħ
29	79	14.7	1254	N	T04047	isoleucine-tRNA li

45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	3	30
72.5	72.5	72.5	73.5	73.5	74	75	75.5	76	76	76.5	76.5	76.5	76.5	77	77.5
13.5	13.5	13.5	13.7	13.7	13.8	13.9	14.0	14.1	14.1	14.2	14.2	14.2	14.2	14.3	14.4
435	301	256	396	393	368	441	449	1266	432	1199	899	662	431	8563	569
N	N	N	N	N	N	N	N	N	N	۳	N	N	N	N	N
C69194	A32498	H83002	A70581	S38875	T35150	T35788	B75451	I59314	T35263	S76549	A41234	I38400	A59474	T30226	T35476
L-asparaginase I -	Mx resistance prot	imidazoleglycerol-	hypothetical prote	methionine adenosy	probable glycosyl	probable transcrip	NADH oxidase - Dei	isoleucine-tRNA li	probable carboxype	transcription-repa	melanocyte-specifi	melanoma-associate	tRNA adenylyltrans	polyketide synthas	probable regulator

## ALIGNMENTS

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isoleucyl-tRNA synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87058
C;Accession: E87058
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler,
R,; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.;
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: E70760

C;Accession: E70760

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc, F(Coller, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Rature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Suleton, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                          A;Accession: E87058
A;Status: preliminary
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1041 <COL>
A;Residues: 1-1041 <COL>
A;Cross-references: UNIPROT:Q10765; UNIPARC:UPI00001364FA; GB:Z74020; GB:AL123456; NID:A;Experimental source: strain H37Rv
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ileS protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 534; DB 2; Length 1041; 99.1%; Pred. No. 9.2e-43;
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                                                                                                                                                        Squares, R.;
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Holroyd,
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A; Gene: DR1335
A; Map position:
C; Superfamily:
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-J
C;Accession: E75407
R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1059 <STO>
A;Cross-references: UNIPROT:Q9X7E5; UNIPARC:UPI00001364F8; GB:AL450380; NID:g13093159; C;Genetics:
A;Gene: 11eS
C;Superfamily: isoleucine-tRNA ligase
                                                                                                                                                                              probable isoleucyl-tRNA synthetase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change C;Accession: T34946
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1078 < WHI>
A; Cross-references: UNIPROT: Q9
A; Experimental source: strain
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: E75407 A;Status: preliminary
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                                  O.A
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                                                                                                                                                             A; Reference number: Z21563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoleucyl-tRNA synthetase - Deinococcus radiodurans (strain R1)
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Best Local S
Matches 86
                                                     ;Status: preliminary; translated fr
;Molecule type: DNA
;Residues: 1-1047 <SAU>
;Cross-references: UNIPROT:Q982X5;
;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Deinococcus radiodurans
Dec-1999 #sequence_revision 03-Dec-1999
                                  Genetics:
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Best Local :
Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: isoleucine-tRNA ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT: Q9RUP8; UNIPARC: UPI00000D3E29;
                  SCOEDB:SC4A10.09
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isoleucine-tRNA ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%; Score 174.5;
37.1%; Pred. No. 1.60
tive 16; Mismatches
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                                                                                                                            from
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Pred. No. 3.5e-32;
                                                                       UNIPARC: UPI00000DB2CC;
                                                                                                                            GB/EMBL/DDBJ
                                                                                                                                                                                   Parkhill, J.; Barrell,
1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                       -GEGFRAEVE 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                       EMBL: AL109663; PIDN: CAB51985
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                                                                                                                                                                                                                                        09-Jul-2004
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T.; Zalewski,
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C.; Ma
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                                                        Superfamily:
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Best Local :
   Query Match
Best Local :
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   Similarity
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Fesidues: 1-1035 <KUR>
A;Cross-references: UNIPROT:Q97ESO; UNIPARC:UPI00000CA6EC;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: TP0452
C;Superfamily: isoleucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1091 <COL>
A;Residues: 1-1091 <COL>
A;Cross-references: UNIPROT:O83466; UNIPARC:UPI0000136505; GB:AE001222; GB:AE000520;
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Praser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                                                                                                                                                                                                 A; Reference number: A96900; A; Accession: G97273
                                                                                                                                                                                                                                                                                                                    R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Marka.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1091 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A71250;
A;Accession: E71322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoleucine-tRNA ligase (EC 6.1.1.5) (ileS) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoleucyl-tRNA synthetase [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 Match 24.5%; Score 132; DB 2; Local Similarity 37.2%; Pred. No. 0.00018; neb 42; Conservative 16; Mismatches 43
                              CAC3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 -- RWTATDPATIAALTDHSGLISDEVLATDPAQGEADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 -VPAEREDWARTHRDLIAGEILATDFEFADLADGVAI----GDGV--RVSIEK 107
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isoleucine-tRNA ligase
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36.7%;
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Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                         Markarova,
Smith, D.R.
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                                                                                                                                                                                                                                                                                                                                                                                        K.S.; Zeng,
                                                                                                                     GB:AE001437; PIDN:AAK80978.1
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                                                                                                                                                                                                                                                                                                                                                                                        Q.; Gibson,
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McD.

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23.9%;

Score Pred.

128.5; DB 2; No. 0.00036;

Length 1035;

Lee

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A;Residues: 1-1066 <KAW>
A;Cross-references: UNIPROT:058792; UNIPARC:UPI00001364PE;
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for C;Genetics:
                                                                                                                                                                               A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome sa;Reference number: A75001
A;Recession: H75139
A;Status: preliminary
A;Status: preliminary
A;Mesidues: 1-1067 <KAW>
A;Residues: 1-1067 <KAW>
A;Cross-references: UNIPROT:Q5V072; UNIPARC:UPI00000344D8; GB:AJ248285; GB:AL096836; A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
H75139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, CDNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: F71100
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
F71100
                                                                                                                                                                                                                                                                                                                              C;Accession: H75139
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision
C;Accession: H75139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: PH1065
C;Superfamily: isoleucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase;
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoleucine-tRNA ligase (BC 6.1.1.5) - C;Species: Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                                                                                       isoleucyl-tRNA synthetase (iles) PAB0616 - Pyrococcus abyssi (strain Orsay)
                                                                           Query Match
Best Local
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Best Local
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                                                        Matches
                                                                                                                              Superfamily:
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                                                      Similarity
39; Conserv
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LPD-----GAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABREDWARTHRDLIAGEILATDFEFADLADGVAIGDGV--RVSIEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPDFLVAEDFEGGRVYVDKTLTRELLAEGLAREFVRRIQEMRKRLDLDVNDRIVVTIETT 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDNRELLQENLDYIMRETRAIEVRFEEAKGYVVEWPEVQAKIGIEK 1064
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                                                                     23.0%;
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; Pred. No. 0.00057;
17; Mismatches 44
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                                                                     Score 123.5;
Pred. No. 0.0
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                                             . 0.0011;
39;
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993

Similarity

20.4%; Score 110; DB 1; Length 1045; 28.1%; Pred. No. 0.021;

Pred. No. 0.02 0; Mismatches

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A;Description: EC 6.1.1.5 [validated, MUID:91244836] C;Superfamily: isoleucine-tRNA ligase C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein
                                                                                                      A;Molecule type: DNA
A;Residues: 1-1045 <JEN>
A;Cross-references: UNIPARC:UPI000016FBA0; GB:M59245;
                                                                                                                                                                                                                                                                                           C;Accession: A40398
R;Jenal, U.; Rechsteiner, T.; Tan,
J. Biol. Chem. 266, 10570-10577, 1
                                                                                                                                                                                                                                                                                                                                                                                                                          isoleucine-tRNA ligase (EC 6.1.1.5) [validated] - Methanobacterium thermoautotrophicum N;Alternate names: isoleucyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1044 <MTH>
A;Residues: 1-1044 <MTH>
A;Cross-references: UNIFROT:027428;
A;Experimental source: strain Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T., Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7155-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fur
                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                A; Reference number: A40398;
                                                                                                                                                                                                                                                                      A; Title: Isoleucyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: isoleucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                               Alternate names: isoleucyl-tRNA synthetase;Species: Methanobacterium thermoautotrophicum;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992
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28.1%; Pred. No. 0.017;
tive 21; Mismatches
                                                                                                                                                                                                                  MUID:91244836; PMID:2037598
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                                                                                                         NID:g149726; PIDN:AAA72950.1;
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A; Molecule type: DNA, A; Molecule type: DNA, A; Residues: 1-1036 (ARN) A; Residues: 1-1036 (ARN) A; Residues: 1-1036 (ARN) A; Cross-references: UNIPROT:084022; UNIPARC:UDI00001364EB; GB:AE001277; GB:AE001273; A; Experimental source: serotype D, strain UW-3/Cx C; Genetics: C; Genetics: 11es C; Superfamily: isoleucine-trna ligase C; Keywords: ligase
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F71565
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.
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A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: F71565
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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A;Residues: 1-986 <KUR>
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A;Accession: E90220
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Best Local S
Matches 27
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Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004;Accession: F71565
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                                             948 FIKSETRASNIILGEAKGDITMDWDIEGESYIIGIKKS 985
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                                                                                                                                                                                                                                          h 19.4%; Score 104.5; DB Similarity 27.6%; Pred. No. 0.065;
                                                                                                                                                                           GLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRD
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                                                                                        LIAGEILATDFEFADLADGVAI-----GDGVRVSIEKT 108
                                                                                                                                  GIVVISKEISESEEEGLIRDIIRRIQFMRKQLKLNVLDYIEISMKVPEERVKTIQKWEE
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Pred. No. 0.062;
.8; Mismatches 48
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                                                                                                                                                                                                                        Mismatches
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                                                                   RESULT 15
F81719
isoleucyl-tRNA synthetase TC0288 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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isoleucyl-trna synthetase, cytoplasmic - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T40751 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, submitted to the EMBL Data Library, March 1998 A;Reference number: Z21948 A;Accession: T40751
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A; Molecule type; DNA
A; Residues: 1-1064 < LYN>
A; Cross-references: UNIPROT:013651; UNIPARC:UPI00001364E3; EMBL:AL022072; PIDN:CAA17821
A; Cross-imental source: strain 972h-; cosmid c8D2
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T40751
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Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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A; Map position: 2
C; Superfamily: isoleucine-tRNA
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                                                                                                                                                                                                                                                                                  A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
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A; Residues: 1-1070 <STO>
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                         Matches
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                                         74 RDLIAGEILATDFEFADLADG 94
                                                                                                                                     15 AGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAER-EDWARTH
                                                                                                                                                                                         27;
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                                                                                                                                                                                                            Similarity
BPLITAETRAR - - BLGEVEDG
                                                                                        AGTVYVDTELNEDVESEGYAREVVRRVQEMRKEMDLAMDAEIRLDVLVFDERVGELVARH
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33.3%; Pred. No. 0.17;
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30.4%; Pred. No. 0.14;
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C;Accession: P81719
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Titte: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Teference number: AB1500; MUID:20150255; PMID:10684935
A;Restaus: preliminary
A;Accession: P81719
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aAA.  e)  soleucinetRNA ligase)  37; ORFNames=MTCY48.29c;  s; Actinomycetales;  sacterium;  1038/31159;  c T., Churcher C.M.,  s S., Barry C.B. III,  Chillingworth T.,  Chillingworth T.,  M.A., Rajandream M.A.,  McLean J., Moule S.,  M.A., Rajandream M.A.,  Majaures S., Squares R.,  tuberculosis from the  Marpenter L., White O.,  Man M.L., Haft D.H.,  Man M.L., Exmolaeva M.D.,  Weidman J.F., Khouri H.M.,  Jr., Venter J.C.,  tuberculosis clinical and  e + tRNA(Ile) = AMP +  (By similarity).  inoacyl-tRNA synthetase	0739al bacillus ce 06ab89 propionibac 058792 pyrococcus 04mhj2 bacillus ce 06hjf2 bacillus th 081r75 bacillus an 083i16 tyropheryma P46214 pyrococcus 083952 tropheryma 083952 tropheryma 081e30 bacillus ce 09v072 pyrococcus 073hw7 wolbachia p 08xhe4 clostridium 06afz0 leifsonia x

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MEDLINB=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
MEDLINB=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.I.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.";
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TIGRAMs; TIGR00392; iles; i.
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PROSITE; PS00178; AA_TRNA_LIGASE I; l.
PROSITE; PS00178; Na_TRNA_LIGASE I; l.
Metal-binding; Nucleotide-binding; Protein biosynthesis; 25
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"HIGH" region.
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IP; P56690; 1ILB.
GO:0005524; F:ATP binding; IEA.
GO:0004522; F:ASOleucine-tRNA ligase activity; IEA.
GO:0016874; F:ligase activity; IEA.
GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
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AAK45854.1;
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99.1%;
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22 ATP (By similarity)
117340 MW; B5023822848E08C
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..3e-39;
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RESULT 3
Q740U6 MYCPA
ID Q740U6,
AC Q740U6,
AC Q740U6,
D7 05-UUL-2
D7 05-UUL-2
D7 05-UUL-2
D8 Acteria
OC COTYNEBA
OC COTYNEBA
OC COTYNEBA
OC MYCOBACT
OC MYCOBACT
OC MYCOBACT
OC MYCOBACT
OC MYCOBACT
OC COTTAINAN
RA Li L. B
RL SUBMitte
DR HSSP; P5
DR GO; GO:0

               RESULT 4
SYI_MYCLS
ID SYI M
AC Q9X7E
AC Q9X7E
DT 30-MA
DT 30-MA
DT 13-SE
DE I801e
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R GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:0004822; F:Isoleucine-tRNA ligase activity; IEA.
R GO; GO:0004824; F:ligase activity; IEA.
R GO; GO:0016874; F:ligase activity; IEA.
R GO; GO:0016874; F:ligase activity; IEA.
R GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
R GO; GO:0006412; P:protein biosynthesis; IEA.
R InterPro; IPR002300; tRNA-synt_1.
R InterPro; IPR001112; tRNA-synt_1.
R InterPro; IPR001301; tRNA-synt_1.
R InterPro; IPR001301; tRNA-synt_1.
R FIGNTS; PR001301; tRNA-synt_1.
R PRINTS; PR001301; tRNA-SYNTHILE.
R FIGNTAMS; TIGR00392; ileS; 1.
R FIGNFAMS; TIGR00392; ileS; 1.
R FOOSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
SEQUENCE 1053 AA; 118304 MW; 0F210268429438E0 CRC64;
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                                   SYI MYCLE
Q9X7E5;
30-MAY-2000
30-MAY-2000
13-SEP-2005
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li L., Bannantine J., Zhang Q., Submitted (SEP-2003) to the EME EMBL; AE017231; ABS03563.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase; Complete proteome; Ligase. SEQUENCE 1041 AA; 117313 MW; 4513382E3248D3AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=k10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ileS; OrderedLocusNames=MAP1246;
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                 [soleucyl-tRNA synthetase
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(TrEMBLrel.
(TrEMBLrel.
(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 48, Last annotation updat
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                                                                                                                                        STANDARD;
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27,
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 454; DB
; Pred. No. 2.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q., Amonsin A., Alt D., Kapur V., EMBL/GenBank/DDBJ databases.
-; Genomic_DNA.
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Last annotation update)
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Pred. No. 1.3e-39;
1; Mismatches 0;
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                    update)
) (Isoleucine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
2.3e-32;
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Best Local S
Matches 86
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TLT 5
(M9 NOCPA OFYW9 NOCPA OFYW9; OCT 2004 25 OCT 2004 25 OCT 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leproma; ML1195; ... TRNA-synt_la.
InterPro; IPR002300; tRNA-synt_l.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_le.
Pfam; PP00133; tRNA-synt_l; 1.
PRINTS; PR00984; TRNASYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL049478; CAB39575.1; -;
EMBL; AL583921; CAC31576.1; -;
PIR; E87058; E87058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterineae; Mycobacteriaceae;
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Bacteria; Actinobacteridae;
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Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = diphosphate + L-isoleucyl-tRNA(Ile). diphosphate = L-isoleucyl-tRNA(Ile). COPACTOR: Binds I zinc ion per subunit (By similarity SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the class-I aminoacyl-tRNA syn
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                                                                                                                                                                                                                                                                                                              SVPAERADWARVHRDFIAREILATSFEFGEPADSVAIGDGVRVSLLK
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                       PRELIMINARY;
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80.4%;
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Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 423;
Pred. No. 1
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Genomic_DNA.
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1 Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

1 Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

1 C -! CATALYTIC ACTIVITY: ATP + L-isocleucine + tRNA(IIe) = AMP

2 diphosphate + L-isoleucyl-rRNA(IIe).

2 -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

2 c -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

3 c GO; GO:0005524; F:ATP binding; IRA.

4 c GO; GO:0005524; F:ATP binding; IRA.

5 c GO; GO:0005822; F:isoleucine-tRNA ligase activity; IEA.

5 c GO; GO:0016874; F:ligase activity; IEA.

5 c GO; GO:0016874; F:isoleucine-tRNA iminoacylation; IEA.

6 c GO:0046872; F:metal ion binding; IEA.

6 c GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.

7 c GO; GO:0006412; P:protein biosynthesis; IEA.

8 c GO; GO:0006412; P:protein biosynthesis; IEA.

8 c GO; GO:0006412; TRNA-synt 1a.

8 InterPro; IPR00230; tRNA-synt 1a.

8 R InterPro; IPR00230; tRNA-synt 1; 1.

8 PRINTS; PR00984; TRNASYNTHILE.

8 PRINTS; PR00984; TRNASYNTHILE.
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Best Local S
                                                                                                                                                             NUCLEALLE SEVENCE: AND 12310 / DSM 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE-22723752; PubMed-12840036; DOI=10.1101/gr.1285603
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.
                                                                                                                                                                                                                                                                                                                                    Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TERMBLrel. 23, Created)
01-MAR-2003 (TERMBLrel. 23, Last sequence update)
01-MAR-2004 (TERMBLrel. 26, Last annotation update)
Putative isoleucyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBFNVO,
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PROSITE; ES00178; AA TRNA LIGASE I; UNKNOWN 1.

ATP-binding; Aminoacyl-trNa synthetase; Complete proteome; Metal-binding; Nucleotide-binding; Protein biosynthesis; Z:

SEQUENCE 1042 AA; 116567 MW; AOBEB64BBD448E4E CRC64;
                    efficiens.";
Genome Res. 13:1572-1579(2003).
                                                                                                                                        Sugimoto S., Matsui
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=CE2043
                                                                                   replacements
                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiba T., Hattori M.;
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Ishikawa J., Yamashita A., Mikami Y., Hoshino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-IFM
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Corynebacterineae; Nocardi
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                                                                                                           Comparative
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  BA000035; BAC18853.1;
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                                                                                   complete genome sequence analysis of the amino acid responsible for the thermostability of Corynebacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Pred. No. 3.5
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); Mismatches
Genomic_DNA
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                                                                                      Corynebacterium
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                                                                                                                                                                                                  Query Match
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Matches 56
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Best Local S
Matches 60
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GO; GO:0004822; F:isoleucine-ENNA ligase activity; IEA.
GO; GO:0006428; P:isoleucine-ENNA ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt 1a.
InterPro; IPR002310; tRNA-synt 1.
InterPro; IPR002301; tRNA-synt ile.
Pfam; PF00133; tRNA-synt ile.
Pfam; PF00133; tRNA-synt il.
PRINTS; PR00984; TRNASYNTHILE.
TIGRFAMS; TIGR0392; ileS; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; UNKNOWN 1.
Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 1103 AA; 123718 MW; B9129E29B1572DEE CRC64;
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SEQUENCE
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TEMBLrel. 31, Last annotation update)
11-SEP-2005 (TEMBLR)
11-SEP-2005 (TREMBLR)
13-SEP-2005 (TREMBLR)
13-SEP-20
                                                                                                                                                                                                                                                                                                                                                Linke B., Tauch A.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR931997; CAI36922.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium jeikeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen Corynebacterium jeikeium K411, a Lipid-Requiring Bacterium of the Human Skin Flora.";
J. Bacteriol. 187:4671-4682 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005; Tauch A., Kaiser O., Hain T., Goesmann A., Weisshaar B., Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoever P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q4JW85_CORJK PRELIMINARY;
Q4JW85;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K411;
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SVPAEKEEWARTHADSIAKEVLATDVKVVVGEQLSHDVAD
                            SVPABREDWARTHRDLIAGEILATDFEFA------DLAD
                                                                                                 VAABPEHTAEVSGQDGLVVLDTQTTPELEAEGWAADRVRGLQEARKAADLQISDRIHLTL
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54.5%;
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Pred. No. 2.4e
L7; Mismatches
                                                                                                                                                                                                                            Score 270.5;
Pred. No. 1e
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GO; GO:0005524; F:ATP binding; IRA.

GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.

GO; GO:0004824; F:isgase activity; IEA.

GO; GO:0016874; F:ligase activity; IEA.

R GO; GO:0016874; F:ligase activity; IEA.

R GO; GO:0016428; P:isoleucyl-tRNA aminoacylation; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R GO; GO:0006412; F:protein biosynthesis; IEA.

R InterPro; IPR002300; tRNA-synt_1a.

R InterPro; IPR002301; tRNA-synt_1i.

R InterPro; IPR002301; tRNA-synt_1i.

R Pfam; PF00133; tRNA-synt_1; 1.

R Pfam; PF00133; tRNA-synt_1i.

R PFINTS; PR00984; TRNASYNTHILE.
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Best Local (
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Q6NGD7_C
Q6NGD7;
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"The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129.";
Nucleic Acids Res. 31:5516-6523(2003).
EMBL; BX248358; CAE50114.1; -; Genomic_DNA.
                                                                                                                                                                 Name=ileS; OrderedLocusNames=Cgl2148, cg2359;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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05-JUL-2004 (TREMBLrel. 27, Last sequence update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
Isoleucyl-tRNA synthetase (BC 6.1.1.5).
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PROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.
Aminoacy1-tRNA synthetase; Complete proteome; Ligase.
SEQUENCE 1052 AA; 118486 MW; 0E045969A137FBCD CRC64;
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                                                NCBI_TaxID=1718;
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MEDLINE=22965443; PubMed=14602910;
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                                                                                                                          Corynebacterineae;
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Pred. No. 2.2e-15;
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A., Dover L.G., Holden M
                                                                                                                                   Corynebacterium
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RESULT Q4H737 ID Q4H737 ID Q4H737 ID Q4H737 ID Q4H 
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GO; GO:0004522; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016878; P:isoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_1ie.
R InterPro; IPR00130; tRNA-synt_1ie.
R InterPro; IPR002301; tRNA-synt_1ie.
R Pfam; PF00133; tRNA-synt_1; 1.
R Pfam; PF00133; tRNA-synt_1; 1.
R PRINTS; PR000944; TRNASYNTHILE.
R RINTS; PR00044; TRNASYNTHILE.
R TICRFAMS; TIGR00392; ileS; 1.
R PROSITE; PS00178; AA, TRNA_LIGASE I; UNKNOWN_1.
R PNOWN 1.
R PROSITE; PS00178; AA, TRNA_LIGASE I; UNKNOWN_1.
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Best Local S
Matches 59
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Nakagawa S.;
"Complete genomic seq
Submitted (MAY-2002)
                                                                                                                                                         "Sequencing DSM 11300.";
                                                                                                                                                                                     STRAIN-SSM 11300;
STRAIN-SSM 11300;
US DOB Joint Genome Institute (JGI-PGP);
COpeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
Hammon N., Israni S., Pitluck S., Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINATCC 13032 / DSM 20300 / NCTB 10025;
STRAINATCC 13032 / DSM 20300 / NCTB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Ralinowski J., Bathe B., Barrels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Rikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
McHardy A.C., Meyer F., Moeckel B., Sahm H., Wendisch V.F., Wiegraebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Creat
13-SEP-2005 (TrEMBLrel. 31, Last
13-SEP-2005 (TrEMBLrel. 31, Last
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J. Biotechnol. 104:5-25(2003).
EMBL; BA000036; BAB99541.1; -;
                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=DSM 11300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aminoacyl-tRNA synthetase, class ORFNames=DgeoDRAFT_0209;
       STRAIN=DSM
                                               NUCLEOTIDE
                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=319795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus geothermalis DSM 11300.
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                                                                                                                      (MAY-2005)
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CAF20488.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus.
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C3333C86C8554B1F CRC64;
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                                                                                                                                                                                                                                    Detter P.;
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                                                                                                                                                                                                                                                                             To the human gastrointestinal tract. ";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

R EMBL; AE014295; AAN25560.1; -; Genomic_DNA.

R HSSP; P56690; IILE.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004622; F:isoleucine-tRNA ligase activity; IE,

GO; GO:0006428; P:isoleucine-tRNA minoacylation; IEA.

R GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.

R InterPro; IPR002300; tRNA-synt la.

R InterPro; IPR002301; tRNA-synt li.

R InterPro; IPR002301; tRNA-synt_li.

R FARM; PF00133; tRNA-synt l; 1.

R Pfam; PF00133; tRNA-synt l; 1.

R PFAM; PR00984; TRNASYNTHILE.

R TIGRPAMs; TIGR00392; 1165; 1.

R PROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.

R RROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.

R RROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.

R RROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.

R PROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.

R SEQUENCE 1103 AA; 124065 MW; B09FBEA401C18C28 CRC
                                                                                                                                                                                       Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GE
STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8G312
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Larimer F., Land M.;
"Annotation of the draft genome assembly
DSM 11300.";
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EMBL; AAHE01000010; E
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                                                                                                                                                                                         Score 185; μο -
No. 5.7e-08;
                                                                                                                                                                                    Pred. No. 5.70
7; Mismatches
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1es 39;
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RESULT 12
Q9RUPB DEIRA
ID Q9RUPB
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AC Q0C
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                                                                     QSTN62;
01-JUN-2002 (TrEMBLrel. 21, Last sequence u
01-JUN-2002 (TrEMBLrel. 26, Last annotation
01-MAR-2004 (TrEMBLrel. 26, Last annotation
18oleucyl-tRNA synthetase.
Name=ileS; OrderediocusNames=MA2431;
Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcina.
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NUCLEOTIDE SEQUENCE.

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;

White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,

Vamathevan J.J., Lam P., McDonald L.A., Winton K.W., Fleischmann R.D.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Karchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
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62 METAC
QBTN62_M
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TIGR; DR1335; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.

GO; GO:0004822; F:isoleucyl-tRNA aminoacylation; IEA.

InterPro; IPR002300; tRNA-synt la.

InterPro; IPR002300; tRNA-synt lie.

Pfam; PF00133; tRNA-synt l; 1.

PFINTS; PR00984; TRNA-SYNTHILE.
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TIGRO0392; 11eS; 1.
AMINOACY1-tRNA SYNTHETABS; Complete proteome.
SECUENCE 1078 AA; 120272 MW; DF007ED70528F70F CRC64;
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01-MAR-2004 (TrEMBLrel.
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  NUCLEOTIDE SEQUENCE
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Pred. No. 4.
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RESULT 14
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A Galagan J.B., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A Allen N., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

A Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Zimmer A., Barber R.D., Cann I., Graham D.B., Grahame D.A., Guss A.M.,

A Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

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and physiological diversity.";

Renower R. 12:52-542(2002).
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01-OCT-2000
01-MAR-2004
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SEQUENCE
                                                                                                                            MEDLINE-20225863; PubMed=10762266; DOI=10.1128/JB.182.9.2611-2618.2000; Boccazzi F., Zhang J.K., Metcalf W.W.; "Generation of dominant selectable markers for pseudomonic acid by cloning and mutagenesis of archaeon Methanosarcina barkeri fusaro."; J. Bacteriol. 182:2611-2618 (2000).

EMBL; AP208389; AAP65673.1; -; Genomic_DNA.
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HSSP; P56690; III.E.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
                        HSSP; P56690; 1ILE.
GO; GO:0005524; F:A
GO; GO:0004822; F:i
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PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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PRINTS; PR00984; TRNASYNTHILE.
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InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002301; tRNA-synt_Ile.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKVLALVETLKOLIAEEVRADVFD-----LGSSIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERE-DWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGTASAESDAGLVYVDANLTPELEAEGYAREVIRRLQDMRKELDLVVDENIRVSVRIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESTAALPDGAGLVVLDGTVTABLEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPA
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) (TrEMBLrel. 15,
4 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                            F:isoleucine-tRNA
                                                                F:ATP binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanomicrobia; Methanosarcinales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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Last annotation update)
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FRNA ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ.
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                                activity;
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Best Local S
Matches 41
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                 R HSSP; P56690; IIIE.

R GO; GO:0005524; F:MTP binding; IEA.

GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.

R GO; GO:0004824; F:ligase activity; IEA.

R GO; GO:0016874; F:ligase activity; IEA.

R GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R InterPro; IPR002300; tRNA-synt 1a.

R InterPro; IPR002301; tRNA-synt 1.

R InterPro; IPR002301; tRNA-synt 1.

R Pfam; PF00133; tRNA-synt 1; 1.

R Pfam; PF00133; tRNA-synt 1; 1.

R PFANYIS; PR00364; TRNASYNTHILE.
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GO; GO:0006428; P:isoleucyl-trnA aminoacylation; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR002300; trNA-synt la.
InterPro; IPR002311; trNA-synt lie.
InterPro; IPR002301; trNA-synt lie.
InterPro; IPR002301; trNA-synt l.
InterPro; IPR002301; trNA-SYNTHILE.
INTERPAMS; TIGR00392; ILES; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.

STRAIN=GOel / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=GOel / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE=22120827; PubMed=12125824;

METLINE=22120827; PubMed=12125824;

MARTHIREZ-ARIAS R., Henne A., Wiezer A., Bacumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsall

Fritz H.-J., Gottschalk G.,
                                                                                                                                      Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fritz H.-J., Gottschalk G.;
"The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
EMBL; AB013550; AAM32663.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=MM2967;
Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8PSV9 METMA PRELIMINARY;
                                                                                                                                                                                                TIGREAMS; TIGR00392; iles; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isoleucyl-tRNA synthetase (EC 6.1.1.5).
                                Local Similarity
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                                                                                                                                      1058 AA;
   Conservative
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                                                                                                                                         120410 MW; 8BA5C0DE0FDCE4F3 CRC64;
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29.0%; Score 156; DB
40.6%; Pred. No. 2.3e
tive 15; Mismatches
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; Pred. No. 1.4e
20; Mismatches
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                                DB 2;
2.3e-05;
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                                                             Length 1058;
   Indels
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Gunsalus R.P.,
10;
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Search completed: 1 Job time : 41.8484 April 14, 14 secs 2006, 17:32:32 문

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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          92
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seq length: 2000000000
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1: /cgm2_6/ptodata/1.

2: /cgm2_6/ptodata/1.

3: /cgm2_6/ptodata/1.

4: /cgm2_6/ptodata/1.

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Copyright (c) 1993 - 2006
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/cgn2_6/ptodata/1/iaa/RCOMB.pep:*
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atch cal s 108 1 1 61	7 <u>0</u> 0.000		74.5 74.5 73.5 73.5 71.5 71.5 70.5 70.5 68.6 69.5
Similarity 8; Conser MAADPESTA MAADPESTA MAADPESTA SVPAEREDW SVPAEREDW	39-4 4, Application to determine the control of the		13.6 13.6 13.7 13.7 13.7 13.7 14.1 15.7 17.8 17.8 17.8 17.8 17.8 17.8 17.8 17
100.0%; Similarity 100.0%; P ; Conservative 0; mandpestantpdggtvvldg	on US Pete Rikke , Tho , Tho S Alter DS, I KATI BALLE DERLY OL-20 NUCLE DERLY NUMBE 1998 NUMBE 1998 1997 1997 1997 1997 1998 1998 1998		1266 327 327 3327 3448 4488 4488 4488 4488 4481 608 608 608 609 608 608 608 608 608 608 608 608 608 608
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CORE 538; DB 2; red. No. 6.1e-59; Mismatches 0; TVTAELEAEGWAKDRIRE TVTAELEAEGWAKDRIRE TVTAELEAEGWAKDRIRE ATDFEFADLADGVAIGDG	RAGMENTS AND .TUBERCULOSIS	ALIGNMENTS	US-09-357-251-32 US-08-463-092B-9 US-08-460-907B-9 US-09-4363-231 US-09-912-363-231 US-09-925-991A-23527 US-09-878-766A-22 US-10-450-369-22 US-09-949-016-8029 US-09-925-991A-26210 US-09-65-703B-2522 US-09-65-703B-2522 US-09-925-991A-19002 US-09-107-532A-5673 US-09-925-991A-24495 US-09-036-987A-6
Length 108;  Indels 0; Gaps 0;  LQELRKSTGLDVSDRIRVVM 60	POLYPEPTIDE FRAGMENTS		Sequence 32, Appli Sequence 9, Appli Sequence 231, App Sequence 231, App Sequence 16722, A Sequence 23527, A Sequence 22, Appl Sequence 22, Appl Sequence 26210, A Sequence 2522, Ap Sequence 19002, A Sequence 24495, A Sequence 24495, A Sequence 6, Appli

US-08-452-083-2 US-08-452-083-2 ; Sequence 2, Application US/08452083 ; Patent No. 5756327

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US-08-898-978-2
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Best Local Similarity 98.0
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application Patent No. 6001602
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/452,083
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,765
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194-08B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-trna
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSI-
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reymolds, P.C.
STREET: Tyo Militia Drive
                 ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                         APPLICANT: Reichard, Raymond W.
APPLICANT: Brown, James R.
APPLICANT: Lawlor, Elizabeth J.
TITLE OF INVENTION: No. 6001602el ileS
NUMBER OF SEQUENCES: 2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,083
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STREET: Lexington
CITY: Lexington
TMATE: Massachusetts
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LENGTH: 1045 amino acids
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                                                                                                                  STREET: 997 Lenox DI CITY: Lawrenceville
COMPUTER:
                                                                               COUNTRY:
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IBM Compatible
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                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Chlamydia trachomatis US-09-372-858-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reichard, Raymond
APPLICANT: Brown, James
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: NOVEL ileS
FILE REFERENCE: GM10051-D1
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/372,858
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 08/898,978
PRIOR FILING DATE: 1997-07-23
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LENGTH: 1041 amino acids
TYPE: amino acid
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                         y Match 19.5%; Score 105; DB 2; Length 1041;
Local Similarity 28.3%; Pred. No. 0.00074;
hes 26; Conservative 18; Mismatches 48; Indels
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                                                                                    931 ASAEGFVARSSASFVAVLDCQLTEPLIMEGIARELVNKINTMRRNRKLHVSDRIAIRLHA 990
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991 PVIVQEAFALHKEYICEETLTTSVSVIDYKEG 1022
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                       PABREDWARTHRDLIAGEILATDFEFADLADG 94
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                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,026
FILING DATE:
FILING DATE:
                                                                                    APPLICANT: Houman, Fariba
TITLE OF INVENTION: Candida Isoleucyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Strains
TITLE OF INVENTION: Comprising Same
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Houman, Fariba
TITLE OF INVENTION: Candio
TITLE OF INVENTION: Compr.
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
STREET: 1 -- STREET: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Mil:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                985 LIILDVNLHPELESEGLARELINRIQRLRKKAGLNTTDDVQVQYRVVKDTIDLPKVIKD 1043
                                                                                                                                                                                                                                                                                                                                                                                                            17 LVVLDGTVTABLBABGWAKDRIRBLQBLRKSTGLDVSDRIRVVMSVPABRBDWARTHRD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                           5885815
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                                                                                                                                                                                                                                                                                      Application US/08742026
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Kaufmann, Christoph
Gallant, Paul L.
Kranz, Janice E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 99; DB 1; 35.6%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida Isoleucyl-tRNA Synthetase Proteins, Nucleic Acids and Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comprising Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
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                                                                                                                                                                                                                              ; ORGANISM: Saccharomyces cerevisiae US-09-357-251-31
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                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                     SEQ ID NO 31
LENGTH: 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09357251
Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.4%; Score 99; DB 1; Length 1088; Best Local Similarity 35.6%; Pred. No. 0.0044; Matches 21; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                          Query Match
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EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Falco, S. Carl
APPLICANT: Fancod, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,026
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                     TYPE: PRT
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LENGTH: 1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVId E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
1031 FDMLS-KTCRSDIAKYDGSKTDPIGD 1055
                                                                        971 LIIMDTNIYSELKSEGLARELVNRIQKLRKKCGLEATDDVLVEYELVKDTIDFEAIVKEH 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                  74 RDLIAGEILATDFEFADLADGVAIGD
                                                                                                                                                                  Similarity
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617-861-9540
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                                                                                                                                                    Conservative
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                                                                                                                                                17.8%; Score 96; DB 2; Length 1072; 26.7%; Pred. No. 0.01; tive 25; Mismatches 34; Indels
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RESULT 8 US-09-902-540-14264

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FILE REFERENCE: PATHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR PILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3245

ENGITH: 209
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; Sequence 43, Application US/08415593
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US-09-583-110-3245
                          RESULT 10
US-08-415-593-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/99/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14264
LENGTH: 1232
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT: Lynn Do
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Best Local Similarity 34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                               --DGEKTGNYILAGEIFTTNEKGISQISYADYAIGL 190
                                                                                                                                                                                                                               GAGSLYIDETKTTRLLDTSDFPEEFKSLAKDQADELDLLRTKNNLNWTFVSPAVDFIP--
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                          14.5%; Score 78; DB 2; Length 209; 30.2%; Pred. No. 0.17; tive 13; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
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Matches
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Patent No. 5912140 5776726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                          GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS A
TITLE OF INVENTION: THEIR USE IN DIAGNO
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-862-9540
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recombinant Pneumoycstis Aminoacyl tRNA
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Ass
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                      NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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TOPOLOGY:
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CLASSIFICATION:
                     STATE: NEW YORK
                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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   amino acid

OGY: linear
                                      NEW YORK
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   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tao, Niajun
Politis-Virk, Karen I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 78; DB 1; Length 978; llarity 32.9%; Pred. No. 1.5; Conservative 12; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435
                                                                                                           THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
126
                                                                                                                                                                  MELANOMA ANTIGENS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/415,593
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121, Application US/08417174 Patent No. 5844075
                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
PILING DATE: 22-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
PILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
PILING DATE: 22-APR-1994
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION UNMER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 14.2%; Score 76.5; Di
Local Similarity 25.2%; Pred. No. 1.3;
nes 30; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: Unku
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 PEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSL 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIREL------QELRKST 48
                                                                                                                                                                                                                                                                                                                                                    T: 345 PARK AVENUE
NEW YORK
                                                                                                                                                                                                                                                                                                                                 NEW YORK
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; MOLECULE TYPE:
US-08-231-565A-27
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US-08-231-565A-27
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Patent No. 5874560
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                                                                                                                                              REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 202(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 661
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              SOFTWARD: CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/231,565A
                                                                                                      SEQUENCE CHARACTERISTICS:
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ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: N
COUNTRY:
                                        TYPE: amino of STRANDEDNESS:
                               TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                   LENGTH:
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                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                         ASCII
                                                   Unknown
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US-09-007-961-27
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Best Local S
Matches 30
                                                                                                                                                                                 Query Match
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                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-41

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KAWAKAMI,
APPLICANT: STEVEN A.
                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCLI
CURRENT APPLICATION DATA:
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ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                        MOLECULE TYPE: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/007,961 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                        STRANDEDNESS: Unkown
                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                               Local
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455
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                                49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
                                                                                                       5 PESTAALPDGAGLVVLDGTVTABLEAEGWAKDRIREL------QBLRKST 48
                                                                                                                                            30;
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                                                                                                                                                           h 14.2%; Score 76.5; DB 1; Length 661; Similarity 25.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                            G--LDVSDRIRVV-MSVPAE----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
GPLLDGTATLKLVKRQVPLDCVLYRYGSFSVTLDIVQG-----IESABILQAVPSGEG
                                                                       PEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSL 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAWAKAMI, YUTAKA; ROSENBERG,
                                                                                                                                                                                                                                                                         Unknown
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25.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                    27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               2026-4124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                              44;
                                                                                                                                                Indels
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US-09-267-439-27
Search completed: April 14, 2006, 17:38:00 Job time : 10.9865 secs
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Unkr
TOPOLOGY: Unknown
MOLECULE TYPE: Prot
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APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 37,341
REFERENCE/DOCKST NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MELANOMA ANTIGENS AND THERAPEUTIC TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
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                                                                                                                                                                                                                                   Local
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STATE: NEW YORK
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
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US-10-620-246-4
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Query Match Best Local Similarity 100.0%; Score 538; DB 3; Length 108; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM	RESULT 1  US-09-791-171-4  US-09-791-171-4  US-09-791-171-4  ISEQUENCE 4, Application US/09791171  Patent No. US20020094336A1  GENERAL INFORMATION: APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: COTTINGER, Thomas APPLICANT: RASMUSSEN, Peter Birk APPLICANT: ROSENKANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WICHEIC ACIDS FRAGMENTS AND POLYPEPTIDE TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS FILE REFERENCE: 670001-2002.1  CURRENT APPLICATION NUMBER: US/09/791,171  CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 0376/97 PRIOR APPLICATION NUMBER: 0376/97 PRIOR PILING DATE: 1997-04-02 PRIOR APPLICATION NUMBER: 60/044,624 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1997-04-10 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOPTWARE: PATENTION SEC ID NOS: 173 SOPTWARE: PATENTION SEC ID NOS: 173 SOPTWARE: PATENTION MUMBER: 60/070,488 TYPE: PRT ORGANISM: Mycobacterium tuberculosis US-09-791-171-4	ALIGNMENTS	28 78.5 14.6 329 4 US-10-282-122A-62051 29 78.5 14.6 1077 4 US-10-128-714-3179 30 78.5 14.6 1077 4 US-10-128-714-8179 31 76.5 14.2 375 4 US-10-287-971-46 32 76.5 14.2 575 4 US-10-287-971-46 33 76.5 14.2 660 4 US-10-287-971-46 36 76.5 14.2 660 4 US-10-245-871-385 36 76.5 14.2 660 4 US-10-245-80A-2 37 76.5 14.2 661 3 US-09-862-260A-2 38 76.5 14.2 661 3 US-09-812-238B-2 39 76.5 14.2 661 3 US-09-812-238B-2 39 76.5 14.2 661 3 US-09-898-860-27 39 76.5 14.2 661 3 US-09-898-860-27 40 76.5 14.2 661 4 US-10-207-655-77 41 76.5 14.2 661 4 US-10-117-937-70 42 76.5 14.2 661 4 US-10-168-417A-2 43 76.5 14.2 661 4 US-10-168-417A-2 45 76.5 14.2 661 4 US-10-685-977-27
pth 108;  lels 0; Gaps 0;  RKSTGLDVSDRIRVVM 60  RKSTGLDVSDRIRVVM 60  IEKT 108  IEKT 108	IDE FRAGMENTS		Sequence 62051, A Sequence 3179, Ap Sequence 8179, Ap Sequence 12584, A Sequence 12584, A Sequence 385, App Sequence 385, App Sequence 27, Appli Sequence 27, Appli Sequence 121, App Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 78, Appli Sequence 79, Appli Sequence 70, Appli Sequence 27, Appli

RESULT 2 US-09-804-980-4

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                                               NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10620246 Publication No. US20040115211A1
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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PLORIO, WAITER
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
FRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
                                                                                                                       PRIOR APPLICATION NUMBER: 1281/98 PRIOR FILING DATE: 1998-10-08
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ORGANISM: Mycobacterium tuberculosis
                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 1277/97
FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/044,624
                                                                                                                                                                  FILING DATE: 1999-01-21
                                                                                                                                                                                 APPLICATION NUMBER: 60/116,673
                                                                                                                                                                                                                            APPLICATION NUMBER: 09/415,884
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/791,171
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 10/138,473
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/070,488 FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-04-18
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RASMUSSEN, Peter Birk
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WELDINGH, Karin
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100.0%; Py
vative 0;
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Pred. No. 6.5e-53;
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US-10-282-122A-62617
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PRIOR FILING DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62617
                                                                            Matches
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Best Local Similarity
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                             TYPE: PRT
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
934 VAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKORIRELQELRKSTGLDVSDRIRVVM 993
                                                                              107;
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                    1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
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: Zamudio, Carlos
: Malone, Cheryl
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Forsyth, R.
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Trawick, John
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, Grant
~ Robert
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io, Carlos
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                                                                          Score 534; DB 4; Length 1041;
Pred. No. 3.5e-51;
1; Mismatches 0; Indels
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RESULT 6
US-10-282-122A-61984

; Sequence 61984, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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SEQ ID NO 64571
LENGTH: 1041
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/230,347
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PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/233,625
PRIOR PELICATION NUMBER: 60/253,625
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Best Local Similarity
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Publication No. US20040029129A1
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APPLICANT: Zamudi
APPLICANT: Malone
APPLICANT: Haselt
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                                                                                                                                                                                   994
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Malone, Cheryl
Haselbeck, Robert
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Trawick, John
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Zyskind, Judith
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dio, Carlos
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US-10-282-122A-63826

Sequence 63826, Application US/10282122A Publication No. US20040029129A1

GENERAL

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robe
APPLICANT: Ohlsen, Kari

Liangsu io, Carlos

APPLICANT:

Ohlsen, Kari Zyskind, Judith

Daniel

Haselbeck, Robert

APPLICANT

APPLICANT: APPLICANT:

Yamamoto, Robert Trawick, John Wall,

Carr, Grant

RESULT 7

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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61984
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APPLICANT:
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                        LENGTH: 10
TYPE: PRT
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FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium avium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                ocal Similarity
1014 SVPAGRAEWAHTHRDLIAGEILATRFEFGEPADPVAIGDGVRVSISK 1060
                                                                                      954 VAADPEFTAALPNGAGLVVLDGTVTPELEAEGWAKDRIRELQELRKSTGLDVSDRISVVM
                        61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK 107
                                                                                                                                                                         92;
                                                                                                        1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM 60
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Zamudio, Carlos
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Yamamoto, Robert
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Malone, Cheryl
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                                                                                                                                                                         Conservative
                                                                                                                                                                                            83.5%;
                                                                                                                                                                       Score 449; DB 4;
Pred. No. 1.5e-41;
4; Mismatches 11
                                                                                                                                                                                                                     DB 4; Length 1061;
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                 Sequence 54011, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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SEQ ID NO 63826
LENGTH: 1059
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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APPLICANT: Xu, H.
FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-02-16
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER: DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN Ver. 3.0
SEQ ID NO 5852
LENGTH: 1054
                                                              ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-5852
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SEQ ID NO 54011
LENGTH: 1052
TYPE: PRT
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                      Query Match
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR PPLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 49.5%; Score 266.5; DB 4; 1 Similarity 49.6%; Pred. No. 7.5e-21; 57; Conservative 18; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGD------GVRVSIEK 107
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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49.5%;
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Score 266.5; DB 3; Pred. No. 7.5e-21;
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                        Length 1054;
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Best Local Similarity

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US-10-156-761-13657; Sequence 13657, Application US/10156761; Publication No. US20030119018A1
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US-10-494-541-76
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                                                                        APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REPERICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-5-30
PRIOR FILING DATE: 2001-5-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SAKAKI, YOSHIYU
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Best Local Similarity
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SEQ ID NO 76
LENGTH: 1063
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILLNG DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13657
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PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 10154180
PRIOR FILING DATE: 2001-11-05
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APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: Genes coding for proteins for genetic stability,
TITLE OF INVENTION: gene expression and folding
FILE REFERENCE: BGI-166US
CURRENT APPLICATION NUMBER: US/10/494,541
CURRENT FILING DATE: 2004-05-03
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APPLICANT: Pompejus, Mai
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Schroder, Hartwig
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Pred. No. 7.6e-21;
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                                                                                                                      ; ORGANISM: Treponema pallidum US-10-282-122A-76512
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US-10-282-122A-76512
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                                                                            Query Match
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                                                           Best Local Similarity
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Best Local Similarity
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APPLICANT:
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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PRIOR
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                                        42; Conservative
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  6 ESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRI--RVVMS--
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Zyskind, Judith
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; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-13657
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                                                                                                                                                                                                                 Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-05-26
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FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/253,625
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                         24.5%; Score 132; DB 4; 37.2%; Pred. No. 1.4e-05;
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t; Pred. No. 2.3e-07;
11; Mismatches 31;
  16; Mismatches
                                                                                                                                                                                                                                                                       See File Wrapper or PALM.
  43; Indels
                                             Length 1091;
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RESULT 14
US-10-503-135-125
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; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51998
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US-10-282-122A-51998
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 51998
LENGTH: 1035
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Best Local (
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
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Trawick, John
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GENERAL INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

IITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

PILE REPERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOPTWARE: PatentIn version 3.1

SEQ ID NO 7198

LENGTH: 1088

TYPE: PRT

ORGANISM: Candida albicans

US-10-032-585-7198
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Search completed: April 14, Job time: 38.999 secs
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APPLICANT: GENIZI GIULIANO

APPLICANT: GENIZI GIULIANO

APPLICANT: GENIZI GIULIANO

APPLICANT: GENIZI GIULIANO

TITLE OP INVENTION: CYTOTOXIC T-CELL EPITOPES FROM CHLAMYDIA

TILLE REFERENCE: 002441.00089

CURRENT APPLICATION NUMBER: US/10/503,135

CURRENT PILING DATE: 2004-08-11

PRIOR APPLICATION NUMBER: PCT/IB03/01161

PRIOR APPLICATION NUMBER: GB-0203403.1

PRIOR FILING DATE: 2002-03-13

PRIOR FILING DATE: 2002-03-13
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LENGTH: 1036
TYPE: PRT
ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7198, Application US/10032585 Publication No. US20030180953A1
                                                                                                                                                                                                                      Query Match 18.2%; Score 98; DB 4; Length 1088 Best Local Similarity 35.6%; Pred. No. 0.099; Matches 21; Conservative 14; Mismatches 24; Indels
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Publication No. US20050152926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 181
SOFTWARE: SegWin99, version 1.02
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                                                                                                            985 LIILDVNLHPELESEGLARELINRIQRLRKKAGLNTTDDVQVQYRVVKDTIDLPKIIKD 1043
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                                                                                                                                                               17 LVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRD 75
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Perfect score:
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1: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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1 MAADPESTAALPDG
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991.565 Million cell updates/sec
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WS-10-506-454-899

US-11-033-039-385

WS-11-1155-288-13

WS-11-119-502-1

US-11-188-298-6318

US-11-188-298-8318

US-11-055-822-564

US-11-055-822-566

US-11-087-084-2

US-11-087-084-2

US-11-188-298-19411

US-11-188-298-19411

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US-11-188-298-19411

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US-11-188-298-10866

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US-11-165-211-37

US-11-165-221-37

US-11-165-221-37

US-11-188-298-10148
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Biocceleration
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           Sequence 5703, Ap

Sequence 899, App

Sequence 385, App

Sequence 13, Appli

Sequence 9, Appli

Sequence 960, Ap

Sequence 564, App

Sequence 564, App

Sequence 2, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 1941, Ap

Sequence 1725, Ap

Sequence 1725, Ap

Sequence 1725, Ap

Sequence 22, Appli

Sequence 22, Appli

Sequence 23, Appli

Sequence 24, Appli

Sequence 37, Appli

Sequence 37, Appli

Sequence 47, Appli
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 Sequence
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US-10-506-454-899
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Query Match Best Local s Matches

ch 25.0%; Score 134.5; DB 7; I Similarity 28.7%; Pred. No. 7.6e-06; 27; Conservative 24; Mismatches 38;

Indels Length 1149;

5

Gaps

Sequence 899, Application US/10506454

Publication No. US20060068386A1

GEMERAL INFORMATION:

APPLICANT: Slesarev, Alexi I

APPLICANT: Mezhevaya, Katja V

APPLICANT: Polushin, Nikolai N

APPLICANT: Shcherbinina, Olga V

APPLICANT: Shcherbinina, Olga V

APPLICANT: Shcherbinina, Olga V

APPLICANT: Shchova, Vera V

APPLICANT: Kozyavkin, Sergei A

TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophil.

6 US-10-6 US-11-6 US-11-7 US-1	RESULT 1  US-11-079-463-5703  Sequence 5703, Application US/11079463  Publication No. US20060073161A1  GENERAL IMPORMATION:  APPLICANT: GATY L. Breton  TITLE OF INVENTION: NUCLEIC ACID AND AMIN  TITLE OF INVENTION: FOR DIAGNOSTICS AND  FILE REFERENCE: PATH00-03DIV2  CURRENT APPLICATION NUMBER: US/11/079,463  CURRENT FILING DATE: 2005-03-14  PRIOR APPLICATION NUMBER: US 60/128,705  PRIOR FILING DATE: 1999-04-09  PRIOR FILING DATE: 2000-04-04  NUMBER OF SEQ ID NOS: 10444  SEQ ID NO 5703  LENGTH: 1149  TYPE: PRT  ORGANISM: B.fragilis  US-11-079-463-5703		26 64.5 12.0 484 27 64.5 12.0 567 28 64.5 12.0 582 29 64 11.9 376 31 64 11.9 376 31 64 11.9 376 32 64 11.9 485 33 64 11.9 485 33 63.5 11.8 129 36 63.5 11.8 239 37 63.5 11.8 239 37 63.5 11.8 506 40 63.5 11.8 506 40 63.5 11.8 506 41 63.5 11.8 506 42 63.5 11.8 506 43 63.5 11.8 506 44 63.5 11.8 506 45 63.5 11.8 506 46 63.5 11.8 506 47 63.5 11.8 506 48 63.5 11.8 506 49 63.5 11.8 506 40 63.5 11.8 506 41 63.5 11.8 506 42 63.5 11.8 506
	5/11079463 LA1  ACID AND AM ACID STICS AN 2 US/11/079,4 33-14 33-14 360/128,705 99 99/540,209	ALIGNMENTS	
	AMINO ACID SEQUENCES RELATING AND THERAPEUTICS 0,463 09		Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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FILE REFERENCE: FID001

CURRENT APPLICATION NUMBER: US/10/506,454

CURRENT FILING DATE: 2004-08-31

PRIOR APPLICATION NUMBER: PCT/US03/06664

PRIOR APPLICATION NUMBER: 60/361,742

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 1722

SOFTWARE: Patentin version 3.2

SEQ ID NO 899

LENGTH: 1080
                                            RESULT 4
US-11-155-288-13
; Sequence 13, Application US/11155288
; Publication No. US20060008468A1
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; ORGANISM: Homo sapiens
US-11-033-039-385
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NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 385
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                                   GENERAL INFORMATION:
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Best Local
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TITILE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

TILE REFERENCE: REH-2017US01

TURRENT APPLICATION NUMBER: US/11/033,039

TURRENT FILING DATE: 2005-01-11

PRIOR APPLICATION NUMBER: 10/245,871

PRIOR FILING DATE: 2002-09-17

PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR APPLICATION NUMBER: 09/396,813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 660
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RESULT 6
US-11-090-439-9
US-11-090-439-9
; Sequence 9, Application US/11090439
; Publication No. US20050266442A1
. GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 661
TYPE: PRT
ORGANISM: Homo mapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/11119502
publication No. US20060014668A1
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Nicolette, Charles A.
TITLE OF INVENTION: Antigenic gp 100 Compounds
TITLE OF INVENTION: for Using Same
                                                                                                                                                                                        Query Match 14.2*; Score 76.5; D
Best Local Similarity 25.2*; Pred. No. 4.5;
Matches 30; Conservative 16; Mismatches
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CURRENT FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: 60/422,620
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
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APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANNK. 050A
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 5247PCT
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                            NAME/KBY: DOMAIN
LOCATION: (209)..(217)
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                                                                                          395 PEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSL
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                                          49 G--LDVSDRIRVV-MSVPAE----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
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                                                                                                                                          5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIREL------OELRKST 48
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GPLLDGTATLRLVKRQVPLDCVLYRYGSFSVTLDIVQG-----IESAEILQAVPSGEG
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                                                                                                                                                                                                                RESULT 8
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US-11-188-298-6318
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Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
Sequence 8860, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452) B
CURRENT APPLICATION NUMBER: US9/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
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Best Local &
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Best Local (
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TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Amgormyolipoma Cell and Method of Use Ther
FILE REFERENCE: 24318-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: 60/556,344
PRIOR PILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 62
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                     52 V-SDRIRVVMSVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT 108
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                                                                                                                                                                                                                                                                                                                                                                                                      3 ADPESTAALPDGAGLVVLD----GTVTAELBAEGWAKDRIRELQELR------KSTGLD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIREL-------QELRKST 48
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Pred. No. 4.5;
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6; Mismatches
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Pred. No. 4.9;
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US-11-188-298-8860
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NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 8860
LENGTH: 435
                                                                                                                      Matches
                                                                                                                                                           Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
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PRIOR
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/142,101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
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                                                                                                                                                                                                                    ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                              OR APPLICATION NUMBER: 60/187,970
OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: DE 19930476.9
OR FILING DATE: 1999-07-01
OR APPLICATION NUMBER: DE 19931415.2
OR FILING DATE: 1999-07-08
OR FILING DATE: 1999-07-08
OR FILING DATE: 1999-07-08
OR APPLICATION NUMBER: DE 19931418.7
OR FILING DATE: 1999-07-08
OR APPLICATION NUMBER: DE 19931419.5
OR FILING DATE: 1999-07-08
                                                                                                                                         Local
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APPLICATION NUMBER: 60/148,613
FILING DATE: 1999-08-12
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE 19931420.9 FILING DATE: 1999-07-08
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59
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                                                                           1 MAADPESTAALEDGAGLVVLDGTVTAELEAEGWAKDRI-RELQELRKSTGLDVSD-RIRV 58
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                                                                                                                                         Similarity
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VMSVPAEREDWARTHRDLIA-----GEILATDFEFADLADGVA-----IGDGV 101
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                                        MAKEGLPAVELPDASGLKV--AVVTARWNAB--ICDRLHKHAVDAGRAAGATVSEYRVIG 56
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Zelder, Oskar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kroger, Burkhard
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o. US20050260707A1
                                                                                                                   Conservative
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                                                                                                                                         13.3%; Score 71.5; 27.1%; Pred. No. 2.
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Pred. No. 6.9;
                                                                                                                      Mismatches
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                                                                                                                                                         Length 159;
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                                                                                                                                                                                                            Sequence 2, Application US/11087100 Publication No. US20050266440A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                          GENERAL INFORMATION:
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                   APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding
TITLE OF INVENTION: System and Uses Thereof
FILE REPERENCE: 2997-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OP INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OP INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
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PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
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PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR APPLICATION NUMBER: 60/187,970
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
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CURRENT FILING DATE: 2005-02-11
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APPLICANT: Kroger, Burkhar
APPLICANT: Schroder, Hartw
CURRENT APPLICATION NUMBER: US/11/087,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DE 19930476.9
FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                              59 VMSVPAEREDWARTHRDLIA-----GEILATDFEFADLADGVA------IGDGV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKEGLPAVELPDASGLKV--AVVTARWNÁE--ICDRLHKHAVDAGRAAGATVSEYRVIG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRI-RELQELRKSTGLDVSD-RIRV 58
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Zelder, Oskar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 71.5; DI
; Pred. No. 2.4;
20; Mismatches
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                                                                          PUFA Polyketide
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; TYPE: PRT
; ORGANISM: Schizochytrium sp.
US-11-087-084-2
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US-11-087-084-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/087,084
CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR FILING DATE: 2001-09-18
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PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR PPLICATION NUMBER: 60/298,796
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 37
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                                                                                                                                                                                           Matches
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LENGTH: 2910
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APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthas
TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 37
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Local Similarity 30.4%;
les 31; Conservative 13
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1937 LSEVQAMLNVEAKDVDALSRTRTVGEVV--DAMKAEIAGGSA 1976
                                                                                           1877 AAAPAPAAAAPAVSSELLEKAETVVMEVLAAKTGYETDMIESDMELETELGIDSIKRVEI 1936
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                                        59 VMSVPA----EREDWARTHRDLIAGEILATDFEFADLADGVA 96
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                                                                                                                                                                                   h 13.1%; Score 70.5; DB 7;
Similarity 30.4%; Pred. No. 1.3e+02;
31; Conservative 13; Mismatches 49
                                                                                                                                      AADPESTAALPD-GAGLVVLDGTVTAELEA--EGWAKDRIRELQELRKSTGLDVSDRIRV 58
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Pred. No. 1.3e+02;
3; Mismatches 49
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US-11-188-298-8241
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US-11-188-298-8241
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CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR PILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452) B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 8241
LENGTH: 328
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 2910
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
TITLE OF INVENTION: System and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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88 -LASIRSAAQQVNGWSDVHKIDVLVNNAGIMATDFKLTE--DG 127
                            59 VMSVPA----EREDWARTHRDLIAGEILATDFEFADLADGVA 96
                                                                                                  28 TTGVSPGGLGALFVEAIAVAEPELAILAGRNÍNKLQQTADHLASKHPNLKTKLLTLDLSS 87
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                                                                                                                                                                                                    Conservative
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Sequence 19411, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION UNDER: US/11/188,298
CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22369
SEQ ID NO 19411
Search completed: April 14, 2006, 18:42:18 Job time : 5.62788 secs
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; TYPE: PRT
; ORGANISM: Magnetospirillum magnetotacticum
US-11-188-298-19411
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US-11-188-298-19411
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                                                                                                                                                                                                                                                                                           5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLD-----VSDRI-RV 58
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                                                                                                                                                                    VGREPSGSPFNSIVQLERENGIPRNPFINAGAIAVTDVILSGHQPREALGEILRFMQFLA 145
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                                                                                                                                                                                                                                               PELAGVDPQAFGLVVIDGDGRA---AVGGDADIPFSIQSISKVFTLTLALGNVGDRLMRR 85
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26.8%; Pred. No. 14;
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Perfect score:
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### ALIGNMENTS

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18-APR-1997;
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97US-0044624P.
97DK-00001277.
98US-0070488P.
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The present sequence represents a Mycobacterium tuberculosis pr Products from the present invention, which describes protein fr and nucleic acid fragments derived from M.tuberculosis, can be the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the of or vaccination against tuberculosis caused by M. tuberculosis

tuberculosis,

diagnosis used

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protein. fragments

ij

New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis.

is - used 1 against

for

N-PSDB;

AAV63918.

WPI; 1998-542705/46.

Andersen P, Oettinger T,

Nielsen , Florio

E 70

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

Claim 1; Page 129-130; 163pp; English.

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RESULT 2
AAY21904
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Best Local Simi
Matches 165;
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05-JAN-1998;
01-APR-1998;
          The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPTS9; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23; CFP25A; CFP30B; CFP7B.
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                                                                                                                                                                                                                                                                                                                               Andersen P,
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                                                                                                                                                                                                                       3; Page 60; 265pp; English.
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98WO-DK000132.
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No. 1.1e-83;
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diagnosing
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Matches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP3OA, RD1-ORF2, RD1-ORF3, RD1-ORF3, MPT59-ESAT6, ESAT6-MPT59, CFP1OA, CFP16, CFP19, CFP23, CFP25A, CFP3OB, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and
                                                                                                                                                                                                                                                                                                                                                                          Vaccine for boosting immunity to mycobacteria when administered in mid-
life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-164602/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orme IM,
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Pred. No. 1.1e-83;
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The present sequence is that of the Mycobacterium current with strain H37Rv gene Rv1932 product, designated Tpx. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAW50725-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom

Claim

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Matches 165
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                     Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protective immunity has waned. The vaccine compositions comprise 1 or more of the 31 purified immunogenic proteins. When used as immunogens the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAM50759), the secreted product of the Rv3084v gend
                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                              Example
                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US012865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological;
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                                                                                                                           SEQ ID NO 23164; 1069pp;
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                                                                                                                                                                    polypeptides and nucleic acids useful for diagnosing infections, especially useful:
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, Jen S, Carter
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                                                                                                                            English.
                                                                                                                                                                                                                                                                     Wang
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are used in
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Matches 103
                                                                                                                                                          Mitcham JI
Zhang Y,
Barth B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the inventi and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                        N-PSDB;
                                                                                                                                    WPI; 2003-381789/36.
                                                                                                                                                                                                                                    15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                             11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                         24-APR-2003
                                                                                                                                                                                                                                                                                                                                         Propionibacterium
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                                                                                                                                                                                                                                                                                                                                                                              Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes predicted ORF-encoded polypeptide #23164
                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2003
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                                                                                                                                                                                                              (CORI-)
                                                                                                                                                                                                                                                                                                                                                                 immunostimulant;
                                                                                                                                    y, Wang S, Jen s, Y, Wang S, Jen s, B, Vallieve-Douglass J;
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                                                                                                                                                                                                                                                                                                                                                                  immune response; vaccine.
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                                                                                                                                                                        Persing DH,
Lodes MJ,
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Pred. No. 1.5e-48;
21; Mismatches 38;
                                                                                                                                                                          Benson
                                                                                                                                                                                     Bhatia
                                                                                                                                                                        DR,
                                                                                                                                                                        Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 170;
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

ç

Example 1;

SEQ ID

NO 23164; 1481pp; English.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
        N-PSDB; ABD16064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa polypeptide #14668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-2004
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                                              WPI; 2003-615309/58
                                                                                                                                Rubenfield MJ,
                                                                                                                                                                                                                                                                                         18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1999;
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                                                                                                                                                                                                            (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADGPMQHLLARAIIVVNAEGKVTYTQLVDEITTEPDYDAALEA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATSVRTENEKAAGLDDTIVLCVSRDLPFAQARFCGAEGIKNVVVASAFRSHFGKDLG
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                                                                                                                           Nolling
                                                                                                                                                                                                            THERAPEUTICS CORP
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98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                                                                         9908-00252991
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                                                                                                                           Deloughery
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C glutamicum
                                 Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG90953 standard; protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ
                                                                                                                                                                                                                                                                                       16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                          18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG90953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html
                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATSYRTED-ERAAASGATYLCVSKDLPFAQKRECGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 MAQVTLKGNPVNVDGQLPQKGAQAPAFSLVGGDLADVTLENFAGKRKVLNIFPSVDTPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IASGPLAGLAARAVVVLDEQNKVLHSELVGEIADEPNYAAALAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterium; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                            ; 99JP-00377484.
; 2000JP-00159162.
; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                 Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 31239; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment SEQ ID NO: 4707.
                                 H, Ando S, Hayashi M, Ikeda M, Ozaki A;
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Pred. No. 2.7e-45;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
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                                                                          Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                              Yokoi
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RESULT 8
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Best Local
25-JUN-1999;
01-JUL-1999;
01-JUL-1999;
08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                       fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide, lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous
                                                                                                                                   23-JUN-2000;
                                                                                                                                                                    04-JAN-2001
                                                                                                                                                                                                                                       Corynebacterium
                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum; stress; resistance; tolerance; SRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB78902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; SEQ ID NO 4707; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                          glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGSPLKGLLARSVIVVDENGKVAYTQLVDEISTEPDYDAALAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATSVRTEDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAKTHFQGNETATSGELFQVGDNLABFNLVNTELGEVSSKDFQGRKLVLNIFFSVDTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                    2000WO-IB000922
                                                                                                                                                                                                                                                                       study; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          SRT protein sequence SEQ ID
99US-0141031P.
99DE-01030429.
99US-0142692P.
99DE-01031413.
99DE-01031457.
99DE-01031541.
99DE-01032209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.0%;
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; Pred. No. 5.3e-44;
24; Mismatches 45
                                                                                                                                                                                                                                                                       vitamin; cofactor; polyketide; enzyme;
hazard; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                            NO:64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
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RESULT 9
AAB79108
ID AAB7
XX
AC AAB7
XX
DT 30-A
XX

AAB79108 AAB79108;

standard;

protein;

165

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119 60

30-APR-2001

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                                                                                                                                                                                                                                                                                                                  CC TARF70984 to AAF71133 encode the Corynebacterium glutamicum stress, CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. CC The C. glutamicum SRT genes (I) can be used in vectors (II) for Cexpression in host cells and production of fine chemicals, such as, an CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC chemical production can be modulated. The presence of (I) or the SRT CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC containing them can be used to map the genomes of organisms related to C. CC clutamicum, to identify and localise (I), (II), (III) and host cells CC containing them can be used to map the genomes of organisms related to C. CC clutamicum, to identify and localise (I) glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein regions required CC for function, in modulating the SRT protein activity, and in modulating the activity of an SRT pathway. (II) are used to permit C. glutamicum to conditions to it. (I) and protein molecules encoded by it increase the CC survive in an environment that is normally environmentally or chemically hazards and CC survive growth conditions. By increasing the growth rate or canintaining a normal growth rate in poor or toxic conditions, the yield, continued are selected or production and/or efficiency or production of fine chemicals from a cculture may be increased.
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1999;
14-JUL-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                                                                                                                                  Sequence 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Corynebacterium glutamicum nucleic acid encoding a tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 211-212; 526pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carbohydrates, or enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061972/07.
N-PSDB; AAF71015.
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121
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                                                                                                                61
                                                                                                                                                       H
                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                         Similarity
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Σ,
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                                    ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                  ATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI
                                                                                                                                                       MAKTHFQGNETATSGELFQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLNIFPSVDTGVC
                                                                                                                                                                           MAQITLEGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFEGKSVLLNIFPSVDTFVC
EGSPLKGLLARSVIVVDENGKVAYTQLVDBIFTEPDYDAALAGL
                                                                             ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
                                                                                                                                                                                                                                56.1%;
ilarity 56.7%;
Conservative 2
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99DB-01032914.
99DB-01040764.
99US-0151214P.
99DB-01041382.
                                                                                                                                                                                                                                                                                                                                                       increased
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                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                    Score 466.5; DB 4
Pred. No. 3.1e-43;
Pred. No. 3.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zelder O,
                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                      Indels
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AAP71138 to AAP71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. Glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated catturated acid, ciatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1999
08-JUL-1999
09-JUL-1999
09-JUL-1999
09-JUL-1999
09-JUL-1999
09-JUL-1999
09-JUL-1999
14-JUL-1999
14-JUL-1999
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14-JUL-1999
14-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering;
                                                                                                                                                                                                                                                                                                New isolated Corynebacterium glutamicum nucleic acid for production modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium
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          The invention relates to new Proteus mirabilis polypeptides and polymeuleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
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                                                                                                                                                                                                                                   New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or
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                                                                                                                                                                                                                                                                                                                            The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                                                                                                              Local Similarity
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  CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGV 117
                                                                                                          MAQ-ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osborne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression vector;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
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                                                                                                                                                                                           50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                              ; Score 418.5; DB 7; pred. No. 7.3e-38; 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Pred. No. 2.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription regulatory element; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                 Gaps
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                                                                                                                                                                      Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                         The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIME) polypeptide activity. The method comprises contacting an NIME polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIME nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIME expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. ANU29379-ANU29379 represent Escherichia coli NIME amino acid sequences of the invention
                                                                                                                                                                                                                                  Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 309-310;
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AIADGPLKGLAARAVVVIDENDNVIFSQLVDBITTBPDYEAALAVLKA
                        TIADGPMAGLLARAIVVIGADGNVAYTELVPBIAQBPNYBAALAALGA
                                                                                                               MSQTVHFQGNEVTVANSIPQAGSKAQTFTLVAKDLSDVTLGQFAGKRKVLNIFPSIDTGV
                                                                                                                                           MAQ-ITLRGNAINTVGBLPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV 59
                                                       CAASVRKFNQLATEIDNTVVLCISADLPFAQSRFCGAEGLNNVITLSTFRNAEFLQAYGV
                                                                                  CATSVRTEDERAA-ASGATVICVSKDIPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV 117
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                                                                                                                                                                                     50.2%; Score 417.5; DB 4; 52.4%; Pred. No. 8.9e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          526pp; English.
                                                                                                                                                                        23; Mismatches
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                                                                                                                                                                                                                                                                                            The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are cources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing theory of the genes in plants, animals or microoyganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Cluminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and genes, proteins, vectors containing the genes and have also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as bioposticides. Other uses of the genes and the area as virulence factors and for identifying targets of human diseases for which P. contains a model (particularly plague and whooping cough). This generals are as of the isolated P. luminescens proteins
                                                                                                                                                             Matches
                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence of Photorhabdus luminescens a useful e.g. as therapeutic antimicrobials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM69123 standard; protein; 168 AA.
                                                                                                                                                                                                                                                        Sequence 168
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Buchrieser
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                                                                                                                                                                                        Similarity
VRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFR-DSFGEDYGVTIAD
                                                                                                                  ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS
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                                                                     VKPQGNDISVSGQFPKSGEKAQDFTLTAKDLSDVSLSHYAGKRKVLNIFPSIDTGVCAAS
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                                                                                                                                                                  25;
                                                                                                                                                             Score 406; DB 6; I
Pred. No. 1.7e-36;
5; Mismatches 53;
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RESULT 14
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                                                                                                                                                                                                           14-JUL-1999;
14-JUL-1999;
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14-JUL-1999
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31-AUG-1999;
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                                                                                                          Kroeger
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99DE-01032920.
99DE-01032922.
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99DE-01033003.
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99DE-01032125
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New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins

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Claim 20;

Page 381; 712pp; English

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RESULT 15
ABB48059
ID ABB48
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Best Local S
Matches 69
                                                                                             Buchrieser C, Prangeul L, Couve E, Rusnlok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaeer P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo P, Gomez-Lopez N; Andendo E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-00004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB48059 standard; protein; 165
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Cossart P;
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Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,

for treatment

and

related

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Search completed: April 14, Job time: 67.931 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the genome sequence of Listeria CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of CC it are useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic composytogenes and related organisms, and for studying genetic composytogenes and other genomes. The present sequence is a protein concoded by the genome sequence of the present invention. Proteins compositely, identification of L. monocytogenes and related organisms, and contributes, identification of L. monocytogenes and related organisms, and contributes, identification of L. monocytogenes and related organisms, and contributes is and biodegradation, especially biosynthesis of vitamin compositions that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are also useful for sequence and proteins encoded by it are useful in pharmaceutical and concodines compositions for the treatment or prevention of infections by L. Compositions for the treatment or prevention, but was obtained contributed in the part of the printed specification, but was obtained contributed in the contributed and the sequence data for this patent in the composition of the printed specification, but was obtained contributed in the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contributed and the contri
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                                                                                                                                                             IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                                                                                                                                                                                                                                                       ATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
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27; Mismatches
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1 MAQITLRGNAINTV
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                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                               283416
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

### SUMMARIES

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RESULT 2
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C;Species: Peeudomonas aeruginosa
C;Species: Peeudomonas aeruginosa
C;Cate: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004
C;Accession: B83328
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Lory, S.; Olson, M.V.

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30
116.5	116.5	117.5	118	118.5	118.5	120.5	121.5	122.5	122.5	122.5	128.5	128.5	133	133.5	135.5
14.0	14.0	14.1	14.2	14.3	14.3	14.5	14.6	14.7	14.7	14.7	15.5	15.5	16.0	16.1	16.3
200	185	198	153	195	157	145	257	576	167	159	155	155	151	157	156
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S76284	AF0661	A57716	AH2203	JC2258	F70870	AH2102	JQ0064	T16005	G70341	AH2118	F97580	AD2801	H75298	E72332	G90434
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## ALIGNMENTS

# RESULT 1

문	Ś	당	Ş	Дb	Ś	Query Ma Best Loc Matches	C; Key	A;Gene: tpx C;Superfami	C;Genetics:	A/Exp	A; Res	A; Mol	A; Stat	A; Ref	A,Tit	Nacur	Rajan	; Con	R;Col	C; Acc	C;Spe	N;Alt	thior	H70635
121 DGPMAGLLARAIVVIGADGNVAYTELVPBIAQEPNYEAALAALGA 165	121 DGPMAGLLARAIVVIGADGNVAYTELVPBIAQBPNYEAALAALGA 165	61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120	61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120	1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC 60	1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC 60	Query Match 100.0%; Score 831; DB 2; Length 165; Best Local Similarity 100.0%; Pred. No. 3.5e-70; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Reywords: oxidoreductase; redox-active disulfide F;60-93/Disulfide bonds: redox-active #status predicted	A;Gene: tpx C;Superfamily: thioredoxin peroxidase	tics:	A,Experimental source: strain H37Ry	A:/Residues: 1-165 <col/> A:/Residues: 1-165 <col/>	A; Molecule type: DNA	A;Accession: H/0635 A;Status: preliminary; nucleic acid sequence not shown; translation not shown	rence number: A70500; MUID:98295987; PMID:9634230	A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	A.A. T. A. S. S. S. S. S. S. S. S. S. S. S. S. S.	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S	h, R.	C:Accession: H70635	C.Species: Mycobacterium tuberculosis	N;Alternate names: scavengase; thiol peroxidase p20	thioredoxin peroxidase (BC 1.11.1) - Mycobacterium tuberculosis (strain H37RV)	

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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pst
A;Reference number: A82950; MUID:2043733
A;Accession: E83328
A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-165 <STO>
A;Cross-references: UNIPROT:P57668; UNIF
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: tpx; PA2532
C;Superfamily: thioredoxin peroxidase
RESULT 4
B85752
thiol perox.
C;Species: |
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C;Superf
C;Keywor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Yersinia pestis
C;Species: 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0285
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, Reparkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davys, P.; Dougan, 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AG0265 A;Status: preliminary
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Best Local S
Matches 85
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: thioredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peroxidase (EC 1.11.1.-) [imported] - Yersinia pestis (strain CO92)
  peroxidase [imported]
cies: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                       85; Conserv
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                                                                                                                                                              GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL
                                                                                                                                                                                                                                               VRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGVTIAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQVTLKGNPVNVDGQLPQKGAQAPAFSLVGGDLADVTLENFAGKRKVLNIFPSVDTPTC
                                                                                                                          GPLAGLTARAVVVLDGQDNVIYSELVNEITTEPNYDAALAAL
                                                                                                                                                                                                           VRKFNQLAGELENTVVLCISSDLPFAQSRFCGAEGLSNVITLSTLRGADFKQAYGVAITE
                                                                                                                                                                                                                                                                                         VHFQGNPVSVAGKLPQIGDKAKDFTLVAKDLSDVALSSFAGKRKVLNIFPSIDTGVCAAS
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ilarity 52.5%;
Conservative 2
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                     Becherichia
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                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 420; DB 2; I
Pred. No. 6.8e-32;
2; Mismatches 53;
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Pred. No. 4.8e-38;
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                       coli
                       (strain 0157:H7,
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                         substrain
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                         EDL933)
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Barrell,
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C;Date: 16-rep-2002. C;Date: 16-rep-2002. C;Accession: B85752
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass, R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass, R;Perna, N.T.; Grotbeck, E.J.; Davie, N.W.; Lim, A.; Dimalanta, 111er, L.; Grotbeck, E.J.; Davie, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-Sep-1997 #sequence revision 19-Sep-1997 #text_change 09-Jul-2004 C;Accession: JC5504; G64881; PC4166 R;Ahou, Y.; Wan, X.Y.; Wang, H.L.; Yan, Z.Y.; Hou, Y.D.; Jin, D.Y. Biochem. Biophys. Res. Commun. 233, 848-852, 1997 A;Title: Bacterial scavengase p20 is structurally and functionally related to A;Reference number: JC5504; MUID:97312505; PMID:9168946 A;Accession: JC5504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P37901; UNIPARC:UPI00000480C8; GB:U93212; A;Experimental source: strain DH5alpha R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thioredoxin peroxidase (EC 1.11.1.-) - Escherichia coli N;Alternate names: scavengase p20; thiol peroxidase p20 C;Species: Escherichia coli
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A;Cross-references: UNIPROT:P37901; UNIPARC:UPI00000480C8;
A;Experimental source: strain 0157:H7, substrain EDL933
A;Cross-references: UNIPARC:UPI000017895B;
A;Experimental source: strain K-12
C;Comment: This enzyme belongs to a novel s
glutamine synthetase from inactivation by n
                                                                                                             A; Molecule type: DNA
A: Residues: 1-35 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-168 < ZI
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                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI00000480C8; GB:AE000230; GB:U00096; NID:gl787578; PIDN:A. A;Experimental source: strain K-12, substrain MG1655 R;Kim, H.K.; Kim, S.J.; Lee, J.W.; Cha, M.K.; Kim, I.H. Biochem. Biochem. Sid; Lee, Commun. 221, 641-646, 1996 A;Title: Identification of promoter in the 5'-flanking region of the E. coli thioredoxia.
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A; Residues: 1-168 <B
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                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                      A; Reference number: PC4166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                         MUID:96205329;
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                                                                                         GB:U33213
                                                                                                                                                                                                         PMID:8630014
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K.; Apodaca,
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chiol peroxidase [imported] - Escherichia coli (strain O157:H7, sub)
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-,
C;Accession: G90866
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yol
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shin
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia of A;Accession: G90866
A;Accession: G90866
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: This enzyme, linked to the thioredoxin as an C;Genetics:
A;Gene: tpx
C;Function:
A;Description: oxidoreductase; antioxidant enzyme; invol
C;Superfamily: thioredoxin peroxidase
C;Keywords: oxidoreductase; redox-active disulfide
F;61-95/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P37901; UNIPARC:UPI00000480C8; GB:BA000007; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Genet ECs1903 A;Gene: ECs1903 C;Superfamily: thioredoxin peroxidase
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A; Residues: 1-168 < HAY>
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                                                                                                                                                              AIADGPLKGLAARAVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA 168
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                                                                                                                                                                                                                                                                                                                                     Score 417.5; DB 2;
Pred. No. 1.2e-31;
3; Mismatches 54;
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Pred. No. 1.2e-31;
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ttori, M.; Shinagawa,
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A; Residues: 1-168 < PAR>
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A; Residues: 1-165 < TIGR>
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th, T.; Cumble, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Anthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Anthors: Complete genome sequence of a multiple drug resistant
A;Title: Complete 3B0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thiol peroxidase [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Dougan, G.; James,
th, T.; Connerton, P.; Cronin, A.;
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                                                                                                                                                                                                                                        MAQ-ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV 59
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                                               TIADGPMAGLLARAI VVI GADGNVAYTEL VPE I AQEPNY EAALAALGA
                                                                                              CAASVRKFNQLATEVENTVVLCVSADLPFAQSRFCGAEGLSNVITLSTLRNNEFLKNYGV
                                                                                                                                           CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV 117
                                                                                                                                                                                             MSQTVHFQDNPVTVANVIPQAGSKAQAFTLVAKDLSDVSLSQYAGKRKVLNIPPSIDTGV
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51.9%; Pred. No. 1.7e-30;
tive 21; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                      peroxidase
                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                     Score 395.5; DB 2;
Pred. No. 1.3e-29;
26; Mismatches 56;
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Davis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AL513382;
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    168
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T
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, L.; White,
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A; Gross-references: UNIPROT:Q93TT8; UNIPARC:UPI00000AFC07; EMBL:U02375; NID:g407281; PIL A; Gross-references: UNIPROT:Q93TT8; UNIPARC:UPI00000AFC07; EMBL:U02375; NID:g407281; PIL A; Karaolis, D.K.R.; Johnson, J.A.; Bailey, C.C.; Boedeker, E.C.; Kaper, J.B.; Reeves, P. Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998

A; Title: A Vibrio cholerae pathogenicity island associated with epidemic and pandemic st A; Reference number: Z16672; MUID:98169509; PMID:9501228

A; Reference number: Z16672; MUID:98169509; PMID:9501228

A; Accession: T09445

A; Accession: T09445

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-4 <KRR>
A; Residues: 1-4 <KRR>
A; Cfenetics:
A; Cross-references: UNIPARC:UPI000011E848; EMBL:AF034434; NID:g3004923; PIDN:AAC12278.1;
Cfenetics:
A; Genetics:
C; Superfamily: thioredoxin peroxidase
C; Keywords: oxidoreductase; redox-active #status predicted
F; 59-93/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable thioredoxin peroxidase (EC 1.11.1.-) - Vibrio cholerae
N;Alternate names: scavengase; thiol peroxidase p20; toxR-activated tagD protein
C;Species: Vibrio cholerae
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: JC2570; T09445
R;Hughes, K.J.; Everiss, K.D.; Harkey, C.W.; Peterson, K.M.
Gene 148, 97-100, 1994
A;Title: Identification of a Vibrio cholerae ToxR-activated gene (tagD) that is p
A;Reference number: JC2570; MUID:95011667; PMID:7523254
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C;Superfamily: thioredoxin peroxidase
C;Keywords: oxidoreductase; redox-active disulfide
F;59-93/Disulfide bonds: redox-active #status pred:
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathon, Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82274
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A; Residues: 1-164 < HUG>
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A; Molecule type: DNA
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Matches 69
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   Conservative
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                                 Score 349; DB 2;
Pred. No. 2.7e-25;
      Mismatches
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H.; Dragoi, I.; Sellers,
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                                                                                                                         Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-l
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                            C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text_change
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change
C;Accession: AGL72
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero,
R;Glaser, B.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
      A; Molecule type: 1
                                                                                          A; Reference number: AB1077; A; Accession: AG1272
                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                       D.; Jones, L.M.; Karst, U.
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AG1272

peroxidases homolog lmo1583 [imported]

Listeria monocytogenes

(strain

EGD-e)

DNA

F.; Kurapkat, G.;

Nat, G.; Madueno, E.;
Vazquez-Boland, J.A.;

Waitournam, A.; M Voss, H.; Wehland

A.; Baquero, E Dussurget, O.;

F.;

Entian,

Berche, P.; tian, K.D.; |

; Bloecke. Fsihi, H

09-Jul-2004

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C;Species:
C;Date: 27-
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AH1635
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Molecule type: DNA
A;Residues: 1-165 <GLA>
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend,
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                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q92BC5; UNIPARC:UPI0000137299; A;Experimental source: strain Clip11262
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   121 MKB---LRLLARSVFVVNAKGBIVYTEVVPEGSDHPNYBAAIBA 161
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Similarity 44.5%;
                      IADGPMAGILARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                              STOTRKFNEEASNLDNTVVLTISVDLPFAOKKWCAAEGLPNAITLSDHRDLSFGEAYGVI
                                                                                           ATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT
                                                                                                                            GALRGLAARAVIVADEFGVITHSELVNEITNEPDYDRILMSL
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                                                                                                                                                                                              Conservative
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                                                                                                                                                                                              Score 342.5; DB 2;
Pred. No. 1.1e-24;
7; Mismatches 59;
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; Entian, K.D.;
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Voss, H.; Wehland
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Fsihi, H
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A; Cross-references: UNIP
A; Experimental source: 8
C; Genetics:
A; Gene: lmo1583
C; Superfamily: thioredox
RESULT 14
A95192
A95192
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2;Date: 03-Aug-2001 #sequence 05-A;Esen, J.A.; Read, T.D.;
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radumnson, T.; Hickey, B.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougher: A;Title: Complete Genome Sequence of a virulent isolate of Streptococc A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus halo
C;Date: 01-Dec-2000 #seq
C;Accession: B84049
R;Takami, H.; Nakasone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9K813; UNIPARC:UPI000013728F; A;Experimental source: strain C-125 C;Genetics: A;Gene: BH3194 C;Superfamily: thioredoxin peroxidase
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <STO>
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A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thioredoxin peroxidase BH3194 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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Matches 75
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;Experimental source: strain EGD-e
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                            IEE---LRLLARAVFVINANDEVTYVEYVSEATNHPDYEKAIEAAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASITFKGNPMTLLGNEVKVGDKAPNFTVLANDLSPVTLDDSKGKVRLISVVPSIDTGVC
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; Pred. No. 5.3e-23;
19; Mismatches 68;
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; Pred. No. 1.7e-24;
27; Mismatches 59
                                                                                                                                                                     03-Aug-2001 #text_change 24-Aug-2001
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                          J.C.; Dougherty, of Streptococcus
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                                                                                                            T.D.; Peterson, S.; Hei
Radune, D.; Holtzapple,
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                        B.A.; Morri
pneumoniae.
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A;Gene:
C;Superf
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J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
J.;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thioredoxilinked thiol peroxidase (EC 1.11.1.-) [imported] - C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #text_char
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <KUR>
A;Cross-references: UNIPARC:UPI0000165A91; GB:AE005672;
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A; Residues: 1-172 < KUR>
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C;Superfamily: thioredoxin
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                                                                                                              64 VRTFDER-AAASGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD 121
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                                                                                                                                                                                                                                                  Similarity
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Similarity 44.5%;
  W---HLLARAVFVLDTDNTIRYVBYVDNINSBPNFEAAIAAAKA
                                  GPMAGLLARAI VVI GADGNVA YTEL VPE I AQEPNY BAALAALGA
                                                                          TRRFNEELAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
                                                                                                                                                  VIFIGNPVSFTGKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQ
                                                                                                                                                                                        ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W---HLLARAVFVLDTDNTIRYVEYVDNINSEPNFEAAIAAAKA 171
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                                                                                                                                                                                                                                                38.6%; Score 320.5; DB 2
44.5%; Pred. No. 1.3e-22;
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1.3e-22;
nes 63;
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Search completed: April 14, 2006, 17:34:20 Job time : 10.6752 secs

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Nature 393:537-544(1998).
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STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed-12218036;

MEDLINE-22206494; PubMed-12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
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Name=tpx; OrderedLocusNames=Rv1932, MT1982; O
                                                                                                                                                                                                                                                     laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-I- FUNCTION: Has antioxidant activity. Could remove peroxides H(2)O(2) (By similarity).
-I- SIMILARITY: Belongs to the ahpC/TSA family. Tpx subfamily.
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AAK46254.1;
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Matches 165
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R InterPro; IPR012336; Thioredoxin-like.

R InterPro; IPR012336; Thioredoxin-like.

Pfam; PF00578; AhpC-TSA; 1.

PROSITE; P801265; TPX; 1.

SEQUENCE 165 Ab.
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InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR002065; TPX;
PANTHER; PTHX10681.SF4; TPX; 1.
Pfam; PF00578; AhpC-TSA; 1.
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GO; GO:0009031; F:thiol peroxidase activity;
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Mycobacterium bovis.
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3D-structure; Antioxidant; Complete
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Best Local Similarity
Matches 138; Conser
                                                                                          Q84G72 MYCAV PRELIMINARY; PRT; 160 AA. Q84G727
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence upda 01-OCT-2003 (TrEMBLrel. 25, Last annotation up Putative thiol peroxidase (Fragment). Mycobacterium avium.

Bacteria, Actinobacteria; Actinobacteridae; Ac Corynebacterineae; Mycobacteriaceae; Mycobacte Mycobacterium avium complex (MAC).
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GO; GO:0009031; F:chiol peroxidase activ
Interpro; IPR00266; AhpC-TSA,
Interpro; IPR012336; Thioredoxin-like.
Interpro; IPR012335; Thioredoxin_fold.
Interpro; IPR012355; TPX;
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
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Q8GP25; Q73ZF0;
Q1-MAR-2003 (TrEMBLrel. 23, C
Q1-MAR-2003 (TrEMBLrel. 23, L
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     Mullerad
                           NUCLEOTIDE SEQUENCE
                                                                      NCBI_TaxID=1764;
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MEDLINE=22511501; PubMed=12623276; DOI=10.1016/S0882-4010(02)00209-7;
Mullerad J. Hovav A.H., Nahary R., Fishman Y., Bercovler H.;
"Immunogenicity of a 16.7 kDa Mycobacterium paratuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium avium complex (MAC).
NCBI_TaxID=1770;
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Bacteria; Actinobacteria; Actinobacteridae; Actinom
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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Pred. No. 5.1e.
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Best Local Sim
Matches 104;
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Best Local Similarity
Matches 137; Conser
                                                                                                                                                            of human skin.";

Science 305:671-673(2004).

SMBL; ARS017283; AAT82345.1; -; Genomic DN
GO; GO:0016491; F:oxidoreductase activity
GO; GO:0009031; F:thiol peroxidase activity
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012365; TPX.
Pfam; PP00578; AhpC-TSA; 1.

Complete proteome; Oxidoreductase; Peroxi
SEQUENCE 167 AA; 17691 MW; BB3F6B60BB
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EMBL; AX176763; AAO21122.1; -; Genomic_DNA.
HSSP; Q57549; 1Q98.
SMR; Q84G72; 2-160.
GO; GO:0009031; F:thiol peroxidase activity; IE
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
Pfam; PF00578; AhpC-TSA; 1.
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PubMed=15286373; DOI=10.1126/science.1100330;
Brueggemann H., Henne A., Hoster F., Liesegang H.,
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
"The complete genome sequence of Propionibacterium of human skin.";
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OGAA71;

OGAA71;

25-OCT-2004 (TrEMBLrel. 28, Created)

25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

25-OCT-2004 (TrEMBLrel. 28, Last annotation updat

Thiol peroxidase (EC 1.11.1.-).

OrderedLocusNames=PPA0590;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium
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                                                                                              Similarity
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17691 MW; BB3F6B60B83CF0F2
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Pred. No. 5.8e-37;
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Pred. No. 1.1e-52;
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Best Local (
                                                                                                    Matches
                                                                                                                                                                                                                                                                                           EMBL; AB016912; AAQ58545.1; -; Genomic_DNA.
HSSP; Q57549; 1Q98.
GO; GO:0016491; F:chiol peroxidase activity; IEA.
GO; GO:0009031; F:thiol peroxidase activity; IE InterPro; IPR010866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin_like.
InterPro; IPR012336; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR01235; TPX.
Pfam; PP00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
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01-MAR-2004 (TrEMBLrel. 26, Last seguence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=tpx; OrderedLocusNames=CV0870;
Chromobacterium violaceum.
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17002 MW; F01AB34A5A637206 CRC64;
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STRAIN=TLS / ATCC 49652 / DSM 12025;

STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;

WA Eisen J.A., Nelson K.E., Paulsen I.T., Heddelberg J.F., Wu M.,

A Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,

WA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,

A Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,

Waterhum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

photosynthetic, anaerobic, green-sulfur bacterium.";

photosynthetic, anaerobic, green-sulfur bacterium.";

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

Proc. Natl. As antioxidant activity. Could remove peroxides or

H(2)0(2) (By similarity).
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28-FEB-2003
13-SEP-2005
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HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR002065; TPX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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                                                                                                                                                                                                                                                                                                                             PROSITE; PS01265; TPX; 1.
Antioxidant; Complete proteome; Oxidoreductase;
SEQUENCE 168 AA; 17714 MW; 4FB46D04B5028073
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Pfam; PF00578; AhpC-TSA; 1.
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CT0754; -.
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AASVRRFNKEAGERGDAVVLCISADLPFAQGRFCTTEGLDNVVPLSVYRSPEFGLDYGLT
                                                 ATSVRTFDERAAASG-ATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT
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                                                                                                                                                                                                                                                                         Score 499;
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No. 3.4e-35;
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CRC64;
                                                                                                                                                                                                                                                                   Length 168
                                                                                                                                                                                                                        Indels
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CSTRAIN=APCC 15692 / PAO1;

X MEDLINE=20437337; Pubmed=10984043; DOI=10.1038/35023079;

X MEDLINE=20437337; Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

XA Reizer J., Saler M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;

XT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

YT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.";

XI Nature 406:959-964(2000).

CC -!- FUNCTION: Has antioxidant activity. Could remove peroxides or

CC -!- FUNCTION: Has antioxidant activity. Tpx subfamily.
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Matches
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P57668;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                           PROSITE; PS01265; TPX; 1.
Antioxidant; Complete proteome; Oxidoreductase; SEQUENCE 165 AA; 17234 MW; 6CBC3A350B57A47E
                                                                                                                                                                                                                                                                                                                                                               PIR; E83328; E83328.
HSSP; P72500; 1PSQ.
HAMAP; MF 00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR01235; TPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restitute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
Probable thiol peroxidase (EC 1.11.1.-).
Name=tpx; OrderedLocusNames=PA2532;
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                                                                                                                                                                                                                           Local
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121
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TB; PS01265; TPX; 1.
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                                                                                                                                                        MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQPRGKSVLLNIPPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                PTHR10681:SF4; TPX; 1.
                                                                                      ATSVRTFD-ERAAASGATVLCVSKDLPFAQKRPCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                    MAQVTLKGNPVNVDGQLPQKGAQAPAFSLVGGDLADVTLENFAGKKKVLNIFPSVDTPTC
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                                                                 ATSVRKFNVEAGKLANTVVLCISADLPFAQKRFCGAEGLENVVNLSTLRGREFLENYGVA
                                                                                                                                                                                                       58.5%;
nilarity 60.0%;
Conservative 2
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                                                                                                                                                                                                   Score 486; DB
Pred. No. 4.5e-
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -; Genomic_DNA.
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                                                                                                                                                                                                                       486; DB 1;
No. 4.5e-34;
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estrictions on its
is statement is not
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RESULT 10

Q7MU37 PORGI PRELIMINARY;
AC Q7MU37;
AC Q7MU37;
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AC Q7MU37;
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AC Q7MU383;
AC Q7MU3833;
AC Q7MU383;
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Q4KCR9_PSEF5
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Best Local S
Matches 96
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GO; GO:0016491; F:oxidoreductase activity; II
GO; GO:0009031; F:thiol peroxidase activity;
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012335; Thioredoxin fold.
InterPro; IPR012335; TPX:
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
                                                                                                                                            QAKCR9_PSEF5 PRELIMINARY; PRT; 166 AA QAKCR9; QAKCR9; 13-SEP-2005 (TrEMBLrel. 31, Last sequence up 13-SEP-2005 (TrEMBLrel. 31, Last annotation Thiol peroxidase (EC 1.11.1.-). QRFNames=PFL 2858; Pseudomonas Fluorescens (strain Pf-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the oral path
Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
EMBL; AE017178; AAQ66736.1; -; Genomic_DNA.
HSSP; P37901; 1QXH.
TIGR; PG1729; -.
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Nelson K.E., Pleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts .
Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L
Haft D.H., Kolonsy J.F., Nelson W.C., Mason T.M., Tallon L., Gr.
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Fraser C.M.;
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OrderedLocusNames=PG1729;
Porphyromonas gingivalis (Bacteroides g
Bacteria; Bacteroidetes; Bacteroidetes
Porphyromonadaceae; Porphyromonas.
                     NUCLEOTIDE SEQUENCE
                                                                                                  Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
                                                                  NCBI_TaxID=220664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAQITLRGNA-INTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMTDGPLKGLLARAVVVVDENGKIIYEELVPEITQEPNYBAAIAAL
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179 AA; 19188 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAASVRRFNQEASSIDNTVVLCLSKDLPFAQARFCGAEGLDKVITVSAFRCDCFEKGYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.5%;
llarity 57.8%;
Conservative 2
                                                                                                                       Gammaproteobacteria;
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Last sequence up
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Pred. No. 2.7
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                                                                                                                            Pseudomonadales;
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RESULT 12
TPX_COLD
ID TPX_COLD
ID TPX_COLD
ID TPX_COLD
AC QBNRG
COBNRG
CO Bacte
OC Coryn
OC Coryn
OX NCBI_
RN (11)
RP NUCLE
RC STRAI
RA NAKAG
RT NUCLE
RC STRAI
RX PUDMI
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Best Local S
Matches 98
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J. Biotechnol.
-!- FUNCTION: H
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28-FEB-2003
28-FEB-2003
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=ARCC 13032 / DSM 20300 / NCIB 10025,

PubMed=12948666; DOI=10.1016/S0168-1656(03)00154-8;

Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,

Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat I

Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,

MCHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,

Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-MAY-2005 (Rel. 47, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.-).
Name=tpx; OrderedLocusNames=cg11086, cg1236;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15980861; DOI=10.1038/nbt1110;
Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodso
Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosov
Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tra
Khouri H.M., Pierson B., Pierson, Weidman J., Watkins K., Tra
Complete genome sequence of the plant commensal Pseudomonas
fluorescens Pf-5.";
                                                                                                                                                                                                                                                                                                         Tauch A.;
"The complete Corynebacterium glutamicum and its impact on the production of L-asg
                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Biotechnol. 23:873-878(2005).
EMBL; CP000076; AAY92130.1; -; Genomic_DNA.
Oxidoreductase; Peroxidase.
SEQUENCE 166 AA; 17418 MW; 198861313AA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
STRAIN=ATCC 13032 /
                                                                                                                                                                                                                                                                  its impact on the productivitamins.";
Biotechnol. 104:5-25(2003).
                                                                                                                                                                               SIMILARITY: Belongs to the ahpC/TSA family. Tpx subfamily.
                                                                                                                                                                                                                FUNCTION: Has antioxidant activity. H(2)O(2) (By similarity).
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DSM 20300 / NCIB 10025;
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per J.;
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Science 307:1463-1465 (2005).

Science 307:1463-1465 (2005).

R EMBL; CRE26927; CAH08472.1; -; Genomic_DNA.

R InterPro; IPR000866; AhpC-TSA.

R InterPro; IPR012336; Thioredoxin_like.

R InterPro; IPR012335; Thioredoxin_fold.

R InterPro; IPR022065; TPX.

R Pfam; PF00578; AhpC-TSA; 1.

R PF0SITE; PS01265; TPX; 1.

R PF0SITE; PS01265; TPX; 1.

Complete proteome; Oxidoreductase; Peroxidase.

OXEQUENCE 166 AA; 17938 MW; DE898C54074EAB68 CRC64;
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EMBL; BX927151; CAR19791.1; ALT_INIT; Genomic_D)
HSSP; P72500; 1PQQ.
HAMAP; MF_00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR012335; TPX:
PANTHER; PFHR10681:SF4; TPX:
PANTHER; PFHR10681:SF4; TPX; 1.
Pfam; PF00578; AhpC-TSA; 1.
Antioxidant; Complete proteome; Oxidored
SEQUENCE 165 AA; 17532 MW; 8A13B9710
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P6_BACFN
Q5LBP6_F
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PubMed=15746427; DOI=10.1126/science.1107008;

Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely (
Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Q.
Barron A., Clark L., Corton C., Doggett J., Holden M.T.G.,

Line A., Lord A., Norbertczak H., Ormond D., Price C.,

Rabbinowitsch B., Woodward J., Barrell B.G., Parkhill J.;

"Extensive DNA inversions in the B. fragilis genome control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Bacteroidetes; Bacteroidetes (class); Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative thiol peroxidase (BC 1.11.1.-)
Name=tpx; OrderedLocusNames=BF2777;
Bacteroides fragilis (strain ATCC 25285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2005
01-FEB-2005
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MATTNEKGQPVKLIGEFIQVGKVAPDFELVKSDLSSFALKDLKGKNIVLNIFPSLDTGVC
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(TrEMBLrel. 29, Last sequence up
(TrEMBLrel. 29, Last annotation
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ALT_INIT, Genomic_DNA.
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Pred. No. 2e-32;
8; Mismatches
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Matches 98
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A Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Ok
A Kuwahara S., Hattori M., Hayashi T., Ohnishi Y.;
A Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
A Fenomic analysis of Bacteroides fragilis reveals extensive DNA
T inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
EMBL; AP006841; BAD49513.1; -; Genomic DNA.
R GO; GO:0016491; F:cxidoreductase activity; IEA.
R GO; GO:009031; F:thiol peroxidase activity; IEA.
R GO; GO:009031; F:thiol peroxidase activity; IEA.
R GO; GO:009031; F:thiol peroxidase activity; IEA.
R GO; GO:001236; Thioredoxin-like.
R InterPro; IPR01236; Thioredoxin-like.
R InterPro; IPR01236; TPX.
R InterPro; IPR01236; TPX.
R InterPro; IPR00265; TPX.
R Pfam; PF00578; AhpC-TSA; 1.
R PGSITE; PS01256; TPX; 1.
R PGSITE; PS01256; TPX; 1.
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R PGSITE; PS01256; TPX; 1.
R PGSITE; PS01256; TPX; 1.
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SAM98 DESPS

QGAM98;

QGAM98;

CS-OCT-2004 (TrEMBLrel. 28, Created)

CS-OCT-2004 (TrEMBLrel. 28, Last sequence update)

CS-OCT-2004 (TrEMBLrel. 28, Last annotation update)

CS-OCT-2004 (TrEMBLrel. 28, Last annotation update)

CS-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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25-OCT-2004 (TrEMBLrel. 28, C:
25-OCT-2004 (TrEMBLrel. 28, L;
25-OCT-2004 (TrEMBLrel. 28, L;
Putative thiol peroxidase.
OrderediccusNames=BF2763;
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STRAIN=YCH46;
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Bacteroidaceae; Bacteroides.
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Pred. No. 2e-32;
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STRAIN=LSv54 / DSM 12343;

K PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;

Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B.,

Bauer M., Zibat A., Lombardot T., Becker I., Amann J.,

A Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N.

VA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N.

VA Rienk H.-P.;

The genome of Desulfotales spychrophila, a sulfate-re
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Matches
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Environ. Microbiol. 6:887-902(2004).
EMBL; CR522879; CA336527.1; -; Genomic DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:00031, F:thiol peroxidase activity; IEA.
InterPro; IPR000866; AppC-TSA;
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR002065; TPX.
Pfam; PF00578; AppC-TSA; 1.
PROSITE; PS01265; TPX; 1.
Complete proteome.
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Complete
SEQUENCE
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ATSVRTFDERAAASGAT-VLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT
                                                                                                                              MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                     MTQVSLNGTIIETIGDLPEVGDMAADFSLTASDLSTKTLDDYTGNTVVLNIFPSIDTPVC
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                                                                                                                                                                                                             17796 MW;
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Pred. No. 3e-32;
20; Mismatches
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                                                                                                                                                                                   2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                  sulfate-reducing bacterium
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Lupas A.N.,
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Search completed: April 14, 2006, 17:32:05 Job time: 62.8796 secs

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Gapop 10.0 , Gapext 0.
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/cgn2 6/ptodata/1/laa/6_COMB.pep:*
/cgn2 6/ptodata/1/laa/H_COMB.pep:*
/cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/laa/RB_COMB.pep:*
/cgn2 6/ptodata/1/laa/RB_COMB.pep:*
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    GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration
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 US-09-050-739-8
US-09-603-20BA-5429
US-09-603-20BA-64
US-09-603-20BA-64
US-09-602-777A-172
US-09-489-039A-716
US-09-489-039A-716
US-09-489-039A-716
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US-09-107-331-5218
US-09-107-29-252
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US-09-765-271-44
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Sequence 8, Appli
Sequence 31239, A
Sequence 64, Appl
Sequence 4608, Ap
Sequence 7716, App
Sequence 7716, App
Sequence 5126, Ap
Sequence 5126, Ap
Sequence 5128, Ap
Sequence 5218, Ap
Sequence 5218, Ap
Sequence 5218, Ap
Sequence 252, App
Sequence 3764, App
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 47, Appl
Sequence 16, Appl
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	17, Appl	14, Appl	<ol><li>Appli</li></ol>	5696, Ap	15, Appl	15, Appl	×	294, App	294, App	294, App	593, App	8377, Ap	1055, Ap	10249, A	6760, Ap	1039, Ap	2, Appli	Z, Appli

## ALIGNMENTS

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RELDINGH, Karin
APPLICANT: PLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED PROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 0376/97
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
LEG ID NOS
LEG ID NOS
                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 165
TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-8
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                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                 Local
121
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                                                                                   ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120
                       DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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Pred. No. 1.2e-85;
; Mismatches 0;
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US-09-252-991A-31239
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Matches
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield of all
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LENGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS PILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/603,208A CURRENT FILING DATE: 2000-06-23 FRIOR APPLICATION NUMBER: 60/141031 PRIOR FILING DATE: 1999-06-25 PRIOR APPLICATION NUMBER: 60/142692 PRIOR FILING DATE: 1999-07-01
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APPLICANT:
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-0
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931541.8
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932209.0
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932230.9
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FILING DATE: 1999-07-01
APPLICATION NUMBER: DE 19931413.6
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931457.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
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o. 6822084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haberhauer, Grego
Lee, Heung-Shick
Kim, Hyung-Joon
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Zelder, Oskar
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                                                                                                                                                                                                                                     1999-08-27
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1999-07-01
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PRIOR FILING DATE: 1999-07-09
PRIOR PELLING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932914.1
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR PELLING DATE: 1999-08-31
PRIOR PELLING DATE: 1999-08-31
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PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR PILING DATE: 1999-07-09
PRIOR PPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR APPLICATION NUMBER: DE 19932129.9
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APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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                                                         APPLICATION NUMBER: DE 19932922.2 FILING DATE: 1999-07-14 APPLICATION NUMBER: DE 19932924.9 FILING DATE: 1999-07-14 APPLICATION NUMBER: DB 19932928.1 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                           FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932920.6
FILING DATE: 1999-07-14
   APPLICATION NUMBER: DE 19932930.3 FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
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DATE:
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US-09-543-681A-4608
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                                                                                                                         US-09-543-681A-4608
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APPLICANT: GARY BERTON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                           SEQ ID NO 4608
LENGTH: 172
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SEQ ID NO 172
LENGTH: 165
                                                      Matches
                                                                                     Query Match
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Best Local Similarity
                                                                        Best
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER: OF SEQ ID NOS: 8344
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PRIOR
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                                                                                                                                                            TYPE: PRT
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                                                                     Local
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APPLICATION NUMBER: DE 19941390.8
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APPLICATION NUMBER: DE 19941378.9
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                                                                      Similarity
QITLRGNAINTVGELPAVGSPAPAPTLTGGDLGVISSDQPRGKSVLLNIFPSVDTPVCAT 62
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                                                      Conservative
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                                                 Score 441; DB 2; L
Pred. No. 1.1e-41;
Pred. Mismatches 50;
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Pred. No. 1.4e-44;
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                                                                                   Length 172;
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CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PRICATION NUMBER: DE 19932125.6
PRIOR PRILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR APPLICATION NUMBER: DE 19932127.2
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US-09-489-039A-7716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 174, Application US/09602777A Patent No. 6831165
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SEQ ID NO 7716
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Grego
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                            APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OP INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OP INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAASVRKFNOLAABLDNTVVLCISADLPFAQSRFCGAEGLSNVVTLSTLRGASFLADYGV
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1999-07-09
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Pred. No. 3.9e-39;
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APPLICATION NUMBER: DE 19932128.0 FILING DATE: 1999-07-09

NUMBER: DE

19932129.9

FILING DATE: 1999-07-14

APPLICATION NUMBER: DE 19932226.0 FILING DATE: 1999-07-09 APPLICATION NUMBER: DE 19932920.6

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                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Corynebacterium glutamicum US-09-602-777A-174
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                    Sequence 3217, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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SEQ ID NO 174
LENGTH: 123
                                                                                           APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOO-07A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: DE 19941391.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE 19941390.8 FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 19941378.9 FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE 19932933.8 FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19933003.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 19932928.1
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                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                       61 ATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI
                                                                                                                                                                                                                                                                                                                                                                       1 MAKTHFQGNETATSGELPQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLNIFPSVDTGVC
                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 57.5
69; Conservative
                                                                                                                                                                                                                                                                                                     ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
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;; Pred. No. 1.1e-30;
14; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5126, Application --,
Sequence 5126, Application --,
Sequence 5126, Application --,
Sequence 5126, Application --,
Patent No. 6800744

Patent No. 6800744

Patent No. 6800744

GENERAL INFORMATION:
GENERAL INFORMATION:
ADD AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-433-5126
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SEQ ID NO 3217
LENGTH: 172
TYPE: PRT
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PRIOR TILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                       TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        APPLICATION NUMBER: US/09/107,433
APPLICATION NUMBER: US/09/107,433
APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
APPLICATION NUMBER: 60/05151
APPLICATION NUMBER: 60/051553
APPLICATION NUMBER: 60/051553
APPLICATION NUMBER: 40/051553
APPLICATION NUMBER: 40,489
ARBERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 W---HLLARAVFVLDTDNTIHYVEYVDNINSEPNFEAAIAAAKA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GPMAGLLARAIVVIGADGNVAYTELVPBIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VTFLGNPVSFTGKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 TRRFNEBLAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 VRTFDER-AAASGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS
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Similarity 44.5%; Pred. No. 5.4e-28;
73; Conservative 23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                LENGTH: 201 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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US-08-956-171E-5218
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Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                        TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5218:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/009,861
PILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
PILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: (B) LOCATION 1...; SEQUENCE DESCRIPTION: SEQ ID NO:
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5218:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 TRRFNEELAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 W---HILARAVFVLDTDNTIHYVEYVDNINSEPNFEAAIAAKA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GPMAGLIARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIFIGNPVSFTGKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: Maryland
                                                                                  LENGTH: 173 amino acids TYPE: amino acid
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                      TOPOLOGY: linear
ULB TYPB: protein
                                                              STRANDEDNESS: single
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STREET: 9410 Key West Avenue
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Patrick S. Dillon
Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.4%; Score 319.5; DB 2
44.5%; Pred. No. 6.7e-28;
tive 23; Mismatches 63
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US-08-781-986A-5218
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                                                                                                                                                    Query Match
Best Local
                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: YELL CITY: Rockville CTATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                    LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                 10 MTBITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
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                                                                                                                                    h 37.8%; Score 314; DB 2;
Similarity 42.3%; Pred. No. 2.3e-27;
69; Conservative 28; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 37.8%;
Similarity 42.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Benson,
DQQTRKFNSDASKEEGIVLTISADLPFAQKRWCASAGLDNVITLSDHRDLSFGENYGVVM
                     ATSVRTFDBRAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38: Human Genome Sciences, Inc.
9410 Key West Avenue
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AVENTION: Staphylococcus aureus Polynucleotides and Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                           5218:
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Pred. No. 2.3e-27;
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                                                                                                                                       62;
                                                                                                                                                                   Length 173
                                                                                                                                     Indels
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124 119 64

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILLING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILLING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3764
LENGTH: 168
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US-09-710-279-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-710-279-252
                                                                                                                      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3764, Application US/09134001C Patent No. 6380370
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                                          Matches
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: BUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GTC-007
                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DSQTRKFNEEASAEDGVVLTISVDLPFAQKRWCASSGLDNVITLSDHKDLSFGRNYGLVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTQITFKNNPIKLSGSEVNEGDIAPNFTVLDNSLNQITLDDYKNKKKLISVIPSIDTGVC
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MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.9%; Score 307; DB 2; ilarity 40.5%; Pred. No. 1.3e-26; Conservative 29; Mismatches 64
                                          Conservative
                                                           36.9%;
                                          29;
                                                         Score 307;
Pred. No. 1
                                          Mismatches
                                                           DB 2;
1.3e-26;
                                          64;
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15283
LENGTH: 00/01-07-10
                                                                                                                                                                                                                                                                                                                                                 Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)8
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Diskett
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CITY: R
                                        COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VRTFDERAAASG--ATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTIA 120
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                                                                                                                                                                                                     Rockville
                                                                                                                                                                                    Maryland
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40.6%; Pred. No. 5e-26;
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PILING DATE:

CLASSIFICATION: 435
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PRIOR APPLICATION UNDER:
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APPLICATION INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION UNDER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 393,09-8504
TILEDHONE: (301) 309-8512
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Maximum Match 100%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006
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     US-09-791-171-8
US-10-620-246-8
US-10-332-512A-9
US-09-804-980-8
US-09-738-626-4707
US-10-617-320-5126
US-10-617-320-5126
US-10-724-972A-5919
US-10-732-624-5218
US-10-732-923-21643
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Sequence 8, Appli
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Sequence 47,07, Ap
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Query Match Best Local Similarity 100.0%; Score 831; DB 3; Length 165; Best Local Similarity 100.0%; Pred. No. 2.4e-79; Matches 165; Conservative 0; Mismitches 0; Indels 0; Gaps  Oy	US-09-791-171-8 US-09-791-171-8 US-09-791-171-8 US-09-791-171-8 US-09-791-171-8  Sequence 8, Application US/09791171  Patent No. US20020094336A1  APPLICANT: ANDERSEN, Peter APPLICANT: ANDERSEN, Peter APPLICANT: OSTTINGER, Thomas APPLICANT: OSTTINGER, Thomas APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter Birk APPLICANT: WELDINGH, Karin APPLICANT: FLORIO, Walter TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS FILE REFERENCE: 670001-2002.1  CURRENT APPLICATION NUMBER: US/09/791,171  CURRENT APPLICATION NUMBER: US/09/791,171  CURRENT APPLICATION NUMBER: 09/050,739  PRIOR APPLICATION NUMBER: 09/050,739  PRIOR APPLICATION NUMBER: 0376/97  PRIOR FILING DATE: 1997-04-02  PRIOR APPLICATION NUMBER: 03/044,624  PRIOR APPLICATION NUMBER: 60/044,624  PRIOR APPLICATION NUMBER: 60/044,624  PRIOR APPLICATION NUMBER: 60/040,4624  PRIOR APPLICATION NUMBER: 60/040,4624  PRIOR FILING DATE: 1998-01-05  PRIOR APPLICATION NUMBER: 60/040,624  PRIOR FILING DATE: 1998-01-05  NUMBER OF SEQ ID NOS: 173  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 8  LENGTH: 165  TYPE: PRT  GRGANISM: Mycobacterium tuberculosis  US-09-791-171-8	ALIGNMENTS	28 130 15.6 155 5 US-10-732-923-21569 Sequence 2154 29 129.5 15.6 257 5 US-10-732-923-21310 Sequence 2133 129 15.5 15.7 5 US-10-732-923-21660 Sequence 216 31 128.5 15.5 15.5 US-10-732-923-21680 Sequence 216 32 128.5 15.1 193 5 US-10-732-923-21240 Sequence 212 33 125.5 15.1 195 5 US-10-732-923-21240 Sequence 214 34 125 15.0 185 5 US-10-732-923-21241 Sequence 214 14.9 15.0 193 5 US-10-732-923-21241 Sequence 214 14.9 15.0 193 5 US-10-732-923-21296 Sequence 215 14.7 14.5 5 US-10-732-923-21596 Sequence 216 14.7 14.7 14.7 14.7 14.7 14.7 14.7 14.7
Gaps 0, SVDTPVC 60 SVDTPVC 60 SVDTPVC 60 DYGVTIA 120 DYGVTIA 120	MENTS		e 21569, A e 21310, A e 21310, A e 21240, A e 21244, A e 21241, A e 21559, A e 21566, A e 21666, A e 21663, A e 21663, A e 21633, A e 21634, A e 21634, A e 21634, A e 21634, A e 21634, A e 21634, A e 21634, A

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APPLICANT: WELDINGH, KARIN

APPLICANT: PLORIO, WAITER

TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1A

CURRENT APPLICATION NUMBER: US/10/620,246

CURRENT PILING DATE: 2003-07-15

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 1277/97

PRIOR APPLICATION NUMBER: 1277/97

PRIOR APPLICATION NUMBER: 60/004,624

PRIOR APPLICATION NUMBER: 60/004,624

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR APPLICATION NUMBER: 10/138,473

PRIOR APPLICATION NUMBER: 10/138,473

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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-8
                                                                                                                                                                                                                                                                   RESULT 3
US-10-332-512A-9
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Sequence 9, Application US/10332512A
publication No. US20040180056A1
GENERAL INFORMATION:
APPLICANT: ORME, Ian M.
APPLICANT: BELISLE, John T.
APPLICANT: INFUNION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMMU
FILE REFERENCE: 38861-186292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10620246
Publication No. US20040115211A1
GENERAL INFORMATION:
APPLICANT: ANDERSEM, Peter
APPLICANT: NIELSEM, Rikke
APPLICANT: OETTINGER, Thomas
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Best Local Similarity 100
Matches 165; Conservative
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SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-01-21 PRIOR APPLICATION NUMBER: 1281/98
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RASMUSSEN, Peter Birk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 831; DB 4; Length 165; 100.0%; Pred. No. 2.4e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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RESULT 5 US-09-738-626-4707

Sequence 4707, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI

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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITILE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOPTWARE: Patentin version 3.0
SEQ ID NO 8
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US-09-804-980-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09804980 Publication No. US20030147897A1 GENERAL INFORMATION:
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Matches
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SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
LENGTH: 165
TYPE: PRT
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 163; Conserv
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CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: PCT/US01/21717
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/217,646
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                         LENGTH: 165
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121 DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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                                                                                             ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120
                                                                                                                                                                    MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                          ATSVRTPDERAAASGSTVLCVSLDLPPAQKRFCGAEGTENVMPASAPRDSFGEDYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120
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                                                                                                                                                                                                                                          98.88;
                                                                                                                                                                                                                                            Score 821; DB 3; Length 165; Pred. No. 2.7e-78;
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                            1; Indels
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APPLICANT:

MIZOGUCHI,

HIROSHI

SEIKO

MIKIRO

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FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOPTWARE: PATENTIN NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOPTWARE: PATENTIN VET: 3.0
SEQ ID NO 4707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-893-671-45
(S-10-893-671-45); Sequence 45, Application US/10893671; Publication No. US20050064527A1; GENERAL INFORMATION:
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US-09-738-626-4707
                                                                                                                     ; OTHER INFORMATION: complement of position 6467-6937 of seq id US-10-893-671-45
                                                                                                                                                                                                                                    SOPTWARE: PatentIn Ver. 2.0 SEQ ID NO 45
                                                       Query Match
Best Local Similarity
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                                       Matches
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US/09/801,563
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/188,362
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Levy, Stuart, et. al.
TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF
FILE REFERENCE: PKZ-043
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APPLICANT:
APPLICANT:
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                                                                                                                                                                    TYPE: PRT
ORGANISM: Bscherichia coli
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                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                   LENGTH: 168
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                                       88;
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  1 MAQ-ITLRGNAINTVGELPAVGSPAPAPTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV 59
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SENOH, AKIHIRO
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                                         Conservative
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57.3%;
                                                       50.2%;
                                       23;
                                     Score 417.5; DB 5;
Pred. No. 1e-35;
3; Mismatches 54;
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                                       Indels
                                                                          Length 168;
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RESULT 8
US-10-617-320-5126
US-10-617-320-5126
; Sequence 5126, Application US/10617320
; Publication No. US20050136404A1
; Publication No. US20050136404A1
; GENERAL INFORMATION:
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US-10-472-928-3396
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CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SegWin99, version 1.03
SEQ ID NO 3396
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Best Local 8
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APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: thiol peroxidase (psaD)
OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15903538 (1.E-96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Streptococcus pneumoniae
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 167
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                             APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 W---HLLARAVFVLDTDNTIRYVEYVDNINSEPNFEAAIAAAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 TIADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TRRFNEELAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VRTFDER-AAASGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
STATE: Massachusetts
                                                                                                                            STREET:
                                                                                                                                             ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAASVRKFNQLATEIDNTVVLCISADLPFAQSRFCGAEGLNNVITLSTFRNAEFLQAYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATSVRTPDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                            100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.6%;
                                                                                                                                                                                                            THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                             CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEINS AND NUCLEIC ACIDS
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-617-320-5126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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INFORMATION FOR SEQ ID NO: 5126:
SEQUENCE CHARACTERISTICS:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 10-Jul-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

PILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131

PILING DATE: May 12, 1998

APPLICATION NUMBER: 60/501553

PILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    AUDIKESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REPERENCE/DOCKET NUMBER: GTC-011 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: «Unknown»
CURRENT APPLICATION NUMBER: US/10/617,320
APPLICATION NUMBER: US/10/617,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 TRRPNEELAGLDNTVVLTVSMDLPPAQKRWCGAEGLDNAIMLSDYPDHSFGRDYALLINE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 W---HLLARAVFVLDTDNTIHYVEYVDNINSEPNFEAAIAAAKA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VRTFDER-AAASGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS 63
                                                                                                                    20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                            Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4%; Score 319.5;
44.5%; Pred. No. 2.9;
tive 23; Mismatches
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                                                                                                                                                                                                                                                                              and Sequences
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; MOLECULE TYPE: protein US-08-781-986A-5218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
PILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
APPLICATION NUMBER: 08/956,171
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Benson, Bob
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                           Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 MTBITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 DQQTRKFNSDASKEEGIVLTISADLPFAQKRWCASAGLDNVITLSDHRDLSFGENYGVVM
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                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human
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(301) 309-8512
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. US20040043037A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patrick S. Dillon
Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8%;
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Pred. No. 8.9e-25;
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US-10-724-972A-5919
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                                                                                                                                                                                                                                                                   ; ORGANISM: S.epidermidis
US-10-724-972A-5919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                문
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                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHO3-16
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
NUMBER OF SEQ ID NOS: 7544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5919, Application US/10724972A Publication No. US20040147734A1
                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 521
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Match 37.8%; Score 314; DB 4; Local Similarity 42.3%; Pred. No. 8.9e-25; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5218:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 EE---LRILARAVEVIDADNKVVYKEIVSEGTDFFDFDAALAA 169
    65
                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 MTEITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVFSIDTGVC 69
                                                                                                                                                                                                                                                                                                                                    168
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  SQTRKFNEEASAEDGVVLTISVDLPFAQKRWCASSGLDNVITLSDHKDLSFGRNYGLVM 124
                             ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                                                MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQQTRKFNSDASKEEGIVLTISADLPFAQKRWCASAGLDNVITLSDHRDLSFGENYGVVM 129
                                                                                       MTQTTFKNNPIKLSGSEVNEGDIAPNPTVLDNSLNQITLDDYKNKKKKLISVIPSIDTGVC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 173 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mark J. Hyman
                                                                                                                                                                              36.9%; Score 307; DB 4; Length 168; ilarity 40.5%; Pred. No. 4.7e-24; Conservative 29; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5218:
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                                                                                       RESULT 13
US-11-106-649-44
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Sequence 44, Application US/11106649
Publication No. US20050181439A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
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RESULT 12
US-09-765-272-44
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 65; Conserva
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Patent No. US2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
APPLICANT: Cho:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
120
                                      133 VVIGADGNVAYTELVPEIAQEPNYE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 DE---LRLLARSVFVLNENNKVVÝKEIVSEGTNYPDFEAALKA 164
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                                                                                                                                      74
                                                                                       63 DNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINEW---HLLARAV 119
                                                                                                                                                                                                                                  15
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FVLDTDNTIRYVEYVDNINSEPNFE 144
                                                                                                                    SGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIADGPMAGLLARAI 132
                                                                                                                                                                                    GKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVFSIDTGICSTQTRRFNSELAGL 62
                                                                                                                                                                                                                                GELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDER-AAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOPTWARE: ASCII Text
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 144 amino acids
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                            34.0%; Score 282.5; DB 3;
44.8%; Pred. No. 1.5e-21;
tive 19; Mismatches 56;
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Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

APPLICANT: FOR RELATING TO HELICOBACTER PYLORI FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 09/765,271
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/536,784
PRIOR APPLICATION NUMBER: US 09/536,083
PRIOR FILING DATE: 2000-03-28
PRIOR PILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
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CURRENT FILING DATE: 2005-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
    INFORMATION
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                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: Windows NT 4.0
SOPTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
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                                                                     REFERENCE/DOCKET NUMBER: GTN-018 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 FYLDTONTIRYVEYYDNINSEPNFE 144
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STATE: Massachusetts
COUNTRY: USA
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
DN FOR SEQ ID NO: 7878:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.5e-21;
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US-10-335-977-7877
; Sequence 7877, Application US/10335977
; Publication No. US20040052799A1
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;
LOCATION: (B) LOCATION 1...166
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7878:
US-10-335-977-7878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH EN APPLICANT
TITLE OF INVENTION: AND THERAPEUTICS
                                                                                                                    INFORMATION FOR SEQ ID NO: 7877: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             APPLICATION NUMBER: US/10/335,977
PILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
PRIOR APPLICATION NUMBER: 08/993,002
PILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
    MOLECULE TYPE: protein HYPOTHETICAL: YES
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                                                 TOPOLOGY: linear
                                                                     TYPE: amino acid
                                                                                                                                                                   TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109-1875
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213361, A 2013, App 5, Appli 17714, Ap 17714, Ap 17714, Ap 17714, Ap 17716, App 15195, Ap 15195, Ap 15066, A 15066, A 15066, A 15066, A 207148, Ap 207148, Ap 30525, A

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Post-processing: Minimum Match 0%
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Listing first 45 s
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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US-11-074-176-70
US-10-642-272A-5
US-10-642-272A-6
US-10-642-272A-4
US-10-642-272A-1038
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US-10-527-771-6
US-11-096-568A-1037
US-11-096-568A-1037
US-11-096-568A-21440
US-10-506-454-553
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Sequence 6489, Ap
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; APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard; APPLICANT: Schroder, Hartwig; APPLICANT: Zelder, Oskar
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US-10-454-437-172
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                                                                                                                                                                                                                           MATTNEKGQPVKLIGBEIQVGKVAPDEELVKSDLSSEALKDLKGKNIVLNIEPSLDTGVC
                                                           Application US/10454437
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US-11-079-185-5
US-11-188-298-13811
US-11-188-298-17714
US-10-506-454-206
US-11-188-298-15480
US-11-188-298-15480
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US-11-188-298-13066
US-11-188-298-13065
US-11-188-298-12207
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US-11-096-568A-27148
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8; Mismatches 47
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; ORGANISM: Corynebacterium glutamicum
US-10-454-437-172
                                                                                                                                                                                                                                                                                                                                                                        Sequence 174, Application US/10454437 Publication No. US20050277115A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 442
SEQ ID NO 172
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                                           CURRENT APPLICATION NUMBER: US/10/454,437 CURRENT FILING DATE: 2003-06-13 PRIOR APPLICATION NUMBER: US 60/141031 PRIOR FILING DATE: 1999-06-25 PRIOR APPLICATION NUMBER: DE 19931636.8 PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                   APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CPCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMBOSTASIS AND ADAPTATION
PRIOR APPLICATION NUMBER: DE 19932125.6 PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                             APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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FILING DATE: 1999-07-19
APPLICATION NUMBER: DE 19932226.0
FILING DATE: 1999-07-09
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Pred. No. 1e-39;
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 252
LENGTH: 164
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US-10-793-626-252
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LENGTH: 123
TYPE: PRT
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Matches
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 442
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                            Local
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APPLICATION NUMBER: DE 19932922.2
FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 19932226.0 FILING DATE: 1999-07-09 APPLICATION NUMBER: DE 19932920.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932127.2
FILING DATE: 1999-07-09
                                   120 ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                             61 DSQTRKFNERASAEDGVVLTISVDLPFAQKRWCASSGLDNVITLSDHKDLSFGRNYGLVM
                                                                                                                  61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATSVRKFNEAAASLENTTVLCISKOLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATSVRTFDERAAA-SGATVLCVSKDLPFAQXRFCGAEGTENVMPASAFRDSFGEDYGVTI 119
                                                                                                                                                            μ
                                                                                                                                                                                                                                          66;
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                                                                                                                                                                                            1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Conserv
                                                                                                                                                                                                                                                            Similarity
DE---LRLLARSVFVLNENNKVVYKEIVSEGTNYPDFEAALKA
                                                                                                                                                          MTQTTFKNNPIKLSGSEVNEGDIAPNFTVLDNSLNQTTLDDYKNKKKLISVIPSIDTGVC
                                                                                                                                                                                                                                        36.9%;
ilarity 40.5%;
Conservative 2
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ilarity 57.5%; Pred. No. 2.6e-27
Conservative 14; Mismatches 36
                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                        Score 307; DB 6;
Pred. No. 1.1e-23;
Pred. No. 64
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                                                                                                                                                                                                                                                                             Length 164;
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CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10841
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                                                                                                                                                                                                                                                             US-11-098-686-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81, Application US/11098686 Publication No. US20060024696A1 GENERAL INFORMATION:
                                                                                                                                                                               Query Match
Best Local
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kapur, Vivok and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METI
FILE REFERENCE: 09531-128001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                   LENGTH: 126
TYPE: PRT
ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 33.7%; Score 280; DB 7; Length 172; Local Similarity 38.7%; Pred. No. 6.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 E---LRILARAVEVVDTNGMITYQEIVPEMTHEPNYTAIFEAV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
  105 SAFRD-SPGEDYGVTIADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                     H
                                                                                                      47 VLLNIFPSVDTPVCATSVRTFDERAAASG--ATVLCVSKDLFFAQKRFCGAEGTENVMPA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 VRTFDERAAASG--ATVLCVSKDLFFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
                                                                                                                                                    h 27.1%; Score 225; DB 7; Length 126; Similarity 42.9%; Pred. No. 1.5e-15; Similarity 42.9%; Mismatches 44; Indels
                                                   TORPNSEAAKLGEKVRILTISCOLPPAQARWCGATGVSAVETLSDHRELSFGYAYGIAIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITFLGNPLTLMGNPVSIGEKAPDFTVLANDLSPRTLSDYANNILILSAVPSLDTGVCDIE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Mismatches
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; TYPE: PRT ; ORGANISM: Lactobacillus acidophilus US-11-074-176-70
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US-11-074-176-70
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                                                                                                                                                          SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 257
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 70
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10642272A Publication No. US20050277606A1
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APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
Best Local Similarity
                                                                                                                                                                                                                                       APPLICANT: Hattori, Pumiyuki
APPLICANT: Sugimura, Keijiro
APPLICANT: Sugimura, Keijiro
APPLICANT: Puruya, Mayumi
TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JP02/01358
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
RIOR SPEDIOR ONE: 30
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                                                                                                            ORGANISM: Rattus norvegicus
                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 QTKTFNKAMDKFPEINFLTISTNTIEDQQTWCAAEDVKNMKLMSDKNLSFGKATGLLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SVRTFDERA-AASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QITLRGNAINTYGELPAYGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPYCAT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PEFGILARSVWVLDPNCKILYRELVDEITHEPNYDAVLNEL 160
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14.6%;
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Score 121.5; DB 6;
Pred. No. 9.6e-05;
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Matches

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RESULT 10
US-10-642-272A-28
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; ORGANISM: Mus sp.
US-10-642-272A-6
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                                                                                                                                                                                                             Sequence 28, Application US/10642272A
Publication No. US20050277606A1
GENERAL INFORMATION:
APPLICANT: Hattori, Fumiyuki
APPLICANT: Sugimura, Keijiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hattori, Fumiyuki
APPLICANT: Sugimura, Keijiro
APPLICANT: Sugimura, Japuni
TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1
FILE REFERENCE: 58777.000012
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SEQ ID NO 6
LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
APPLICANT: Sugimura, Keijiro
APPLICANT: Buruya, Mayumi
ITILE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JP02/01358
PRIOR APPLICATION NUMBER: JP 41003/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/642,272A CURRENT FILING DATE: 2003-08-18 PRIOR APPLICATION NUMBER: PCT/JP02/01358 PRIOR FILING DATE: 2001-02-18 PRIOR APPLICATION NUMBER: JP 41003/2001 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 HDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNITLLSDITKOISRDYGVLLES---A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GLLARAIVVIGADGNVAYTEL----VPEIAQEP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 HDVNCEVVAVSVDSHFSHLAWINTPAKNGGLGHMNITLLSDLTKQISRDYGVLLES---A 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GIALRGLFIIDPNGVVKH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ĞIALRGLFIİDPNĞVIKHLSVNDLPVGRSVEEP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 PAVGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDERAAA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 -- SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%; Score 121.5; DB 6 ilarity 29.0%; Pred. No. 9.6e-05; Conservative 19; Mismatches 64
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                                                                           RESULT 12
US-10-821-234-1038
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US-10-642-272A-4
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28
LENGTH: 198
     Sequence 1038, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10642272A Publication No. US20050277606A1 GENERAL INFORMATION:
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APPLICANT: Sugimura, Keijiro
APPLICANT: Sugimura, Keijiro
APPLICANT: Puruya, Mayumi
TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JP02/01358
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.1%; Score 117.5; DB 6; Local Similarity 29.0%; Pred. No. 0.00024;
                                                                                                                                                                                                                       126 GLLARAIVVIGADGNVAY 143
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                                                                                                                                                                                                                                                                         123 HDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNIALLSDLTKQISRDYGV-LLEG--S
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                                                                                                                                                                                                                                                                                                                                                                      63 PAVTQHAPYFKGTAVVNGEFKDLSLDDFKGKYLVLFFYPLDFTFVCPTEIVAFSDKANEF 122
                                                                                                                                                                                                                                                                                                                                                                                                                   18 PAVGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDERAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 LGCEVLGVSVDSQPTHLAWINTPRKEGGLGPLNIPLLADVTKSLSQNYGVLKND---EGI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMAGL 127
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                                                                                                                                                                                                                                                                                                                      74 --SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMA 125
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US-10-821-234-1038
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10527771 Publication No. US20050271683A1
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Best Local :
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SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1038
LENGTH: 206
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: University Gent
TITLE OF INVENTION: Ostertagia vaccine
FILE REFERENCE: 2002-015
CURRENT EPPLICATION NUMBER: US/10/527,771
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 10/243,319
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                      TYPE: PRI
ORGANISM: Ostertagia ostertagi
PEATURE:
NAME/KEY: misc feature
LOCATION: (72) ... (72)
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Local Similarity 29.9%;
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128 LARAIVVIGADG
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                                                                                                                                                    20 VGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDERA---AA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNA-----RIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNAINTVGELPAVGSPAPAFTLTG----GDLGVISSDQFRGKSVLLNIFPSVDTPVCATSV 64
                                      IDAAVLACSXDSVFSHLAWINTPRKMGGLGDMNIPVLADTNHQIAKDYGVLKED---EGI 119
                                                                          SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMAGL 127
                                                                                                                IĞKPAPDFATKAVYNĞDFIDVKLSDYKĞKYTVLFFYPLDFTFVCPTBIIAFSDRVEEFKK 62
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                                                                                                                                                                                                            Score 106.5; DB Pred. No. 0.0021;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                              DB 6;
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US-11-096-568A-1037
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, NAME/KEY: misc feature
; LOCATION: (1). \( \tilde{(16)} \)
; OTHER INFORMATION: Ceres Seq. ID no. 13599403
US-11-096-568A-1038
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US-11-096-568A-1038
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LENGTH: 216
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1038, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1037
                                                                                                                                      Matches
                                                                                                                                                        Query Match
Best Local Similarity
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TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                     LENGTH: 226
TYPE: PRT
ORGANISM: Zea mays subsp. mays
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(226)
OTHER INFORMATION: Ceres Seq. ID no. 13599402
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                                                                                     21 GSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC---ATSVRTFDERAAASGAT 77
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VLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS---FGEDYGVTIADGPMAGLL-ARAIV 133
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                                              GOSAPDFTLKDQNGKPVSLKKYKGKPVVVYFYPADETPGCTKQACAFRDSYEKFKKAGAE
                                                                                                                                      Conservative
                                                                                                                                                        11.9%; Score 99; DB 7; Length 226; 28.1%; Pred. No. 0.015;
                                                                                                                                 25; Mismatches
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Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

							17 394.5	403	15 403.5	403	13 407.5	12 407.5		10 431.5	460	460	7 465.5	6 494.5	5 607		-	2 961	1	No. Score	Result
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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 134-135; 163pp; English.

WPI; 1998-542705/46. N-PSDB; AAV63920.

Andersen P, Oettinger T,

Nielsen R, Florio W;

Rosenkrands I,

Weldingh K,

Rasmussen PB;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
352	352	358.5	358.5	358.5	359	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	370	373	374
36.6	36.6	37.3	37.3	37.3	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	38.5	38.8	38.9
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Abo17619	Aau12175	Adb11380	Adb11382	Adb11384	Abb68747	Aam79775	Adx08011	Adv44275	Adc39067	Aao15043	Abo53082	Aao15041	Aam78791	Adm24600	Aam43579	Adm24670	Aam43649	Aag33047	Aag33046	Aag08599
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### ALIGNMENTS

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10-NOV-1997;
05-JAN-1998;
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97US-0044624P.
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98US-0070488P.
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Best Local Simi
Matches 182;
The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic; Mycobacterium tuberculosis; immune response; intuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; Mt pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP7B; CFP19; CFP27; CFP3OA; RD1-ORF; CFP1OA; CFP16; CFP19;
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                                                                                                                                                                             New immunogenic fragment of Mycobacterium tuberculosis.
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01-APR-1998;
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                                                                                                                                                   3; Page 60;
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Best Local :
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Tateishi
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N-PSDB; AAH65004.
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07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium; amino organic acid synthesis.
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; 2000JP-00159162.
; 2000JP-00280988.
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Senoh A,
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Ikeda M,
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Pred. No. 3.2e-93;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

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Best Local S
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02-JUN-2000;
07-JUL-2000;
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                        WPI; 2001-616774/71.
                                                                                                                                                                                                                                                    Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #6074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU45178 standard; protein; 182
                                                                                                                                                                                                                       L'maisonneuve
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                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPHIARRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIDGFMIQGGDPTGTGRGGPGYTFADBFHPBLRFDRAYLLAMANAGPGTNGSQFFITVTP
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                                                                                                                                                                                                                    Persing DH, |
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                      2000US-0199047P.
2000US-0208841P.
2000US-0216747P.
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79.9%;
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Pred. No. 2.9e-67;
1; Mismatches 23
                                                                                                                                                                                                                    JL, Wang
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uvestis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CE lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a comple with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and ctherefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins, by central integration of activity of the acnes protein, by contact did not form part of the printed specification, but was contacted in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                              Mitcham JL, Skeiky YAW, Pe
Zhang Y, Wang S, Jen S, I
Barth B, Vallieve-Douglass
WPI; 2003-381789/36
                                                                                                                                  15-OCT-2001; 2001US-00978825
                                                                                                                                                                  11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                     24-APR-2003.
                                                                                                                                                                                                                                                                       Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             ABM41697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM41697 standard; protein; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                      Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; immunogenic.
                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic polypeptide #6373
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                                                                                                    CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATLHTWRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQGFMIQGGDPTGTGRGGBGYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKT
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                                                 Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 607; DB 4; I
Pred. No. 9.9e-56;
6; Mismatches 37;
                                                 Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 182
                                                 Maisonneuve JL;
Jones R, Carte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC encoding a Proplenibacterium acnes protein. The invention also relates to CC polypeptides encoded by the polynucleotides (ABM3524-ABM64536) and to CC immunogenic fragments of P. acnes polypeptides. The invention also relates to CC additionally encompasses expression vectors and host cells comprising a CC method for stimulating an immune response specific for a P. acnes cC method for stimulating an immune response specific for a P. acnes cC method for stimulating an immune response specific for a P. acnes cC polypeptide and an isolated T cell population comprising P. acnes polypeptides, cC polypeptide and an isolated T cell population comprising P. acnes polypeptides, cC polypeptide antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit cC for detecting or determining the presence or absence of P. acnes in a CC patient; and a method for inhibiting the development of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for dagnosing, preventing or treating acnes CC polypeptides are useful for dagnosing, preventing or treating acnes CC polypeptides are useful for dagnosing, preventing or treating acnes CC protein. The polynucleotides can also be used as probes or primers for useful call not form naver of the primers for antiset of the polynucleotides are septiment of the present sequence represents a specifically claimed P. acnes polypeptide which is thought to contain an immunogenic region. Note: The sequence data for the primers for the present sequence data for the primers of the primers for the present sequence data for the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the primers of the 
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Matches 115
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                                                                                                                                                                                                        M. xanthus
                                                                     US6833447-B1
                                                                                                                Myxococcus xanthus
                                                                                                                                                           Transgenic
                                                                                                                                                                                                                                                        02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                 ABM94799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATTHTURGDIKIALFGNHAPKTVANFYGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6373; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHLNRRHTIFGEVADEESRKVVDBIAQVRTGRMDRPVEPVVIESVELA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDGFMIQGGCFLGTGTGGFGYRFADEFHFELTFSKFYLLAMANAGFGTNGSQFFITVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQGFMIQGGDPTGTGRGGPGYKFADBFHPBLQFDKPYLLAMANAGPGTNGSQFFITVGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATLRTNHGDI VLNLFADQAPKT VDNFVGLAGGTKEYVDPHTGQPTTGKFYDGLTFHRV
                                                                                                                                                           plant; DNA
                                                                                                                                                                                                        protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                              protein; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%;
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                                                                                                                                                             replication; gene regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 607; DB 6; 1
Pred. No. 9.9e-56;
6; Mismatches 37;
                                                                                                                                                                                                      seq id 13998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 182;
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                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDs 9692-16825 represent a group of 7134 Mayococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldman
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                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                      182
YLNNRHTIFGEVVSGYD--VVEKISNVQRDPRDKPLEPVVIQKIAMS
                               HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIBSITIS 182
                                                                                              QGFMIQGGDPTGTGRGGPGYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP
                                                                                                                                   ATLETNOGAIVVRLFSKDAPKTVANFVGLATGEKAWTDPKTGQRVEGKPLYDGVIFHRVI
                                                                                                                                                                  ATLHTNRGDIKIAL FGNHAPKTVAN FYGLAQGTKDYSTQNASGGPSG-PFYDGAVFHRVI
                                                                    PGFMIQGGDPTGTGRGDPGYRFEDEFQSGRTFDKKGLLAMANAGPGTNGSQFFITTSTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13998;
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                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25pp; English.
                                                                                                                                                                                                                   Score 494.5; DB 9
Pred. No. 8.2e-44;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiegand RC
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                                                                                                                                                                                                       51;
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RESULT 7
ABB66190
ID ABB6
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ABP66140 standard; protein; 182 AA

ABP66140;

19-NOV-2002 (first entry)

Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ij NO:884.

antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;

Bifidobacterium longum

rotavirus;

food

composition; pharmaceutical

30-JAN-2001; 2001EP-00102050

30-JAN-2001; 2001EP-00102050

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC sequences given in ABQ81842 and ABQ81843, or a sequence given in CC (1) as the sequence of the control of the sequence given in CC ABQ81842 and ABQ81843. Also described is a polymucleotide (II) encoding a CC fusion protein, comprising a sequence selected from 197 sequences given in ABP65258 to ABP66354 ligated in frame to a polymucleotide encoding a CC heterologous polymeptide. (I) has antidiarrheic and antibacterial CC activities, and can be used as an inhibitor of Salmonella. (I) (which is CC a probe) is useful for the detection and/or identification of CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM 1-2618) can be CC used for preventing and/or treating diarrhoea brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected CC products, ice-creams, fermented cereal based products, milk based CC products, infant formula, pet food or a pharmaceutical composition selected CC products, infant formula, pet food or a pharmaceutical composition concellected from tablets, liquid bacterial suspensions, dried oral CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent confidence of the pathoacterium relared melectida sequence of the the Sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of 
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Best Local
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                                                                                                                                                                              detection;
                                                                                                                                                                                                                                                                                   08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     AEB41604 standard; protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium related nucleotide sequences given in the Sequence listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of a Bifidobacterium genome selected sequences given in ABQ81842 and ABQ81843, or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum
                                                                               WO2005049642-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 884; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                 pneumophila protein SEQ ID NO 5936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRFTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAG-----PGTNGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIIMNTSEGSITINLEDDKAPNTVANFLGLATGEKEWA-DPYTGQPSHGKFYNGLTFHRI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS-GPFYDGAVFHRV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I KQFMI QGGCPLGTGTGGPGYEFDDEI DPSLKFDKPYLLAMANAGLRRGMDGKVHGTNGS
                                                                                                                            pneumophila
                                                                                                                                                                              infection; Antibacterial; Vaccine.
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Pred. No. 9.6e-41;
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RESULT 9
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a protein contain (I) are useful as vaccines and immunogenic compositions.
                                                            WO2005049642-A2
                                                                                        Legionella pneumophila
                                                                                                                       detection; infection; Antibacterial; Vaccine.
                                                                                                                                                      L. pneumophila protein SEQ ID NO 2657
                                                                                                                                                                                       08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides, useful for detection or ident for treatment and prevention of infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genome of Legionella pneumophila Paris strain and polypeptides, useful for detection or identification o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchrieser C, Tichit M, Rusniok C, Bouchier C, Jarraud S;
                                                                                                                                                                                                                                                  ABB38325 standard; protein; 205
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                                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                             136 HLWRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                              84 AGEMIQGGDELGNGTGGEGGTEDNE-NTNASENKEGVLAMANAGENTNGSQFFITVAPTP
                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TÄIIKTSEGNITCELFTKEAPNTVANFVGLATGTKEFKDVKTGEMVKRPFYNGLIFHRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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INSTRAIT ANTE & RECHUNIV LYON 1 BERNARD CLAUDE.
CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                              BLQGNYNVFGQVI--SGQEVVDKISKMPTDPQDKPIKPVVIENITI
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Zidane N, |
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Pred. No. 3.4e-40;
17; Mismatches 52
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Vandenesch
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23-SEP-2004; 2004WO-IB003578.

02-JUN-2005

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RESULT 10
AAW44191
ID AAW44
XX AAW44
XX 17-OC
DT 17-OC
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Best Local Similarity
Matches 94; Conserv
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Rusniok C,
Jarraud S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated or purified nucleotide sequences (I) from Legionalla pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the strain for treatment and prevention of infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSP)
(INRM)
(UYLY-)
(CNRS)
                                                                    Halobacterium
                                                                                               Cyclophilin cyclosporin
                                                                                                                                                                         17-OCT-2003
08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compositions, for treatment and prevention of intectic pneumophils. The present squence represents the amino
                                           JP09313184-A
                                                                                                                                            Cyclophilin
                                                                                                                                                                                                                                               AAW44191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 2657; 660pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-388305/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2003; 2003FR-00013687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumophila protein.
                                                                                                                                                                                                                                                                                                                                   136 HLWRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                            101
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INSERM INST NAT SANTE & RECHUNIV LYON 1 BERNARD CLAUDE.
CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                            AGFMIQGGDPLGNGTGGPGYTFDNE-NTNASFNKPGVLAMANAGPNTNGSQFFITVAPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                   TAIIKTSEGNITCELFTKEAPNTVANFVGLATGTKEFKDVKTGEMVKRPFYNGLIFHRVI
                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                    ELQGNYNVFGQVI--SGQEVVDKISKMPTDPQDKPIKPVVIENITI
                                                                                                                                                                                                                                                                                                                                                                                              QGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 AA;
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Bouchier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.9%;
llarity 56.6%;
Conservative 1:
                                                                                                  PPIase; halophilic;
                                                                                                                                           type PPIase.
                                                                                                                                                                       (revised)
(first entry)
                                                                      salinarum
                                                                                                                                                                                                                                            protein;
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Zidane N,
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                                                                                                                                                                                                                                               180
                                                                                                                archaebacterium;
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                                                                                                                1mmunosuppressant;
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Vandenesch F;
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RESULT 11
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N-PSDB; ABX07287.
                                                                                                                                                                                                                                      Bacterial meningitis; pneumonia;
antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                             23-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a cyclophilin type PPIase gene from a halophilic archaebacterium, Halobacterium cutirubrum. The cyclophilin type PPIase may be combined with an immunosuppressant cyclosporin A. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cyclophilin type archaebacterium.
                                                                                                                                        27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                        Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                            gene therapy;
                                                                                                                                                                                                                                                                       S. pneumoniae type 4 strain protein from coding region
                                                                                                                                                                                                                                                                                                                             ABU01998;
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                                                              Masignani V,
                                                                                                                   27-MAR-2001; 2001GB-00007658
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                                                                                  (GENO-)
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                                                                                               CHIR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 YAGVSFHRIIEGFMIQGGDPTGTGRGGPGYEFADEFHDDLTHDGPGVLSMANSGPDTNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA-----SGGPSG-PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                  CHIRON SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                        QFFITLDAQPHLDGRHAVFGAVTD--GMDVVETIGDVETDANDAPASEITIDRVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADEFHPELQFDKFYLLAMANAGPGTNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.9%; Score 431.5; larity 50.0%; Pred. No. 3.86 Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                            (revised)
(first en
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                                                                                                                                                                                                                                                                                             entry)
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                                                               Fraser C;
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                                                                                                                                                                                                                                       sepsis; otitis media; ear infection;
immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purified from halophilic
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3.8e-37;
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New proteins and nucleic acid molecules from useful as medicaments for treating or prevent

preventing

Streptococcus ting a disease

pneumoniae, or infection

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RESULT 12
ABP81616
ID ABP81617
XX ABP81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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                                          Streptococcus pneumoniae; diagnosis; gene therapy.
    Streptococcus pneumoniae
                                                                                                            Streptococcus
                                                                                                                                                      04-MAR-2003
                                                                                                                                                                                                                                      ABP81616 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003
andardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to streptococcus bacteria, such as pneumonia, sepsis, otitis media infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                  376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
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                                                                                                                                                                                                                                                                                                                                                YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGTNGSQFFI -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3150; 56pp; English
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                                                                                                                                                      (first entry)
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                                                                                                          pneumoniae polypeptide SEQ ID NO 694.
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                                                                  infection; otitis media; antibacterial;
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Pred. No. 4.8e-34;
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03-JUN-2004

ADM92196

ADM92196 standard; protein; 466

B

119

317

375

62

7

152

S pneumoniae

antigenic (first entry)

protein

sequence

SeqID393

antibacterial;

gene therapy; Streptococcus pneumoniae infection;

Streptococcus

pneumoniae

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                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                      a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABB81299-ABB91674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
                                                                                                                                                                                                                                                                                                                                                       Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 42; Page 987-989; 1091pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABZ42464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001US-0283948P
18-APR-2001; 2001US-0284443P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zagursky RJ,
Wooters JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002WO-US011524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200283855-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-093010/08
                                                                                                                                           318 -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                               277 DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD------
436 YAVLDAIAAVETGAMDKPVEDVVIETIEI
                                  153 QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                            63
                                                                                                                                                                                                                                     3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                    PGTNGSQFFI---------TVGKTPHLNRHTIFGEVIDAES
                                                                                                                                                               GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGF---GYKFADEFHPELQFDKPYLLAMANAG
                                                                   PNTNGSQFFIVQNQHLPYSKKBITRGGWPBPIABIYANQGGTPHLDKKHTVFGQLADBAS
                                                                                                                                                                                                                                                                                   42.4%;
ilarity 45.0%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green BA,
                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                   Score 407.5; DB 6;
Pred. No. 4.8e-34;
3; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chakravarti DN,
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                    Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l for treating or c diseases, e.g. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Russell DP;
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RESULT 14
ADK46830
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 466 AA;
                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus pneumoniae infection. The present sequence is that of an S pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus pneumoniae nucleic acid molecules, useful diagnosing, treating and preventing active infections of Strpneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2002; 2002US-0407082P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-2003; 2003WO-US027401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004020609-A2
 02-JUL-1997;
                     26-MAY-2000;
                                            02-MAR-2004.
                                                                  US6699703-B1.
                                                                                       Streptococcus
                                                                                                            Antibacterial;
                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                ADK46830 standard; protein; 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 393; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camilli A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-239189/22
                                                                                                                                                                                                                                                                                                  376
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                                                                                                                                                                                                                                                                             153
                                                                                                                                                                                                                                                                                                                                                                 63 GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                94;
                                                                                                                                                                                                                                                                                                                                                                                                             3 DCDSVTNSPLATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                         YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                          QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                  PNTNGSQFFIVQNQHLPYSKKBITRGGWPEPIAEIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                                                                                                                                                                                                                                              -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                                                                                                                                        DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD
                                                                                                                                                                                                                                                                                                                        PGTNGSQFFI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hava DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                      2000US-00583110.
                                                                                                                                                       (first entry)
                                                                                                                                pneumoniae protein, Seq ID No 3345.
                                                                                       pneumoniae
                                                                                                          Gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                            42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 407.5; DB 8
Pred. No. 4.8e-34;
3; Mismatches 41
                                                                                                           Vaccine; Streptococcus
                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                         -TVGKTPHLNRRHTIFGEVIDAES
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
                                                                                                           pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
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ARESULT 15
ADR95835
ID PAR95
XX ADR95
XX ADR95
XX ADR95
XX HOVel
DE NOVel
XX Menir
XX Menir
XX Strep
XX Strep
XX US680
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PM US680
PF 30-JI
PR 02-JI
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Best Local S
 02-JUL-1997;
12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 466
                                  30-JUN-1998;
                                                      05-OCT-2004.
                                                                                                                                                        Novel S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                       bacterial
                                                                                                                                                                              16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1998;
30-JUN-1998;
                                                                                                                                                   Streptococcus
                                                                                                                                                                                                   Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
                                                                                                                                                                                                                                                                                                                                   ADR95835 standard; protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3345; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doucette-Stamm L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-212399/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP----GYKFADEFHPELQFDKPYLLAMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRVVEAISKTATDGNDRPTDPVVIBSITI
                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTNGSQFFI--------TVGKTPHLNRRHTIFGEVIDAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
A
                                                                                                                                                    pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0085131P.
98US-00107433.
97US-0051553P
98US-0085131P
                                                  98US-00107433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bueh
                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%;
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                                                                                                                                                                                                                                    sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 403.5; DB 8
Pred. No. 1.3e-33;
Pred. No. 1.3e-33; Mismatches 42
                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                                                                                      4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC encoding a Streptococcus pneumoniae ADR91365 Dypeptide, or its CADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95682, CC ADR96079) or any of the fully defined sequences (appearing as ADR94308, CC ADR96079) or any of the fully defined sequences appearing as ADR91705, CC ADR91886, ADR92197, ADR92234, ADR93039, ADR992253, ADR95682, CC ADR91866, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or CC ADR93476 or at least 40, 60 or 300 consecutive nucleotides, which is CC hybridisable under high stringency conditions to the nucleotide sequence. CC The nucleic acids and proteins are chosen from 5206 disclosed sequences. CC Also included are a recombinant expression vector comprising the isolated completed acid cited above operably linked to a transcription regulatory CC element, a cell comprising the recombinant expression vector and a probe CC comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the present conditions resulting from bacterial infection by Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and CC pathological conditions resulting from bacterial infection by Ctitis media. The present sequence is one of the 2603 disclosed S. CC pneumoniae protein sequences. Note: The sequence data for this patent did conditions are the printed specification, but was obtained in CC celetronic format directly from USPTO at the conditions of the printed specification, but was obtained in conditions and directly from USPTO at the conditions of the conditions of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segdata.uspto.gov/sequence.html?DocID=6800744B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4470; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
                                                153
                                                                                                 382
  442
                                                                                                                                               120
                                                                                                                                                                                                                                                                                              324 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG 381
                                                                                                                                                                                                                         63 GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAG 119
|:: |: | |:| : ||||:| | 470
                            QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                 PNTNGSQPPIVQNQHLPYSKKEITRGGWPEPIABIYANQGGTPHLDRRHTVPGQLADEAS 441
                                                                                                                                     PGTNGSQPFI-------------TVGKTPHLNRRHTIFGEVIDAES 152
                                                                                                                                                                                                                                                                                                                                                                                                42.0%; Score 403.5; DB 8; Length 472; nilarity 44.5%; Pred. No. 1.3e-33; Conservative 23; Mismatches 42; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                42; Indels 51;
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Search completed: April 14, 2006, 17:18:40 Job time: 73.5178 secs

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### Searched: Scoring table: Sequence: Title: Perfect score: Run on: OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-620-246-12 961 1 MADCDSVTNSPLATATATLH.....ATDGNDRPTDPVVIESITIS 182 April 14, 2006, 17:19:08; Search time 10.6721 Seconds (without alignments) 1640.866 Million cell updates/sec 283416 seqs, 96216763 residues GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	v	4.	ω	2	٦	NO.	Result	
314.5	315	318	319.5	322	322.5	331	332	332	333.5	334.5	336	w	339.5	350	351	358.5	374	380	394.5	395	403.5	407.5	431.5	434	526.5	527.5	881	961	Score		
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peptidyl-prolyl ci	peptidylprolyl iso	peptidyl prolyl ci	peptidylprolyl iso	ğ	ሯ	peptidyl-prolyl ci	peptidylprolyl iso	cyclophilin-like p	_	-	peptidyl-prolyl ci		hypothetical prote	peptidylprolyl iso	probable cyclophil	peptidylprolyl iso	F22M8.7 protein -	hypothetical prote	2	~	prot	껉	peptidylprolyl iso	peptidyl-prolyl is	peptidylprolyl iso	rolyl	ä	peptidylprolyl iso	Description		

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## ALIGNMENTS

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181 18 182	181 IS 182	121 GTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESIT 180 	61 PSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGP 120 	1 MADCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGG 60 	Query Match 100.0%; Score 961; DB 2; Length 182; Best Local Similarity 100.0%; Pred. No. 4.5e-80; Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	F;Gene: ppiA A;Gene: ppiA C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase F;9-182/Domain: cyclophilin homology <cyp></cyp>	A;Rocecute type: DNA A;Residues: 1-182 <col/> A;Cross-references: UNIPROT:P71578; UNIPARC:UPI000013206D; GB:Z80233; GB:AL123456; NID: A;Experimental source: strain H37Rv	A;Accession: 67/698 A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230		N;CUNIGAINS: CYCLOPHAIH C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C.Accomics. G70608	RESULT 1 G70698 Peptidylprolyl isomerase (EC 5.2.1.8) ppiA [similarity] - Mycobacterium tuberculosis (s

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137

LMRRHTIFGEVIDAESQRVVEAISKTATD-GNDRPTDPVVIESITI 181

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Nature 409, 1007-1011, 2001

A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simonds, M.; Ske A; Title: Massive gene decay in the leprosy bacillus.

A; Reference number: A86909; MUID:21128732; PMID:11234002

A; Accession: C86910

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-182 <STO>

A; Croos-references: UNIPROT:Q9CDE9; UNIPARC:UPI000013206C; GB:A
C; Genetics:

A; Gene: pplA

C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
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N;Alternate names: cyclophilin; peptidyl-prolyl cis-trans
C;Species: Streptomyces chrysomallus
C;Date: 18-Aug-2000 #sequence revision 10
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                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T51359
R;Pahl, A.; Gewies, A.; Keller, U.
Microbiology 143, 117-126, 1997
A;Title: SCCypB is a novel second cytosolic cyclophilin
A;Reference number: Z25383
A;Accession: T51359
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R;Cole, S.T.; Eiglmeier, K.; Parkhill,
R.; Davies, R.M.; Devlin, K.; Duthoy,
eam, M.A.; Rutherford, K.M.
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A; Residues: 1-175 < PAH>
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                                                                                                                                            Query Match
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                   GFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPH 136
                                                                                          ATLHINRGDIKIALEGNHAPKTVANFVGLAQGIKDYSTQNASGGPSGPFYDGAVFHRVIQ 76
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GFMIQGGDPLGNGTGGPGYKFADBFHPELGFTQPYLLAMANAGPGTNGSQFFLTVSPTAW
                                                                     ATLKTNRGDIEIRLLPNHAPKTVRNFVELATGQREWVNPETGEKSTDRLYDGTVFHRVIS
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90.1%;
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Pred. No. 8.4e-73;
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Fraser, A
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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Las Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84342
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C;Accession: T36725
R;Muxphy, L.; Harris, D.; Bentley, S.D.;
submitted to the EMBL Data Library, June
A;Reference number: Z21612
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
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C;Superfamily: peptidylprolyl isomerase;
C;Keywords: cis-trans-isomerase
                                                                                                                                                                  A; Gene: ppiA
C; Superfamily:
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A; Residues: 1-189 <STO>
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A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9HNW6; UNIPARC:UPI00000639D6; GB:AE004437; NID:g10581353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-177 <MUR>
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                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 HLNRRHTIFGEVIDAESQRVVEAISKTATD-GNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
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                                        N
                                                                                                      Similarity
                                     ADCDSVTNSPLATATILHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGFMIQGGDPLGNGTGDPGYQFPDEFHPDLAFDKPYLMAMANAGPGTNGSQFFITVSPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
-MPVDATVHTSEGEFDIELYDERAPRTVENFLNLARHEPAADADPAPDTV
                                                                                                    45.2%;
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                                                                                21;
                                                                                                    Score 434; DB 2;
Pred. No. 3.6e-32;
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Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIPARC: UPI00000B11B; EMBL: AL079308; PIDN: CAB45223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                    Mismatches
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                                                                                  Indels
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                                                                                    18;
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                                                                                  Gaps
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58
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G.; Jable
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RESULT 7
A95179
A95179
hypothetical protein SP1538 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Apte: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95179
R;Tettelin, H; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, B.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: A95179
A;Accession: A95179
A;Accession: A95179
A;Accession: Aysidatus: preliminary
A.MClevile tree. Nux
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-180 <IID>
A;Cross-references: UNIPROT:O50586; UNIPARC:UPI0000062A42; EMBL:AB002414; NID:g2760611;
A;Cross-references: UNIPROT:O50586; UNIPARC:UPI0000062A42; EMBL:AB002414; NID:g2760611;
A;Note: the source is designated as Halobacterium cutirubrum
C;Genetics:
A;Gene: Cyp
C;Function: A;Description: cyclophilin-type peptidyl-prolyl cis-trans isomerase [validated, MUID:980]
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;1-179/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T43805

R;Iida, T.; Furutani, M.; Iwabuchi, T.; Maruyama, T.

Gene 204, 139-144, 1997

A;Title: Gene for a cyclophilin-type peptidyl-prolyl cis-trans isomerase from A;Accession: T43805

A;Accession: T43805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local S
Matches 88
                               Molecule type: DNA
Residues: 1-466 <KUR>
        Cross-references: UNIPROT:Q97PR4; UNIPARC:UPI00000518B5; GB:AE005672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLLAMANAGPGTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWEDPESGEIRGDSLYAGVSFHRIIEGFMIQGGDPTGTGRGGPGYEFADEFHPELQFDKP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA-----SGGPSG-PF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASEITIDRVEI 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPPITLDAQPHLDGRHAVFGAVTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAGVSFHRIIBGFMIQGGDPTGTGRGGPGYEFADEFHDDLTHDGPGVLSMANSGPDTNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 431.5; DB 2;
; Pred. No. 5.7e-32;
20; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GMDVVBTIGDVBTDANDAPASBITIDRVBI
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     PIDN: AAK75626.1;
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                                                                                                              RESULT
A71261
peptidylprolyl isomerase (BC 5.2.1.8) TP0947 [similarity] - syphili N;Contains: cyclophilin C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-
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hypothetical protein spr1393 [imported] - Streptococcus pneumoniae (strain R6) (;Species: Streptococcus pneumoniae (;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: H98045 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B., e. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowltz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P. M.; Winkler, M.B. J. Bacteriol. 183, 5709-5717, 2001 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Atcession: H98045 A;Accession: H98045
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C;Genetics:
A;Gene: SP1538
                                                                                                                                                                                                                                                                                                                                     A;Gene: spr1393
                                                                                                                                                                                                                                                                                                                                                                                        A;Residues:
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Best Local
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436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 DISTV-SGPL----ATIKINHGDLRIKLFPSHAPKTVANFVSL---SKD-------
                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                     93;
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                                                                                                                                                                                                                                                                                                                                                                                      1-466 <KUR>
                                                                                                                                                                                                                                                                                   h 42.0%;
Similarity 44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 42.4%;
Similarity 45.0%;
94; Conservative :
YAVLDVIAAVETGAMDKPVEDVVIETIEI 464
                               QRVVEAISKTATDGNDRPTDPVVIBSITI 181
                                                              PGTNGSQFFI ----
                                                                                                                              -GYYDGVIFHRIIXDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                               GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAG 119
                                                                                                                                                                                                     DIETV-EGPL----ÄTIKTNHGDLRIKLFPEHÄPKTVANFVSL---SKD-------
                                                                                                                                                                                                                     DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNTNGSQFFIVQNQHLPYSKKEITRGGWPEPIAEIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGTNGSQFFI-----
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                      UNIPROT: Q8CYJ1;
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                                                                                                                                                                                                                                                                                   Score 403.5; DB 2
Pred. No. 6.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 407.5; DB 2;
Pred. No. 2.8e-29;
                                                                                                                                                                                                                                                                                                                                                                      UNIPARC:UPI00000E4733; GB:AE007317; PIDN:AAL00197.1
                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TVGKTPHLNRRHTIFGEVIDAES 152
                                                                                                  TVGKTPHLNRRHTIFGEVIDAES 152
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(BC 5.2.1.8) TP0947 [similarity] - syphilis spirochete

#text\_change 09-Jul-2004

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-215 <COL>
A;Cross-references: UNIPROT:O66105; UNIPARC:UPI0000132074; GB:AE001263; GB:AE000520; A;Experimental source: strain Nichols
C;Genetics:
C;Genetics: TP0947
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
C;Keywords: cis-trans-isomerase
C;Keywords: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A71261
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, Pthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-196 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9CH46; UNIPARC:UPI00000C6930; GB:AE005176; PID:g12723824; A;Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
167
                                            119 KNLPYPKDSLIQGGWPEEVAETYTGGGTPHLDGRHTVFGQLVDEESYKVLDEIAAVRVGA 176
                                                                                         130
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                                                                                                                                                                                                                                                                    16 TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                  84;
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                                                                                                                                                                               QGFMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFI---
                                                                                                                                   KDFMVQGGDPTGTGMGGSSIYGEKFEDEFSMDL-FNLRGALSMANAGPNTNGSQFFIVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTN
NDRPTDPVVIESITI
                                                                                                                                                                                                                            TAIINTNHGKMTVKLFDNLAPKTVKNFIELSK------EGYYDGVIFHRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSQFFITHVATPWLDGKHTVFGKVV--EGMEVVHAI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSOFFITVGKTPHLNRRHTIFGEVIDAESORVVEAI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFYQGLTFHRVIKDFMIQGGDPQGNGTGGPGYQFPDECDPALRHDSPGVLSMANAGPGTN
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                       41.1%; Score 394.5; DB 2
43.1%; Pred. No. 1.4e-28;
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                                                                                                                                                                                                                                                                                                                  26; Mismatches
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Pred. No. 1.5e
15; Mismatches
                                                                                      TVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                             Length 196;
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                                                                                                                                                                                                                                                                                                                45;
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M.; Utterback,
                                                                                                                                                                                                                                                                                                                  Gaps
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nypothetical protein F14L2.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48940
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T48940
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A;Residues: 1-629 <JOR>
A;Residues: 1-629 <JOR>
A;Cross-references: UNIPROT:Q9LXM7; UNIPARC:UPI0000A046D; EMBL:AL353818; GSPDB:GN00061;
A;Experimental source: cultivar Columbia; BAC clone F14L2
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                                                                                                                                                                                                                                                                                                                                                                                     A;Intron8: 62/2; 91/1; 120/3; 200/3; 241/2; 266/3; 302/3; 361/3; 434/2; 476/3; 551/2;
                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T48940
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                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                         Matches
583 WLDNKHIVFGRVV--KGMDVVQGIBKVKIDKNDRPYQDVKILNVIV
                                               136 HLWRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                              523 MIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTLSMANAGPNTNGSQFFITTVATP
                                                                                                                                                                                               478 MHTTLGDIHMKLYPEBCPKTVENF
                                                                                                                                                                                                                                                                                    79;
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179 QDKPVDDVVIESVEI
                                                                                                                                      79 MIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                                                                                                                             19 LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGF 78
                                                                                                                                                                                                                                                                                                          h 39.5%; Score 380; DB 2; Length 629; Similarity 47.6%; Pred. No. 1.3e-26;
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                         21; Mismatches 46;
                                                                                                                                                                                               -----YYDNHLFHRVIRGF
                                                                                                                                                                                                                                                                                         Indels
    626
                                                                                                                                                                                                                                                                                         20;
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                                                                                                 582
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Rytheologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li., J.H.; Li., Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
C86151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F22M8.7 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-160 <STO>
                                                                                                                   A; Map position: 1
C; Superfamily: per
                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9LPC7; UNIPARC:UPI000000BB15; GB:AE005172; NID:g8570445;
                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: C86151
                                                                                                                                                                                                 Genetics:
                                                                                                                       peptidylprolyl isomerase; cyclophilin homology
38.9%; Score 374; DB 2; 47.3%; Pred. No. 8.2e-27;
                                Length 160;
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δ

Matches

Similarity

Conservative

22;

Mismatches

Indels

20;

Gaps

P

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probable cyclophilin-related peptidyl prolyl cis-trans isomerase - fission yeast (Sch: C;Species: Schizosaccharomyces pombe C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 C;Accession: T41399 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D. submitted to the EMBL Data Library, May 1998 A;Reference number: Z21991 A;Accession: T41399 A;Accession: T41399 A;Accession: T41399 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-610 <WOO> A;Residues: 1-610 <WOO> A;Residues: 1-610 <WOO> A;Experimental source: strain 972h-; cosmid c553 C;Genetics: SPDB:SPCC553.04 A;Map position: 3 A;Introns: 24/1 F;449-608/Domain: cyclophilin homology <CYP>
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A;Accession: T38930
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-155 <BAD>
A;Cross-references: UNIFROT:P87051; UNIFARC:UPI0000128C69;
A;Experimental source: strain 972h-; cosmid c57A10
C;Genetics:
A;Gene: SPDB:SPAC57A10.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidylprolyl isomerase (EC 5.2.1.8) SPAC57A10.03 [similarity] - fission y. N;Contains: cyclophilin (;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38930 R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.: Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
A;Introns: 10/3; 24/3; 42/3; 69/2; 101/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;1-155/Domain: cyclophilin homology <CYP>
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T38930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                           Cross-references: UNIPROT:074942; UNIPARC:UPI000069EF1; EMBL:AL023704; PIDN:CAA19257
Experimental source: strain 972h-; cosmid c553
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Best Local :
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Search completed: April 14, Job time : 12.6721 secs

2006, 17:34:32

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A;Introns: 69/1; 102/1
C;Superfamily: peptidylprolyl isomerase;
C;Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-169 < DUZ>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid
A;Reference number: Z20600
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A;Experimental source: strain Bristol N2; clone C34D4
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                                                                  MIQGGDPTGTGRGGASIYGDKFSDEIDERLKHTGAGILSMANAGPNTNGSQFFITLAPTQ 118
                                                                                                   MIQGGDPTGTGRGGP---GYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                                       LDTTMGKIALBLYWNHAPRTCQNFSQLAKRN--
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HLDGKHTIFGRV--AAGMKVIANMGRVDTDNHDRP
                                                                                                                                                                      LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGF 78
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Pred. No. 1.3e-24;
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Q8NUAS_CORDL
Q8PU19_CORBP
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Q82PC6_STRAW
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              Query Match
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Result No.

100.0%;

Score 961; DB 1; Pred. No. 3.7e-84;

Length 182;

Minimum Maximum

Database

Sequence:

45	44	43	42	41	40	39	38	37	36	35	ω <b>4</b>	ω W	32
386	386	387	388	388.5	388.5	392	393	394	394.5	395	395	397	398.5
40.2	40.2	40.3	40.4	40.4	40.4	40.8	40.9	41.0	41.1	41.1	41.1	41.3	41.5
423	181	159	466	468	468	470	466	471	196	344	215	470	253
N	N	N	N	N	N	N	N	N	N	N	ب	N	N
Q6ZJ09_ORYSA	Q7XXQ2_ORYSA	Q6MC42_PARUW	Q8E747_STRA3	Q5M569_STRT2	Q5MON3_STRT1	Q8P009_STRP8	Q8E1N1_STRAS	Q8DVJ7_STRMU	Q9CH46_LACLA	Q6AMQ1_DESPS	PPIB_TREPA	Q5XAQ1_STRP6	Q5BXXN7_SCHJA
Q6zj09 oryza sativ	Q7xxq2 oryza sativ	Q6mc42 parachlamyd	Q8e747 streptococc	Q5m569 streptococc	Q5m0n3 streptococc	Q8p009 streptococc	Q8eln1 streptococc	Q8dvj7 streptococc	Q9ch46 lactococcus	Q6amq1 desulfotale	066105 treponema p	Q5xaq1 streptococc	Q5bxn7 schistosoma

# ALIGNMENTS

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R EMBL; BX248334; CAD92871.1; -; Genomic_DNA.
R HSSP; P52013; 110P.
R SMR; P65763; 12-182.
R InterPro; IPR002130; CSA_PPIase.
R Pfam; PF00160; Pro isomerase; 1.
R PFAM; PF00153; CSAPPISMRASE.
R PRINTS; PR00170; CSA_PPISMRASE.
R PROSITE; PS00170; CSA_PPIASE_1; 1.
R PROSITE; PS00170; CSA_PPIASE_2; 1.
R PROSITE; PS00172; CSA_PPIASE_2; 1.
COmplete proteome; Isomerase; Rotamase.
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Pryor M., Duthoy S., Grondin S., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-i- FUNCTION: Pplases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of prolline imidic peptide bonds in oligopeptides (By similarity).

-i- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the cyclophilin-type PPIase family.
-!- SIMILARITY: Contains 1 PPIase cyclophilin-type domain.
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NCBI_TaxID=1765;
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WEDLINE=B8295997; PubMed=9634230; DOI=10.1038/31159;

M Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

A Cole S.T., Brosch R.V., Eiglmeier K., Gas S., Barry C.E. III,

A Harris D.B., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

A Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

A Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,

A Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares R.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence.";

RL Nature 393:537-544(1998).
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[2]
NUCLEOTIDE S
STRAIN=CDC
                                                                                                                                                                          J. Bacteriol. 184:5479-5490(2002).

-I- FUNCTION: PPIABES accelerate the folding of proteins. the cis-trans isomerization of proline imidic peptide oligopeptides (By similarity).

-I- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = pept
                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.194.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Feterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Peterson J.D., DeBoy R.T., Nolson W.C., Umayam L.A., Ernolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg N.G., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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01-NOV-1997 (Rel. 35, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase
(Rotamase A).
Name=ppiA; OrderedLocusNames=Rv0009, MT0011;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
MCBI_TaxID=1773;
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Fraser C.M.;
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                                                     (omega=0).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the cyclophilin-type PPIase fam.
SIMILARITY: Contains 1 PPIase cyclophilin-type domain.
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Best Local Sim
Matches 182;
                                                                  Holroyd S., Hornsby T., (Murphy L.D., Oliver K., (Rutter S., Seeger K., 58 Squares S., Stevens K., 18 Barrell B.G.;
                                                                                                                                                                                                                                                                                                                Z8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase
(Rotamase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; G70698; G700
PDB; 1W74; X-ray
TIGR; MT0011; -
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PFINTS; PR00153; CSAPPISMRASE.

PROSITE; PS00170; CSA PPIASE 1; 1.

PROSITE; PS00172; CSA PPIASE 2; 1.

PROSITE; PS0072; CSA PPIASE 2; 1.

PROSITE; PS0072; CSA PPIASE 2; 1.

PROSITE; PS0072; CSA PPIASE 2; 1.

PPIASE cyclophilin-type.

DOMAIN 13 181 PPIASE cyclophilin-type.
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Q9CDE9;
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-I- FUNCTION: PPIases accelerate the folding of proteins.
                                                                            Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitchead S., Woodward J.R.,
                                                                                                                                                                                              STRAIN=TN;
MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
                                                                                                                                                                                                                                                Corynebacterineae;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BX842572; CAB02430.1; -; EMBL; AE000516; AAK44233.1; -;
                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                         SEQUENCE
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Matches 164
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Pfam; PF00160; Pro isomerase; 1.
PRINTS; PR00153; CSA_PPISMRASE.
PROSITE; PS00170; CSA_PPIASE 1; 1.
PROSITE; PS00172; CSA_PPIASE 2; 1.
Complete proteome; Isomerase; Rotama DOMAIN 13 181 PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004
05-JUL-2004
05-JUL-2004
Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

-- SIMIIARITY: Contains 1 PPIase cyclophilin-type domai EMBL, AE017227; AAS02328.1; -; Genomic_DNA.

HSSP; Q27450; 1A58.

SMR; Q744Q3; 14-182.

GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase ac GO; GO:0006457; P:protein folding; IEA.
                                                                                                                                                                                                                                                                                                                Name=ppiA; OrderedLocusNames=MAP0011;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q744Q3 MYCPA PRELIMINARY;
Q744Q3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                 STRAIN=k10;
                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                              Mycobacterium avium
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Leproma; ML0011; -.
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SUBCELLUTY: Belongs to the cyclophilin-type PPIas
SIMILARITY: Contains 1 PPIase cyclophilin-type do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY:
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Last seq
Last ann
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Pred. No. 1.8e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Rotamase.
PPIase cyclophilin-type.
; 6A6D8004348A9544 CRC64;
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.8e-76;
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                             activity; IEA
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Matches 163
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Q4YYC5;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8).
Name=ppiA; ORFNames=jk003;
Corynebacterium jeikeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                 Linke B., Tauch A.;
Submitted (DEC-2004) to the
EMBL; CR931997; CAI36182.1;
                                                                                                                                                                                                                Nosocomial Pathogen Corynebacterium Bacterium of the Human Skin Flora."; J. Bacteriol. 187:4671-4682 (2005).
                                                                                                                                                                                                                                                                                 PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005; PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005; Tauch A., Kaiser O., Hain T., Goesmann A., Weisshaar B., Albersmeier A., Bekel T., Bischoff N., Brune I., Chakrabot Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoever
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SEQUENCE
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NCBI_TaxID=306537;
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Pfam; PP00160; Pro isomerase; 1.
PRINTS; PR00153; CSAPPIASE 1; 1.
PROSITE; PS00170; CSA_PPIASE 1; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
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               VTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGBSGFFY
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182 AA; 19327 MW; 7FBB403D7091A12E
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 MTNK---TATAILHTNQGDIAIDLFGNHAPETVANFVGLAQGTKEYSQPNASGTNEGPFY
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                                                                                                        174 AA; 18825
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                                                                 74.78;
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Pred. No. 4.4e-76;
1; Mismatches 8
                                                                   Score 717.5;
Pred. No. 9.
                                                    Pred. No. 9.20
2; Mismatches
                                                                                                         B72873CD42C381B6
                                                                                                                                  Genomic_DNA
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QBNUAS CORGL ID QBNUAS;
AC QBNUAS;
DT 01-CCT-2002 (7
DT 01-MAR-2004 (7)
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Best Local S
Matches 135
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SMR; Q6MBV0; 5-173.

G0; G0:0016853; P:isomerase activity; IEA.

G0; G0:0016857; P:peptidyl-prolyl cis-trans is:

G0; G0:0006457; P:protein folding; IEA.

InterPro; IPR000130; CSA PPIASE; 1.

PRINTS; PR00153; CSA PPIASE; 1.

PROSITE; PS00170; CSA PPIASE; 1.

PROSITE; PS00172; CSA PPIASE; 1.
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CORGL
Q6M8Y0
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STRAINAATCC 13032 / DSM 20300 / NCIB 10025;
STRAINAATCC 13032 / DSM 20300 / NCIB 10025;
PubMeda-12948626; DOI=10.1016/S0168-1656(03)00154-8;
Ralinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Ekmanns B.J., Gaigalat L.
Burkovski A., Dusch N., Eggeling L., Ekmanns B.J., Gaigalat L.
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
MCHardy A.C., Meyer F., Moeckel B., Sahm H., Wendisch V.F., Wiegrae
                                                                                                                                                                                                                                                                                                                                          EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                  Name=ppiA; OrderedLocusNames=cg0048;
                                                                                                                                                                                                                                              Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                          Tauch A.,
                                                                                                                                                                                                                                                                                                                                                                                        its impact
                                                                                                                                                                                                                                                                                                                                                                                      complete Corynebacterium glutamicum ATCC 13032 genome sequence its impact on the production of L-aspartate-derived amino acids
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174 AA;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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llarity 79.9%;
Conservative 1
                                      PRELIMINARY;
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26,22
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Created)
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Pred. No. 1.3e-60;
1; Mismatches 23;
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                                      PRT;
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RASE B (EC 5.2.1.8)
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Query Match
Best Local Similarity
Matches 135; Conserv
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GO; GO:0016853; F:1somerase activity; IEA.

GO; GO:0003755; F:peptidyl-prolyl cis-trans i
GO; GO:0006457; P:protein folding; IEA.

InterPro; IPR002130; CSA PPIASE.

Pfam; PF00160; Pro_isomerase; 1.

PRINTS; PR00133; CSAPPISMASE.

PROSITE; PS00170; CSA PPIASE 1; 1.

PROSITE; PS00170; CSA PPIASE 2; 1.

PROSITE; PS00170; CSA PPIASE 2; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

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PROSITE; PS00170; CSA PPIASE 3; 1.

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PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.

PROSITE; PS00170; CSA PPIASE 3; 1.
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T. Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch B., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J., "The complete genome sequence and analysis of Corynebacteriu diphtheriae NCTC13129.", Nucleic Acids Res. 31:6516-6523(2003).

-!-SIMILARITY: Contains 1 PPlase cyclophilin-type domain. EMBL; BX248354; CAE48536.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence applated to the probable peptidyl-prolyl cis-trans isomerase A (E
Name-ppiA; OrderedLocusNames=DIP0025;
Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BC 5.6.1.0).
OrderedLocusNames=Cgl0034;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycet
                                                                                                                                                                                                                                                                                                                   STRAIN=Biotype gravis / NCTC 13129; MEDLINE=22965443; PubMed=14602910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterineae;
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-i-SIMILARITY: Contains 1 PPIase cyclophilin-type domair EMBL; BA00036; BAB97427.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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R SMR; Q6NKJ3; 9-179.

R GO; GO:0016853; F:15omerase activity; IEA.

DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR002130; CSA PPlase.

DR InterPro; IPR00215; Prot_inh_serpin.

Pfam; PF00160; Pro isomerase; 1.

DR Pfam; PF00160; Pro isomerase; 1.

PROSITE; PS00170; CSA PPIASE 1; 1.

PR PROSITE; PS00170; CSA PPIASE 1; 1.

DR PROSITE; PS00170; CSA PPIASE 2; 1.

DR PROSITE; PS000284; SERPIN; UNKNOWN 1.

KW Complete proteome; Isomerase; Rotamase.

"" "CONTENCE 180 AA; 19442 MW; F04683573BDDF598 CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC64; CRC6
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Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                               Genome Res. 13:1572-1579(2003).

-!- SIMILARITY: Contains 1 PPIASE cyclophilin-type EMBL; BA000035; BAC16839.1; -; Genomic_DNA.
HSSP; P30412; ZRWC.
SMR; Q8FUI9; 31-200.
GO; GO:0016853; F:180cmerase activity; IEA.
GO; GO:0016853; F:peptidyl-prolyl cis-trans isomera GO; GO:0003755; F:peptidyl-prolyl cis-trans isomera GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR002130; CSA_PPIASE.
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Genome Bor
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                                                                                                                                     Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASRASE;
PROSITE; PS00170; CSA_PPIASE 1; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
Complete proteome; Isomerase; Rotal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
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STRAIN=YS-314 / AJ 1
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Bacteria; Actinobacteria;
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                                                                                                           SEQUENCE
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   Similarity
                                                                                                       proteome; Isomerase; Rotamase.
202 AA; 21829 MW; 814495B2E7C3A818
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78.4%;
73.7%;
76.0%;
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Pred. No. 5e-60;
1; Mismatches
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the thermostability
Score 708; DB 2
Pred. No. 9e-60;
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                                    Length
                                                                                                           CRC64;
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RESULT 11
Q82FC6\_STRAW
ID Q82FC6\_STRAW 1
AC Q82FC6;
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DT 01-JUN-2003 (7

PRELIMINARY;

PRT;

186

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(TrEMBLrel.

24,

Created) Last seq

sequence update)

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RESULT 10
Q6A9U1 PROAC
Q6A9U1 PROAC
AC Q6A9U1;
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Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00160; Pro isomerase; 1.
PEAM; PF00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
Complete proteome; Isomerase; Rotamal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINERAI17202 / DSM 16379;
STRAINERAI17202 / DSM 16379;
PubMed=15286373; DOI=10.1126/science.1100330;
Brueggemann H., Henne A., Hoster P., Liesegang H.,
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase A (EC OrderedLocusNames=PPA0718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterineae,
NCBI_TaxID=1747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 305:671-673(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of human skin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 PPIase cyclophilin-type L; AE017283; AAT82475.1; -; Genomic DNA. GO:0016853; F:isomerase activity; TEA.
                                         135
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123
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                                                                                        63
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                           PHINRRHTIFGEVIDAESQRVVBAISKTATDGNDRPTDPVVIESITIS
                                                                                                                 IQGFMIQGGDFTGTGRGGGFGYKFADEFHPELQFDKFYLLAMANAGFGTNGSQFFITVGKT
                                                                                                                                                                                 STATLRINHGDIVVNLFADQAPKTVDNFVGLAGGTKEYVDPHTGQPTTGKFYDGLTFHRV
                                                                                                                                                                                                                                  ATATLHTNRGDI KIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV
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                                                                                           IDGFMIQGGCPLGT
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PHLNRRHTIFGEVADEESRRVVDEIAQVRTGRMDRPVEPVVIESVELA
                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                              63.6%; Score 611; DI
69.0%; Pred. No. 1.60
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacteriaceae;
                                                                                      GGPGYRFADEFHPBLTFSKPYLLAMANAGPGTNGSQFFITVAPT
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EADFB1A883EE6546
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Best Local Sim
Matches 109;
                                                                                                              25-OCT-2004 (TREMBLrel. 28, Last sequence update)
25-OCT-2004 (TREMBLrel. 28, Last sequence update)
25-OCT-2004 (TREMBLrel. 28, Last annotation update)
25-OCT-2004 (TREMBLrel. 28, Last annotation update)
Peptidyl-prolyl cis-trans isomerase.
Peptidyl-prolyl cis-trans isomerase.
Name=ppiB; OrderedLocusNames=Lxx00160;
Leifsonia xyli (subsp. xyli).
Leifsonia xyli (subsp. xyli).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitiis.";

Nat. Biotechnol. 21:526-531(2003).

-1- SIMILARITY: Contains 1 PPIase cyclophilin-type domain.

EMBL; BA00030; BAC72041.1; -; Genomic_DNA.

HSSP; Q27450; IASB.

G0; G0:0016853; F:isomerase activity; IEA.

G0; G0:0016853; F:isomerase activity; IEA.

G0; G0:000457; P:protein folding; IEA.

InterPro; IPR001310; CSA-PPIASE.

PFam; PP00100; Pro isomerase; 1.

PRINTS; PR00153; CSA-PPIASE.
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STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed-11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Q6AHM5
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PROSITE; PS50072; CSA_PPIASE_2; 1.
Complete proteome; Isomerase; Rotamase.
Complete proteome; Isomerase; Rotamase.
SEQUENCE 186 AA; 20307 MW; 80BB7CC577A5EE05 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      Q6AHM5_LEIXX PRELIMINARY;
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STRAIN=MA-4680 / AT
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NCBI_TaxID=33903;
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Putative peptidyl-prolyl cis-trans isomerase.
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                                                                                           Microbacteriaceae;
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A Kitajama J.P., Truffi D., do Amaral A.M., Harakava R.,

A de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,

A de Oliveira J.C.F., Mood D., de Oliveira M.C., Miyaki C.Y.,

A Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,

A lmeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,

Perro M.I.T., Gagliardi P.R., Gilylioti E., Goldman M.H.S.,

A Coldman G.H., Kimura B.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,

A Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,

Numes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,

Teai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

A Teai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;

Mol. plant Microbe Interact. 17:827-836 (2004).

L. Mol. plant Microbe Interact. 191827-836 (2004).

EMBL, ABO16822, AAT88120.1; -; Genomic DNA.
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P77949;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8)
(Rotamase B) (Cyclophilin ScCypB) (S-cyclophilin).
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PRINTS; PR00153; CSA.PPISMASE.
PROSITE; PS00170; CSA.PPIASE 1; 1.
PROSITE; PS50072; CSA.PPIASE 2; 1.
Complete proteome; Isomerase; Rotal
SEQUENCE 179 AA; 19233 MW; 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; NCBI_TaxID=1892;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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EMBL, AB016822; AAT88120.1; -; Genomic DNA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0003755; F:peptidy1-proly1 cis-trans isomerase activity;
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006457; CSA_PPIase.
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CATALYTIC ACTIVITY:
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   LOCATION: Cytoplasmic
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                                          Inhibited by
                                                                                                                Peptidylproline
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4204C1783128784F CRC64;
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                                          cyclosporin A (CsA)
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'va R.,
'vi C.Y.,
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Best Local S
Matches 104
                                                                          Hopwood D.A.,
"Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: Contains 1 PP EWBL; AL939118; CAB45223.1; -PIR; T36725; T36725.
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01-NOV-1999 (TREMBLrel. 12, Created)
01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-NOV-1999 (TREMBLrel. 26, Last annotation update)
Putative peptidyl-prolyl cis-trans isomerase.
OrderedLocusNamees-SCO386; ORFNames-SCH69.26c;
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                           MEDLINE-2196410; PubMed=12000953; DOI=10.1038/417141a; MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver T., Howarth S., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=A3(2) / M145;
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PIR; T51359; T51359.
HSSP; P30412; 2RMC.
GO; GO:0016853; P:isomerase activity; IEA.
GO; GO:0003755; P:peptidyl-prolyl cis-trans
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InterPro; IPRO02130; CSA_PPIase.
Pfam; PF00160; Pro isomerase; 1.
PRINTS; PR00153; CSAPPISNEASE.
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Interpro; IPR002130; CSA PPIASE.
Pfam; PF00150; Pro isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; UNKNOWN_1
PROSITE; PS50072; CSA_PPIASE_2; 1.
Complete proteome; ISOmerase; Rotamase.
SEQUENCE 177 AA; 19418 MW; PCF8ADED9C
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Q4NK35;
13-SEP-2005 ('
13-SEP-2005 ('
13-SEP-2005 ('
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Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=ArthDRAFT 3560;
Arthrobacter sp. FB24.
Bacteria; Actinobacteria;
                                                                                                                                                  Larimer F., Land M.;
"Annotation of the draft genome assembly of Arthrobacter Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                           PROSITE; PS50072; CSA_PPIASE_1; PROSITE; PS50072; CSA_PPIASE_2;
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STRAIN=PB24
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EMBL/GenBank/DDBJ whole genome shotgun
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Sequence 12, Appl
Sequence 3345, Ap
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wlegand, Roger C.
APPLICANT: Wlegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Set FILE REFERENCE: 38-10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
VIMBER OF SEQ ID NOS: 16825
SEQ ID NO 13998
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CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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Matches 93
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lynn Dou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13998, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                  LENGTH: 466
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                            ch 42.0%; Score 403.5; DB 2; Similarity 44.5%; Pred. No. 5.1e-36; 93; Conservative 23; Mismatches 42;
3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Pred. No. 1.3e-46;
L2; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences
                                                                                                 Length 466;
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                                                              Indels 51;
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...472;
SEQUENCE DESCRIPTION: SEQ ID NO: 4470:
US-09-107-433-4470
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US-09-107-433-4470
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                                                           Query Match
Best Local S
Matches 93
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                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION UNMER: «Unknown»
SOPTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/107,433
PILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/ 085131
APPLICATION NUMBER: 60/ 085131
PILING DATE: May 12, 1998
APPLICATION NUMBER: 60/55153
PILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-507
TELEPAX: (781)893-8277
                                                           Y Match 42.0%; Score 403.5; DB 2; Local Similarity 44.5%; Pred. No. 5.2e-36; nes 93; Conservative 23; Mismatches 42;
                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 YAVLDVIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
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3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNTNGSQFFIVQNQHLPYSKKEITRGGWPEPIAEIYANQGGTPHLDRRHTVFGQLADEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 472 amino acids
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                                                               Indels
                                                                                               Length 472;
                                                               51;
                                                               Gaps
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US-09-270-767-49073
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US-09-270-767-33856
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                                                                                                                                ; ORGANISM: Drosophila melanogaster US-09-270-767-49073
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US-09-270-767-33856
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33856
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49073
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49073, Application US/09270767 Patent No. 6703491
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Best Local S
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                                                                Query Match
Best Local Similarity
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                                                                                                                                                                          LENGTH: 186
TYPE: PRT
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    18 TLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQG 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHINRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAVLDVIAAVETGAMDKPVEDVVIETIEI 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMIQGGDPTGTGRGGASIYGSEFADELHGDLRHTGAGILSMANSGPDTNGSQFFITLAPT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP----GYKFADBFHPBLQFDKPYLLAMANAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.4%; Score 359; DB 2; Length 186; ilarity 46.9%; Pred. No. 1.2e-31; Conservative 21; Mismatches 45; Indels
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09270767
                                          37.4%; Score 359; DB 2; Length 186;
46.9%; Pred. No. 1.2e-31;
ative 21; Mismatches 45; Indels
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                                            Gaps
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US-09-440-828-1
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS/TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 161
TYPE: PRT
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                                                                SOFTWARE: PERL Program SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09440828 Patent No. 6458575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09136442 Patent No. 6030825
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                                                                                                     CURRENT APPLICATION NUMBER: US/09/440,828
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 09/136,442
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 4
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CURRENT FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Patterson, Chandra
TITLE OF INVENTION: CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS/TRANS ISOMERASE
FILE REFERENCE: PF-0582 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennii
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                  FILE REFERENCE: PF-0582 US
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 2925455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QWLDGKHTIFGRVY--TGMEVVKRIGMVETDKNDRPVDPLRI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMIQGGDPTGTGRGGASIYGSEFADELHGDLRHTGAGILSMANSGPDTNGSQFFITLAPT 138
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44.4%; Pred. No. 1.8e-30;
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US-09-134-001C-3111
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/ OTHER INFORMATION: 2925455
US-09-440-828-1
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                                                                                                                           RESULT 10
US-09-134-000C-3739
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3111
LENGTH: 203
             Sequence 3739, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 81; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR PILING DATE: 1997-11-08

PRIOR PILING DATE: 1997-11-08

PRIOR PILING DATE: 1997-11-08
FILE
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REFERENCE:
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                                                                                                                                                                                                      188
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                                                                                                                                                                                                                                                                                                                                                     MVQGGDPTATGMGGESIYGSAFEDEFSLE-AFNLYGALSMANAGPNTNGSQFFIVQMKEV
                                                                                                                                                                                                      DKPVYDVVIESIDV 201
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ilarity 44.4%;
Conservative 2
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3739
LENGTH: 175
TYPE: PRT
ORGANISM: Enterococcus faecalis
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BANDMAN, OLGA
APPLICANT: LAL, PRESTI
APPLICANT: CORLEY, NEIL C.
APPLICANT: PATTERSON, CHANDRA
APPLICANT: BAUGHM, MARIAH R.
TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS
NUMBER OF SEQUENCES: 4
                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows Version SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 31
                                                                                                                                                                                                                                                                                        COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
TELEFAX:
                  TELEPHONE:
                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:::: |
163 FDVVMDTVEI 172
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3174 Porter Drive
650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                        USA
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                    650-855-0555
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                                                                                                                                                                                                                                  US/09/088,425
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                                                        PF-0529
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INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

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RESULT 13
US-09-999-833A-245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil
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TITLE OF INVENTION: HUMAN PEPTIDYL-PROLYL ISOMERSASES
FILE REFERENCE: PF-0529-1 DIV
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IMMEDIATE SOURCE:
LIBRARY: BRAINONO:
CLONE: 2291164
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6524838 2291164CD1
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Local Similarity 40.8%; Pred. No. 2.8
                                                                                                                                                                                                                                                                               Local Similarity tes 71; Conserv
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                                                                                                                                                                         71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
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                                                                     FFTLGRADELNNKHTIFGKVTGDTVYNMLR-LSEVDIDDDERPHNPHKIKSCEV 166
                                                                                         FITVGKTPHLNRRHTIFGEVIDAESQRVVBAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                              FHRVIQGFMIQGGDPTGTGRGGP---GYKFADBFHPBLQFDKPYLLAMANAGPGTNGSQF 127
                                                                                                                                                                                                                                              PLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAV 70
                                                                                                                                          PHRVVPGFIVQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
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Corley, Neil. C.
Patterson, Chandra
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Pred. No. 2.8e-28;
4; Mismatches 60;
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Sequence 245, Application US/09999833A Patent No. 6916648 GENERAL INFORMATION:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
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PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 2001-07-30
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APPLICANT: Baker Kevin P
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OR FILING DATE: 1998-03-13
OR PILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/078939
                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
                                        APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26
                                                                              APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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Stewart, Timothy A.
Tumas, Daniel
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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f, Ellen
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DR FILING DATE: 1998-03-27
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DR APPLICATION NUMBER: 60/079920
DR FILING DATE: 1998-03-30
DR APPLICATION NUMBER: 60/079923
DR APPLICATION NUMBER: 60/079923
DR APPLICATION NUMBER: 60/080105
DR FILING DATE: 1998-03-30
DR APPLICATION NUMBER: 60/080105
DR APPLICATION NUMBER: 60/080105
DR APPLICATION NUMBER: 60/080107
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R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081955
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-09
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/081070
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71; Conservative
                                                                                                                                         PLATATATLHTNRGDIKIAL FGNHAPKTVAN FVGLAQGTKDYSTQNASGGPSGPFYDGAV
                                             FHRVIQGEMIQGGDPTGTGRGGP---
                                                                                           PPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEA------YYDNTI
                                                                                                                                                                                                              34.7%;
  24;
                                                                                                                                                                                      Score 333.5;
Pred. No. 2.8e
24; Mismatches
                                                                                                                                                                                      i.8e-28;
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114 128

FTTLGRADELNNKHTIFGKVTGDTVYNMLR-LSEVDIDDDERPHNPHKIKSCEV FITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181

Indels Length

Gaps

127 53 70

472; 19;

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US-10-020-445A-245
Sequence 245, Application US/10020445A
Patent No. 6667297
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT FILING DATE: 2001-10-24
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: 60/07/450
OR PILING DATE: 2001-07-30
OR PILING DATE: 2001-07-30
OR PILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06/250
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/06/5311
OR PILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/06/364
OR APPLICATION NUMBER: 60/07/450
OR APPLICATION NUMBER: 60/07/450
OR APPLICATION NUMBER: 60/07/632
OR PILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/07/632
OR APPLICATION NUMBER: 60/07/632
OR PILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/07/632
OR APPLICATION NUMBER: 60/07/632
                                                                                                                                                           DR FILING DATE: 1998-03-13
DR APPLICATION NUMBER: 60/078886
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078936
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078910
DR FILING DATE: 1998-03-20
DR FILING DATE: 1998-03-20
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078939
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
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                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paoni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Napier, Mary A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Na
Filvaroff,
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Sophia S.
                   NUMBER: 60/079664
: 1998-03-27
                                                                                                                         NUMBER:
                                                                                                                                                                                                                                                                                                                                  NUMBER: 60/078004
                                                                               NUMBER:
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                                                          1998-03-26
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f, Ellen
60/079689
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PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079726
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PRIOR APPLICATION NUMBER: 60/081826
PRIOR PILING DATE: 1998-04-22
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PRIOR PILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082706
PRIOR PILING DATE: 1998-04-22
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PRIOR
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APPLICATION NUMBER: 60/085704
PTI-ING DATE: 1998-05-15
COURSEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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114
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                                                                        FHRVIQGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQF
                            PITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
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                                                                                                                                                                                                                                                                                                          NUMBER: 60/085697
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                                                                                                                                                                                                                             34.7%; Score 333.5; DB 2;
40.8%; Pred. No. 2.8e-28;
tive 24; Mismatches 60;
                                                                                                                                                                                                                                                                    Length 472;
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113 127 53 70

Search completed: April 14, Job time: 17.829 secs

2006, 17:37:58

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Sequence 8, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
ITITLE OF INVENTION: No. 5968802e1
NUMBER OF SEQUENCES: 21
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US-08-482-728A-8
                                                                                                                                                                                                                                                                                US-08-482-728A-8
                                                                                                                                                                                                                             Best
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 398-32:
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                              TOPOLOGY: ur
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           LENGTH: 123 amino
TYPE: amino acid
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STATE: California
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106
                                141 HTIFGEVIDAESQRVVEAIS 160
                                                                    46
                                                                                        84 DPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRR 140
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                                                                                                                                                                                                                           Similarity
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                                                                                                                                       GDIHTKLEPVECPKTVENE------CVHSRNG-----YYNGHTEHRIIKGEMIQTG
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Four Embarcadero
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TKGMEVVQRIS
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                                                                                                                                                                                                                          Score 323; DB 1;
Pred. No. 6.5e-28;
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 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 3400
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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388
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   Gapop 10.0 ,
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961
1 MADCDSVTNSPLATATATLH.....ATDGNDRPTDPVVIESITIS
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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US-10-820-246-12
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US-10-167-761-11863
US-10-477-76-994
US-10-477-928-3150
US-10-477-939-168022
US-10-437-963-144839
US-10-437-963-196266
US-10-767-701-61368
US-10-767-701-61368
US-10-767-701-61368
US-10-767-701-61368
US-10-424-599-12566
US-10-424-599-12566
US-10-425-115-237088
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US-10-188-057-327
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US-10-188-057-327
US-10-188-057-257
US-10-501-282-5678
US-10-501-282-5678
US-10-625-115-278418
US-10-028-072-8
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Biocceleration
Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11863, Appl Sequence 594, App Sequence 3150, App Sequence 3150, App Sequence 144839, Sequence 19626, A Sequence 61368, A Sequence 212565, Sequence 237087, App Sequence 237087, App Sequence 327, App Sequence 327, App Sequence 327, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 5678, App Sequence 578418, Sequence 8, Appli
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121 GTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESIT

OY 61 PSGPFYDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADBEHPELQFDKPYLLAMANAGP	MADCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQ 	9 961; DB 3; Length 182; NO. 6e-94; matches 0; Indels 0;	RESULT 1 US-09-791-171-12 US-09-791-171-12 Sequence 12, Application US/09791171 Patent No. US20020094336A1 GENERAL INFORMATION: APPLICANT: NIELSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: ROSENKRANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: FLORIO, Walter TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENT TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENT CURRENT APPLICATION NUMBER: US/09/791,171 CURRENT APPLICATION NUMBER: US/09/791,171 CURRENT APPLICATION NUMBER: 0301-02-20 PRIOR APPLICATION NUMBER: 0376/97 PRIOR FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 0376/97 PRIOR PILING DATE: 1997-04-02 PRIOR APPLICATION NUMBER: 03/044,624 PRIOR PILING DATE: 1997-04-18 PRIOR PILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOFTWARE: PATENTING NUMBER: 60/070,488 PRIOR FILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOFTWARE: PATENTING N	ALIGNMENTS	28 352 36.6 166 4 US-10-121-049-8 Sequence 8, 30 352 36.6 166 4 US-10-123-904-8 Sequence 8, 31 352 36.6 166 4 US-10-140-470-8 Sequence 8, 32 352 36.6 166 4 US-10-176-918-8 Sequence 8, 33 352 36.6 166 4 US-10-176-918-8 Sequence 8, 35 352 36.6 166 4 US-10-176-921-8 Sequence 8, 35 352 36.6 166 4 US-10-176-921-8 Sequence 8, 35 352 36.6 166 4 US-10-140-474-8 Sequence 8, 36 352 36.6 166 4 US-10-142-431-8 Sequence 8, 37 352 36.6 166 4 US-10-142-431-8 Sequence 8, 39 352 36.6 166 4 US-10-142-423-8 Sequence 8, 39 352 36.6 166 4 US-10-142-423-8 Sequence 8, 36 36.6 166 4 US-10-123-262-8 Sequence 8, 36 36.6 166 4 US-10-123-263-8 Sequence 8, 37 352 36.6 166 4 US-10-123-263-8 Sequence 8, 38 352 36.6 166 4 US-10-142-423-8 Sequence 8, 39 352 36.6 166 4 US-10-142-423-8 Sequence 8, 36 36 166 4 US-10-142-353-8 Sequence 8, 36 36 166 4 US-10-143-032-8 Sequence 8, 36 36.6 166 4 US-10-143-032-8 Sequence 8, 36 36.6 166 4 US-10-123-236-8 Sequence 8, 36 36.6 166 4 US-10-123-236-8 Sequence 8, 36 36 166 166 166 166 166 166 166 166 1
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181

182

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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 182
TYPE: PRT
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US-09-804-980-12
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PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILLING DATE: 1998-03-30
PRIOR PELICATION NUMBER: 0376/97
PRIOR PELICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILLING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/070,4624
PRIOR PILLING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thon
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Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 182; Conservative 0; Mismatches
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                                                                                                                                                                                                          APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WILDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
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; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3539
                                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION UNMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR RILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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PRIOR FILLING DATE: 2002-05-02
PRIOR PELLORITION NUMBER: 09/791,171
PRIOR FILLING DATE: 2001-02-20
PRIOR FILLING DATE: 2001-02-20
PRIOR FILLING DATE: 1999-10-08
PRIOR PELLORITION NUMBER: 60/116,673
PRIOR PELLORITION NUMBER: 60/116,673
PRIOR PELLORITION NUMBER: 1281/98
PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILLING DATE: 1999-10-08
PRIOR FILLING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                             SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 3539
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SEQ ID NO 12
LENGTH: 182
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3539, Application US/09738626 Publication No. US20020197605A1
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Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 182; Conservative 0; Mismatches
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                                                                                                                                          PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                         LENGTH: 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
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180 120

180

60

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120

Query Match

74.5%;

Score 716;

DB 3;

Length 187;

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US-10-474-776-694
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEMA, THADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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            Sequence 694, Application US/10474776

Publication No. US20040110181A1

GENERAL INFORMATION:
APPLICANT: Byeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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LENGTH: 186
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SOPTWARE: PatentIn version 3.1
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Local Similarity 65.3%;
hes 109; Conservative 1;
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                                                                                                                                                                                                                                                                                                                                                                               SGEMIQGGDELGNGTGDEGYQEQDEFHEDLREDKEYLLAMANAGEGTNGSQEFITVAETA 125
                                                                                                                                                                                                                                                                                                                           HLNRRHTIFGEVIDAESQRVVEAISKTATD-GNDRFTDFVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                    QGFMIQGGDPTGTGRGGPGYKFADBFHPBLQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS-GPFYDGAVFHRVI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIDGEMIQGGDFTGTGTGGGGGYTFADEFHFELREDRAYLLAMANAGFGTNGSQFFITVTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIQGFMIQGGDPTGTGRGGPGYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATLKTSQGDIAVRLLPNHAPKTVRNFVELATGEREW-TNPATGEKSKDKLYDGTVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPHLNNAHTIFGEVTDAESQKVVDAIATTATDRYDRPADAVVIESVEIT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPHLARRHTIFGEVIDAESQRVVEAISKTATDGNDRFTDFVVIESITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 543.5; DB 4
Pred. No. 1.9e-49;
7; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHIRON SpA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
ITILE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PRO
FILE REFERENCE: P026926WO
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SegWin99, Version 1.03
SEQ ID NO 3150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3150, Application US/10472928 Publication No. US20050020813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 694
LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: cof family protein/peptidyl-prolyl cis-trans isomerase, cyclophi OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15903436 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Streptococcus pneumoniae FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                      y Match 42.4%; Score 407.5; DB
Local Similarity 45.0%; Pred. No. 2e-34;
heb 94; Conservative 23; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                 318 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
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                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                    3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                       YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                            QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                  PGTNGSQFFI----------TVGKTPHLNRRHTIFGEVIDAES 152
                                                                                                                                                                                                                                      GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP---GYKFADBFHPBLQFDKPYLLAMANAG 119
                                                                                                                                                                                                                                                                               DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 407.5; DB Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                          41;
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US-10-617-320-4470
US-10-617-320-4470
; Sequence 4470, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                              ;
IAME/KEY: misc feature
;
LOCATION: (B) LOCATION 1...472
;
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-617-320-4470
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/ 08513:
PILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
PILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/617,320 FILING DATE: 10-Jul-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
442
                                                                             382 PNTNGSQFFIVQNQHLPYSKKEITRGGWPEPIABIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                     120 PGTNGSQFFI----
                                                                                                                                                             324 -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                   153 QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                             283 DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD------
                                                                                                                                                                                    3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
YAVLDVIAAVETGAMDKPVEDVVIETIEI 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                              42.0%;
                                                                                                                                                                                                                                                                                                                         Score 403.5; DB 5
Pred. No. 5.4e-34;
3; Mismatches 42
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                                                                                                                   ----TVGKTPHLNRRHTIFGEVIDAES 152
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                                                                               441
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                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144839
LENGTH: 651
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39256, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Koyalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 39256
LENGTH: 195
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                                            Matches
                                                                  Query Match
Best Local Similarity
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Best Local S
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Sorghum bicolor PEATURE:
                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT4530_45616C.1.pep
                                                                                                                                                                                                      ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 SQFFITTVATPWLDNKHTVFGRVV--KGMDVVQQIEKVKTDKNDKPYQDVKILNVTV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SOFFITVGKTPHLNRRHTIFGEVIDAESORVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNG 124
14 TATATL-----HTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 NLIFHRVIKGFMIQTGDPLGDGTGGQSIWGTEFEDEFHKSLRHDRPFTLSMANAGPNTNG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 TATTSLPDNLVLHTSMGDIHLRLYPEECPKTVENF-----TTHCRNG----YYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 TATAT-----LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
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Similarity 46.3%; Pr
82; Conservative 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbazuk, Brad
                                               Conservative
                                                                  46.3%;
                                               23/
                                            Score 386; DB 4;
Pred. No. 6.1e-32;
3; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 386; DB 4;
Pred. No. 1.2e-32;
3; Mismatches 46
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                                                                                         Length 651;
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                                               Indels
                                               26;
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                                               Gaps
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US-10-424-599-168022
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US-10-437-963-196266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-168022
       APPLICANT: Boxharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 203-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 196266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                        Sequence 196266, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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LENGTH: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION UMBER: 38/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                    APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_12273C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
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                                                                                                                                                                                                                                                                                                                                                                                             QGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLIFHRVIKGFMIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTLSMANAGPNTNG 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVTLHTNLGDIKCEIFCDEVPKTSENFLALC------ASG-----YYDGTIFHRNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAVEHRVIQGEMIQGGDPTGTGRGGP---GYKEADEEHPELQEDKPYLLAMANAGPGTNG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGFMIQGGDPTGTGKGGTSIWGKKFNDEIRESLKHNARGILAMANSGPNTNGSQFFLTYA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu, Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 384; DB 4; Length 160; 
; Pred. No. 1.5e-32; 
22; Mismatches 46; Indels
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US-10-739-930-8097
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US-10-767-701-61368
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Sequence 8097, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
GENERAL INFORMATION: David K.
APPLICANT: KOVALIC, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)8
FULE REFERENCE: 38-21(53377)8
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
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SEQ ID NO 61368
LENGTH: 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT4530_92133C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 39.6%;
Local Similarity 47.3%;
                                                                                                                                                                                                                                                                                                                113
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                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                    76 QGFMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVG 132 :||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVI 75
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                                                                                                                                                                                                                                                                                                                                                                                                              KGFMIQGGDPTGTGKGGTSIWGTKFADEFRESLKHNARGIMSMANSGPNTNGSQFFITYA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVTLHTNLGDIKCEVFCDQVPRTAENFLALC-----ASG-----YYDGTVFHRNI
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47.3%; Pred. No. 2e-32;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 212565
LENGTH: 616
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clome ID: PAT_MRT3847_33973C.1.pep
US-10-424-599-212565
Search completed: April 14, 2006, 18:40:38 Job time: 64.9683 secs
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US-10-424-599-212565
; Sequence 212565, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(639)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C38338_1.p
US-10-739-930-8097
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SEQ ID NO 8097
LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.5%; Score 380; DB 4; Length 616; Best Local Similarity 46.4%; Pred. No. 2.5e-31; Matches 83; Conservative 21; Mismatches 53; Indels
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                                                                                                                                 123 NGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVZAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                 497 YDNLIFHRVIKGFMIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTVSMANAGPNT
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                                                                                                                                                                                                                             66 YDGAVFHRVIQGFMIQGGDFTGTGRGGF---GYKFADEFFFELQFDKFYLLAMANAGFGT 122
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                                                                                                ID NOS: 11088
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration
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Sequence 3153, App
Sequence 21481, A
Sequence 21481, A
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Sequence 3154, A
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Sequence 414, App
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Sequence 426, App	•	Sequence 317, App	•	Sequence 306, App	Sequence 21248, A	Sequence 21249, A	Sequence 21250, A	•	Sequence 879, App	•	Sequence 314, App	Sequence 323, App	•	•	•		•	Sequence 44, Appl	Sequence 302, App

ALIGNMENTS

# APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maurean APPLICANT: Beresini, Maurean APPLICANT: Desnoyers, Luc APPLICANT: Desnoyers, Luc APPLICANT: Desnoyers, Luc APPLICANT: Desnoyers, Luc APPLICANT: Desnoyers, Luc APPLICANT: Gao, Mei-Qiang APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Georetiesen, Mary E. APPLICANT: Sherwood, Steven APPLICANT: Sherwood, Miliam APPLICANT: Machanbe, Colin K APPLICANT: Mood, Mililiam APPLICANT: Mililiam APPLICANT: Mood, Mililiam APPLICANT: Mililiam APPLICANT: Mood, Milil RESULT 1 US-10-131-826A-8 GENERAL INFORMATION Sequence 8, Application US/10131826A Publication No. US20050245730A1

Application data removed - See File Wrapper or PALM

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APPLICANT: PURUKAWA, YUSUKE
APPLICANT: PURUKAWA, YOSCHI
APPLICANT: PURUKAWA, YOSCHI
APPLICANT: The University of Tokyo
TITLE OF INVENTION: Genes and Polypeptides Rel.
TITLE OF INVENTION: Colorectal Carcinoma
FILE REFERENCE: 082379-000400US
CURRENT APPLICATION NUMBER: US/10/517,151
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/386,985
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 111
SOSTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 166
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ORGANISM: Homo Sapien
                                                                              US-10-973-115B-8
                                                                                                    RESULT 3
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                 Sequence 8, Application US/10973115B Publication No. US20060040351A1 GENERAL INFORMATION:
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10517151 Publication No. US20060019252A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                              136 HLWRRHTIFGEVIDAESQRVVBAISKTATDGNDRPTDPVVI 176
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                                                                                                                                                                   121 WLDGKHTIFGRV--CQGIGMVNRVGMVETNSQDRPVDDVKI 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%; Score 352; DB 6; Length 166; llarity 46.6%; Pred. No. 2.5e-28; Conservative 20; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.6%; Score 352; DB 6; llarity 46.6%; Pred. No. 2.5e-28; Conservative 20; Mismatches 46
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APPLICANT:

Gerritsen, Mary E. Goddard, Audrey

APPLICANT

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Sequence 8, Application US/11290153
Publication No. US20060073568A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForger, Laura
APPLICANT: DeForger, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Pilvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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US-11-290-153-8
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CURRENT PILING DATE: 2004-10-22
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2002-05-14
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 1909-05-25
PRIOR APPLICATION NUMBER: US 60/123,090
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
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PRIOR PILING DATE: 1999-05-25
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LENGTH: 166
TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desnoyers, Luc
Filvaroff, Ellen
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DeForge, Laura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.6%; Score 352; DB 6; llarity 46.6%; Pred. No. 2.5e-28; Conservative 20; Mismatches 46
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                                      APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGOR, MURRAY ROBER
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: LUND, STEVEN TROY
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MODRZYCKI, BOB
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PRIOR FILING DATE: 2002-05-15
PRIOR PELICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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Best Local S
Matches 75
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Publication No. US20060010516A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
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APPLICANT:
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APPLICANT:
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P3330R1C321
CURRENT APPLICATION NUMBER: US/11/290,153
CURRENT FILING DATE: 2005-11-30
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ORGANISM: Homo Sapien
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FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
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FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                           121 WLDGKHTIFGRV--CQGIGMVNRVGMVETNSQDRPVDDVKI
                                                                                                                                                                                                                                                                                                                                                                                                                 136 HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
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T: KODRZYCKI, BOB
INVENTION: CELL CYCLE GENES AND RELATED METHODS
ERENCE: 044463-0360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 36.6%; Score 352; DB 7; Length 166; Similarity 46.6%; Pred. No. 2.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIQGGDPTGTGRGGP---GYKFADEFHPBLQFDKPYLLAMANAGFGTNGSQFFITVGKTP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETSMGI I VLELYWKHAPKTCKNFAELAR-----RGYYNGTKFHR I I KDF
                                                                                                         CONNETT, MARIE B.
EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, William
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RESULT 7
US-11-024-959-435
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US-11-096-568A-21480
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 310
ILEMACH.
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21480
LENGTH: 164
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CURRENT FILING DATE: 2004-12-30
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PRIOR FILING DATE: 2003-12-30
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)..(164)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Zea mays subsp. FEATURE:
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                                                                                                           131 VGKTPHLNRRHTIFGEVIDABSORVVEAISKTATDGNDRPTDPVVI 176
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                                                                                                                                                54 IIKDFIVQGGDFTGTGRGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFIT 113
                                                                                                                                                                          74 VIQGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFIT 130
                                                                                                                                                                                                                                                          14 TATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHR 73
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                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                          LAPCQSLDGKHTIFGRV--CRGMEIVKRLGSVQTDKNDRPIHEVKI
                                                                                                                                                                                                                             TPEVTLETSMGAVSVEMYYRHAPKTCRNFVELAR------RGYYDNVIFHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIVQGGDPTGTGRGGESIYGKKFEDEIKPELKHTGAGILSMANAGPNTNGSQFFITLAPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLETSMGSFTVELYFKHAPRTSRNFIELSR------RGYYDNVKFHRIIKD
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                                                                                                                                                                                                                                                                                                   Score 347; DB 7;
Pred. No. 7.9e-28;
Pred. No. 7.9e-28;
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Pred. No. 6.2e-28;
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Sequence 435, Applic Publication No. US20 GENERAL INFORMATION:

Application US/11024959 5. US20060010516A1

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SEQ ID NO 435
LENGTH: 163
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Best Local 9
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APPLICANT:
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430R10312 CURRENT APPLICATION NUMBER: US/10/194,487 CURRENT FILLING DATE: 2002-07-12
                                                                                                                                                                    PRIOR
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR PILING DATE: 2003-12-30
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TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
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                                                                                                                       APPLICATION NUMBER: 60/059266
FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/062250
                                                                               APPLICATION NUMBER: 60/063120
                                                                                                   FILING DATE: 1997-10-17
                   FILING DATE:
                                       APPLICATION NUMBER: 60/063121
                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LAPTPWLDEKHTIFGRV--CKGMDVVKRLGNVQTDKNDRPIHDVKILRTTV 161
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EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
LUND, STEVEN TROY
MAGUSIN, ANDREAS
KODRZYCKI, BOB
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Godowski, Paul J.
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                      1997-10-24
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60/063486
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; Prior Application removed - St; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 98; LENGTH: 472; TYPE: PRT; ORGANISM: Homo Sapien
US-10-195-883-98
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PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
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Matches
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Best Local Similarity 40.8
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/195,883

CURRENT FILING DATE: 2002-07-15
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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ORGANISM: Homo Sapien
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5<u>4</u>
                                    71 FHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQF 127
                                                                                                                                                                                                   11 PLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAV 70
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                                                                                                                                      PPTNGKVLLKTTAGDIDIBLWSKBAPKACRNFIQLCLEA--
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PHRVVPGFIVQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                             34.7%;
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                                                                                                                                                                                                                                                                     ; Score 333.5; DB 6;
; Pred. No. 7.4e-26;
24; Mismatches 60;
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Pred. No. 7.4e-26;
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FITVGKTPHLNRRHTIFGEVIDABSQRVVEAISKTATDGNDRPTDPVVIESITI

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; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 98; LENGTH: 472; TYPE: PRT; ORGANISM: Homo Sapien
US-10-195-888-98
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US-10-195-888-98
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
                  APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C329
CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430R1C324
CURRENT APPLICATION NUMBER: US/10/195,888
CURRENT FILING DATE: 2002-07-15
                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                               Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHRVVPGFIVQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
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                                                                                                                                                                                                                                                                               Desnoyers, Luc
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Smith, Victoria
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Goddard, Audrey
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ilarity 40.8%;
Conservative 2
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Pred. No. 7.4e-26;
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; Sequence 442, Application US/1102495
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
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                                                                                                                                                       RESULT 13
US-11-024-959-442
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US-11-096-568A-33153
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TITLE OF INVENTION: Sequence-Determined DNJ
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 33153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 164
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (164)
OTHER INFORMATION: Ceres Seq. ID no. 13
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                                                                                                                                                                                                                                                                                                               PIVOGGDPTGTGRGGESIYGSKPEDEINKELKHTGAGILSMANAGPNTNGSQFFITLAPQ 117
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                                                                                                                   Application US/11024959
o. US20060010516A1
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40.8%; Pred. No. 7.4e-26;
tive 24; Mismatches 60;
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US-11-096-568A-21481
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; ORGANISM: Pinus radiata
US-11-024-959-442
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Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21481
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21481, Application US/11096568A Philication No. US20060048240A1 GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOPTWARE: Patentin version 3.3
SEQ ID NO 442
                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                       Matches
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KNY: misc_feature
LOCATION: (1)..(147)
OTHER INFORMATION: Ceres Seq. ID no. 12404719
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                                                                                                                                                                                                                                   Local
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Local Similarity 48.4%;
 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 DDKHVVFGEVIKGKS--IVRAIENYPTASGDVPTSPIIISA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 NRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIES 178
                                  141 HTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
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                                                                                                         84 DPTGTGRGGP---GYKFADSFHPSLQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRR 140
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                                                                                                                                                                                 24 GDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGFMIQGG
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                                                                                                                                                                                                                     69;
                                                                                                                                               N
                                                                                                                                                                                                                                         Similarity
HTIFGRV--CRGMEIVKRLGSVQTDKNDRPIHEVKI 140
                                                                      DPTGTGRGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFITLAPCQSLDGK 106
                                                                                                                                               GAVSVEMYYRHAPKTCRNFVELAR-------RGYYDNVIFHRIIKDFIVQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGDPT-GTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHL
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Pred. No. 3.6e-26;
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Pred. No. 7.7e-26;
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; OTHER INFORMATION: Ceres Seq. ID no.
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Matches
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APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21482
LENGTH: 140
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays subsp.
FEATURE:
106
                                        147 VIDAESQRVVEAISKTATDGNDRPTDPVVI 176
                                                                                                                                                                                                                                                        68;
                                                                                  46 RGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFITLAPCQSLDGKHTIFGR
                                                                                                                  90 RGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRRHTIFGE 146
                                                                                                                                                                                                  30 LFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGFMIQGGDPTGTG
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                                                                                                                                                                       1 MYYRHAPKTCRNFVELAR-------RGYYDNVIFHRIIKDFIVQGGDPTGTG
V--CRGMEIVKRLGSVQTDKNDRPIHEVKI
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Pred. No. 2.7e-25;
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Search completed: April 14, Job time: 7.79883 secs 2006, 18:42:15

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Pred. No. is the score greater the and is derived be the number of results predicted by chance to have a r than or equal to the score of the result being printed, ed by analysis of the total score distribution.

Result No.	Score	Query Match	Length	BB	ID	Description
1	1348	100.0	265	2	AAW72891	Aaw72891 Mycobacte
2	1348	100.0	265	N	AAY21908	
ω	147	10.9	287	9	ABM95900	
4.	108	8.0	1574	σ	AAE37002	Mic
<sub>5</sub>	103	7.6	8805	4	ABB67112	Abb67112 Drosophil
თ	100	7.4	19	N	AAW72898	
7	100	7.4	19	N	AAY21915	Aay21915 N-termina
œ	99.5	7.4	755	ហ	ABB91978	Abb91978 Herbicida
9	96	7.1	565	œ	ADN26519	Adn26519 Bacterial
10	96	7.1	579	æ	ADN26762	Adn26762 Bacterial
11	96	7.1	614	œ	ADS28471	Ads28471 Bacterial
12	96	7.1	621	4.	ABB66212	Abb66212 Drosophil
13	95	7.0	4038	4	ABG99871	Abg99871 S. cinnam
14	94.5	7.0	853	ω	AAB26917	Aab26917 Large sub
15	94.5	7.0	853	7	ABU62618	Abu62618 Pseudomon
16	93.5	6.9	269	7	AB071472	Abo71472 Pseudomon
17	92.5	6.9	583	œ	ADJ49538	Adj49538 Oil-assoc
18	92	6.8	728	æ	ADX92106	Adx92106 Plant ful
19	91.5	6.8	2194	4	AAM40114	Aam40114 Human pol
20	91	6.8	381	7	AB061838	
21	91	6.8	383	w	AAG29504	Aag29504 Arabidops
22	91	6.8	441	7	ADM26564	
23	91	6.8	442	4	ABU52687	-
24	91	6.8	469	w	AAG29503	Aag29503 Arabidops

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 140; 163pp; English.

WPI; 1998-542705/46. N-PSDB; AAV63922.

Oettinger Andersen P,

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Rosenkrands I,

Weldingh'K,

Rasmussen

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6.6	6.6	6.6	6.6	6.6	6.6	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7		6.8	
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Aau98656	Aau97744	Abp66019	Adn24843	Adn22084	Abo84045	Abj18816	Abu38650	Aau36373	Abo71541	Ads27020	Ads26629	Ads26263	Abu43515	Abg24318	Ads29018	Adr24079	Adr24082	Abu24332	Adt59335	Adn72195
Mycobacte	Mycobacte	Bifidobac	Bacterial	Bacterial	Pseudomon	Pseudomon	Protein e	Pseudomon	Pseudomon	Bacterial	Bacterial	Bacterial	Protein e	Novel hum	Bacterial	Pyrococcu	Pyrococcu	Protein e	Plant pol	Thale cre

#### ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
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                                                                                                                                                                                   WO9844119-A1
                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                               Mycobacterium tuberculosis; antigen; vaccine;
                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen CFP29.
                                                                                                                                                                                                                                       21-JAN-1999
                                                                                                                                                                                                                                                  AAW72891;
                                                                                                                                                                                                                                                              AAW72891 standard; protein; 265 AA.
                                                                                                                                                                                                          infection.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                              97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                97DK-00000376.
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RESULT 2
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ID ANY2
XX ANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1997;
05-JAN-1998;
01-APR-1998;
The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of antigen CFP29.
                                                                                                                                                                                                                                         New immunogenic fragment of Mycobacterium
                                                                                                                                                                                                                                                                                                                        WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP3OA; pharmaceutical; vaccination; M. africanum; M. bovis; CFP16; CFP23; CFP7B; CFP19; CFP23;
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98US-0070488P.
98WO-DK000132.
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                                                                                                                                                                                   60-61; 265pp; English
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Pred. No. 2.3e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second CC different amino acid sequence from M. tuberculosis, and/or including a CC sequence which protects the first amino acid sequence from in vivo CC degradation or post-translational processing; (3) a nucleic acid fragment CC that encodes the above polypeptides. The polypeptides and nucleic acid care useful as pharmaceuticals, for diagnosis of and as antigens for CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or CC povis. The polypeptides are also useful for diagnosing ongoing or CC previous sensitization in an animal with bacteria belonging to the CC tuberculosis complex. The invention also describes the use of CFP7A or CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for the in a mammal by performing a DTH type skin CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin CC tuse of CFP27, CFP30A, CFP16, CFP19, CFP23, CFP23B, CFP79 or AT-CC cell epitope of for the preparation of an immunological composition; and CC for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                        Matches 265;
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Best Local
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                       TERLYLQETLTFLCYTAEASVALSH
                                                                             VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD
                                                                                                    VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD
                                                                                                                                                             EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK
                                                                                                                                                                                      EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK
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                                                                                                                                                                                                                                                                    PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVBRGSKDSDWBPVKEAAKKLAFVEDRTIF
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100.0%; Pred. No. 2.3e-130;
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ID ABM9
XX ABM9
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XX 10-0
XX (MON
XX WPI;
XX WPI;
                                                                                                                                                           Transgenic plant; DNA replication; gene regulation; gene expression
                                                                                                                                                                            M. xanthus protein sequence, seq id 15099.
                                                                                                                                                                                                02-JUN-2005
                                                                                                                                                                                                                 ABM95900;
                                                                                                                                                                                                                                    ABM95900 standard;
                                                                                                                                         Myxococcus xanthus.
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                    protein;
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WPI; 2005-028716/03 Goldman BS, Hinkle GJ, 10-JUL-2000;

2000US-0217883P.

(MONS)

MONSANTO TECHNOLOGY LLC.

Slater SC,

Wiegand

RC;

10-JUL-2001; 2001US-00902540

21-DEC-2004. US6833447-B1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDS 9692-16825 represent a group of 71314 Mayococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                            23-OCT-2003
07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression identifying mutations in a gene of interest, and for constructing
   WPI; 2003-343556/33
                                                                                    26-JUL-2001; 2001US-0307629P.
                                                                                                                 26-JUL-2002; 2002CA-02391131
                                                                                                                                              19-NOV-2002
                                                                                                                                                                                                      Micromonospora
                                                                                                                                                                                                                                    Macrolide;
                                                                                                                                                                                                                                                              Micromonospora carbonacea polyketide synthase (PKS) type I
                                                                                                                                                                                                                                                                                                                                        AAE37002;
                                                                                                                                                                                                                                                                                                                                                                AAE37002 standard; protein; 1574 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 287
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                                                         ECOPIA BIOSCIENCES INC
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                           Staffa A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KAPTNGVIAHLRASKPLVRLRVPPTLSRNEIDDVERGSKDSDWEPVKEAAKKLAPVEDR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEQETAMVFTDARKFKTIPIIYKDFLLHWRDIEAARTHNMPLDVSAAAGAAALCAQQEDE
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                                                                                                                                                                                                                                 rosaramicin; polyketide; polyketide synthase; PKS; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
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                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                       carbonacea.
                              Parnet CM
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Pred. No. 4e-06;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reactions, in vitro or in vivo, to direct or enhance the synthesis or modification of polyketide, polyketide substrate or its precursor. The present sequence is M. carbonacca polyketide synthase (PKS) type I protein. (Updated on 2-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to genes and proteins involved in the biosynth of macrolides by microorganisms. In particular it relates to the nuc acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Micromonospora carbonacea. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 158-163; 206pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide involved in biosynthesis of macrolides by microorganisms, useful for biosynthesis of macrolides by microorganisms, preferably for biosynthesis of rosaramicin.
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                                                                                                        DGDIIWAPAIDGAFV-----LTTRGGDFDLQL-----GTDV-----AIGYASHDTDTBR
                                                                                                                                                                             LTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIREHLNRLV 199
                                                                                                                                                                                                              GAAGSPPLDRVDVLQPVSWAVMVSLAQVWRSLGVEPDAVV-
                                                                                                                                                                                                                                                                                                                       LIDVKAPTN------GVIAHLRASKPLV---RLRVPFTLSRN---EIDDVER
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L-RABLLTVL
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                                                                                                                                           LTLPDAARVVA-LRSQVIGRV-LSGRGGMASVQL-----
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ABB67112 standard; protein; 8805
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ABB67112

26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 28128

Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001.

23-MAR-2001; 2001WO-US009231.

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11-JUL-2000; 2000US-00614150.
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10-NOV-1997; 05-JAN-1998; 01-APR-1998;

97DK-00001277. 98US-0070488P. 98WO-DK000132. 20-MAY-1999. 08-OCT-1998;

98WO-DK000438

WPI; 1999-347282/29

Andersen P,

Skjot R;

(STAT-) STATENS SERUM

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Best
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18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                               tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; T pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A CFP7B; CFP10A; CFP10A; CFP10A; CFP19; CFP23;
                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Mycobacterium tuberculosis N-terminal peptide. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                 N-terminal sequence of antigen
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                                                                                                                                                                                        AAY21915;
                                                                                                                                                                                                                    AAY21915 standard;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 144; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersen P,
Oettinger T,
WO9924577-A1
                         Mycobacterium
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                                                                                                        Immunogenic; Mycobacterium tuberculosis;
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97US-0044624P.
97DK-00001277.
98US-0070488P.
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                                                    CFP7B.
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                                                                                                          immune response; infection;
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7A; CFP30A;
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immunogenic fragment of Mycobacterium tuberculosis

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Best Local
                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                     (FARB )
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                                                                                                                                                                                                                                                                                                                              Weidler
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100.0%; Pr
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Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 755
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CFHTRRVMYGLSLDDLGDDGSLSSIA----TRKYLABESLT
                              VLTTRGGDFDL---QLGTDVAIGYASHDTDTERLYLQETLT
                                                                                                                                   VGDEKEVPHVVYISREKRPNHFHHYKAGAMNFLVRVSGLMTNAPYMLNVDCDMYVNEADV
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                                                                 VRQAMCIFLQKSMDSNHCAFVQYPQDFYDSNVGBLTVLQLYLGRGIAG
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20.8%; Pred. No. 1
                                                                                     SDH----GYP-----IREHLNRLVDGDIIWAPAIDGAF
                                                                                                                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                                                                                                                                                                                112;
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                                                                   --IQGPQYAGSG
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nitrogen;
bacterial
                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                     Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial polypeptide #9172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN26519 standard;
(HINK/)
                                                                                        21-FEB-2002; 2002US-0360039P
                                                                                                                                  20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                         US2003233675-A1
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                                            (CAOY/) CAO Y
HINKLE
SLATER
                                                                                                                                                                                                                                                                                                                phosphorus; photosynthesis;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
  ທຸດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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                                                                                                                                                                                                                                                                                                                                       lignin; galactomannan,
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Claim 5; SEQ ID

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1189; 261pp + Sequence Listing; English

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RESULT 10
ADN26762
ID ADN26
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AC ADN26
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AC ADN26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc microbial source: The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cc transformed plant taxing an improved property. The plant is a crop plant cc transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transforming plant with the cc recombinant DNA construct is useful for improving plant with the cc improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, cc increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate of content, improved yield by modification of carbohydrate, nitrogen or cc phosphorus use and/or uptake, by modification of carbohydrate, nitrogen or cc phosphorus use and/or uptake, by modification of photosynthesis or by cc providing improved plant growth and development under at least one stress condition, improved plant production or improved galactomannan cc production. Note: The sequence expressed in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic forms after the sequence represents and the content of the printed specification but was obtained in electronic complete. The sequence can be content to the printed specification but was obtained in electronic complete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                      02-DEC-2004
                                                            ADN26762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 9172; 122pp; English.
                                                                                                   ADN26762 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
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(GOLD/) GOLDMAN B
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                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ention relates to a recombinant DNA construct comprising a r functional in a plant cell, where the promoter is positioned for expression of a polynucleotide encoding a polypeptide from
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                                                                                                                                                                                                                                          DLQLGTDVAIGYASHDTDTERL
                                                                                                                                                                                                                                                                                                                         TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF------VLTTRGGDF
                                                                                                                                                                                                                                                                                                                                                              ATMPPQIRRI-----AQTYLQDPIB----VTIATKTTTAANIRQRYWWVSGLHKLDAL
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                      (first entry)
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                                                                                                                                                                                                       ----AARGLDVERI 315
                                                                                                   protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
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                                                                                                     579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111;
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63 NGVIAHL-RASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFE

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                                                                                                                                                                 The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant to the combinant DNA construct and growing the transformed plant, where the CC recombinant DNA construct is useful for improving plant with the CC recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant, where the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, pathogens or pests, content, improved yield by modification of carbohydrate, nitrogen or CC content, improved yield by modification of carbohydrate, nitrogen or CC providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan CC growth intended specification or improved galactomannan CC growth intended specification but was obtained in electronic CC form part of the printed specification but was obtained in electronic CC format from USPTO at segdata.uspto.gov/sequence.html.
                                                                         Matches
                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAOY/)
(HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-061375/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; SEQ ID
                                     æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
HINKLE G J
SLATER S C
CHEN X.
GOLDMAN B
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinkle
phosphorus; photosynthesis; lignin; galactomannan; polypeptide.
                                                                       7.1%;
llarity 26.0%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater
                                                                     31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC,
                                                                       Score 96; DB
Pred. No. 2.2;
31; Mismatches
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                                                                           Indels
                                                                           52;
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The invention relates to a recombinant DNA construct comprising a compromer functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitrogen;
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HINK/)
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polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                     New isolated nucleic a
                                                              N-PSDB;
                                                                                                   Venter JC,
                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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2000US-00614150
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                                                                                                     PWD,
                     detection reagent for detecting for elucidating cell signaling a
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                                                                                                     Myers
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 New DNA sequence encoding polyketide synthase, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                   S. cinnamonensis MonAIV/polyketide synthase multi-enzyme MONS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 621 AA;
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                                                                                                                                                                                                                                                                                                        Streptomyces cinnamonensis
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                                                   WPI; 2001-611393/70
                                                                                                                                                             28-MAY-1999;
                                                                                                                                                                                               30-MAY-2000; 2000WO-GB002072
                                                                                                                                                                                                                                                                                                                                                                               insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                Monensin;
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                                                                                                                                                                                                                                                                                                                                             BI; mon
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                                                                                         PF,
                                                                                                                          BIOTICA TECHNOLOGY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEIELEAARTFKRHIA------GRRVVDVSDPGGP-----VTAAVSTGRLIDVKAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGDLILEVETEKKAHAVLKYREHESQQEKI 363
                                                                                                                                                                                                                                                                                                                                                          gene cluster; polyketide synthase; antibiotic; antihelminthic;
de; immunosuppressant; antifungal; antibacterial; polyether;
on BII; mon CI; mon CII; mon H; mon RI; mon RII; mon T; mon AIX
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                                                                                         Oliynyk M;
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of polyketides such as antibiotic monensin

CC cluster (and is capable of expressing a corresponding polypeptide), a condition probe derived from the gene cluster (for identification and condition of the same or analogous gene cluster, e.g. one which binds specifically to a region of the monensin gene cluster selected from mon condition and condition a The invention relates to a DNA sequence which is a fully defined sequence of 103551 base pairs appearing as ABX04971, or its variant, that it is not a sequence encoding all or part amino acids 1-920 encoded by mon AI as given in the specification. The DNA is the S. cinnamonensis polyketide antibiotic momensin biosynthetic gene cluster. Also included are a recombinant cloning or expression vector comprising the gene cluster, a transformed host cell which has been transformed to contain the gene Sequence 4038 AA; monensin gene cluster

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Best Local
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                                                                                                                                                                                                                         1176 LLPPTDAEQVWLPFAWNDVALHAVRATTVRVRLTPLGERI----DQGLRITVADAVG---
                                                                                                                                                 1229 ---APVL-TVRDLR-SRPTDTGRLAAAATRD-----RHGLFDLEWIAPENAAENAA----
                                    177
                                                                                                                                                                                                                                                                                                 60;
                                                                                                                                                                                    57 DVKAPTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVED
                                                                                                                                                                                                                                                            8 LAPVTEA-----AWABIBLEAARTFKRHI----AGRRVVDVSDPGGPVTAAVSTGRLI
                                                                                                                                                                                                                                                                                                                  Similarity
V---EPDRTDDGLALATHVLDLVQ---TWLASPLHDSRLVLVTRGAVTDADV--DVA
                                VYTKVSETSDHGYPIREHLMRLVDGDIIW--APAIDGAFVLTTRGGDFDLQLGTDVA 231
                                                                                                          RTIFEGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSAD
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                  7.0%;
                                                                           -GPARDASEGWVTLGEDAASLADLLASV----EAGAPAPQ--LVAAP 1314
                                                                                                                                                                                                                                                                                                 29,
                                                                                                                                                                                                                                                                                               Score 95; DB 4; Length 4038; Pred. No. 57; 9; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                  Gaps
   1363
                                                                                                                                                     1274
                                                                                                                                                                                                                             1228
                                                                                                                                                                                                                                                                56
                                                                                                                176
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## RESULT 14 AAB26917

S

AAB26917 standard; protein; 853

#### SXAXEXBXBXXXX AAB26917;

12-JAN-2001 (first entry)

Large subunit of periplasmic nitrate reductase NapA

NapA; toxic periplasmic nitrate reductase; enzyme; transgenic organism; waste denitrification; denitrifying bacteria. denitrifying bacteria.

Pseudomonas sp.

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                                                                                                                                                                                                                                                                           Periplasmic nitrate reductase subunit; enzyme; NapA; NapB; NapC; denitrification; water purification; industrial waste purification; denitrifying bacteria; nitric oxide reductase subunit; NorB; NorC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2003
02-SEP-2003
                                       06-AUG-2002
                                                                                                        US6429003-B1
                                                                                                                                                                         Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU62618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU62618 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 853 AA;
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Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunits. Also included are a chimaeric gene comprising the Nap nucleic acid linked to regulatory sequences, a transformed cell comprising the chimaeric gene and a nucleic acid fragment encoding an enzymatically active bacterial periphaemic nitrate reductase subunit, obtained by probing a library with the Nap nucleic acid and sequencing the isolated clone. The Nap nucleic acid is useful for producing enzymes useful in denitrifying reactions (for water purification and industrial waste purifying) and for identifying other denitrifying bacteria. Also disclosed are the nucleic acid and protein sequences for the nitric oxide reductase subunit genes NorB, NorC, NorQ and NorD. The present sequence represents the NapA protein. Note: The present sequence is stated to be encoded by the DNA appearing as ACD26043 but is not encoded by it.

(Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid fragment encoding enzymatically active bacterial periplasmic nitrate reductase subunit periplasmic periplasmic page and NapC pseudomonas sp. strain G-179, which comprises NapA, NapB and NapC subunits. Also included are a chimaeric gene comprising the Nap nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 35-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Pseudomonas bacterial periplasmic nitrate reductase subunit nucleic acid, for producing enzymes used in water purification.
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                                                                                                                                                                                                                                                                                                                                                       RLRVPFTLSRNEIDDVERGSKDSDWEPV-----KEAAKKLAFVEDR------
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### ALIGNMENTS

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RESULT 1

E70520

hypothetical protein Rv0798c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: E70520

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 밁 δ 밁 5 문 S 문 S A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-265 <COL> A;Cross-references: UNIPROT:007181; UNIPARC:UPI00000D5E0 A;Experimental source: strain H37Rv A;Gene: A; Accession: Query Match Best Local Simi Matches 264; Genetics: Rv0798c 241 181 181 121 121 13 61 -,\_ Similarity TERLYLQETLIFICYTAEASVALSH 265 VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180 PTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVERGSKDSDWEPVKGAAKKLAFVEDRTIF 120 MNNLYRDLAPVTEAAWABIBLEAARTFKRHIAGBRVVDVSDPGGPVTAAVSTGRLIDVKA 60 EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180 PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF MNNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA Conservative 99.5%; Score 1341; DB: Pred. No. 2e-98; 0; Mismatches UNIPARC: UPI00000D5E0F; GB:Z96797; GB:AL123456; NID 2 ۲, Length Indels translation not shown 265; 0 Gaps

sensor histidine k hypothetical prote hydroxymethylbilan hypothetical prote

RESULT 2

B72333
bacteriocin - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

241

240

240

120

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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and A;Title: Evidence for lateral gene transfer between Archaea and A;Accession: B7233
A;Accession: B7233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <ARN>
A;Residues: 1-262 <ARN>
A;Cross-references: UNIPROT:Q9WZP2; UNIPARC:UPI00000D7358; GB:AE
A;Experimental source: strain MSB8
C;Genetics:
A;Genetics:
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young
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R; Nelson, K.E.; Clayton, R.A.;
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A; Residues: 1-281 <AQF>
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A;Status: prelimina
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                                                                                                                                                                                                                                          A;Gene: aq_1760
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                   GVCEVKPGQEYKVCEPVRTGERKHV----PVPTLYKDFVISWRDLEHWRQFNLPVDTTGV
                                                    VTAAVSTGRLIDVKAPT-NGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKDSDWBPV 104
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son, D.;
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A; Residues: 1-492 < BO
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 201
                                       191
                                                                            148
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                                                                                                                                                                                                                                                                                                                                         76;
                                                                                                                                                                                                                            66 IAHLRAS-----
                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                    13 EAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDV-----KAPTNGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-492 <BOR>
                                       RVLTVGGGFIS-VEFAGIFNAYKPKDGQVTLCYRGEM---ILRGFDH--TLREELTKQLT
                                                                        EIPDVISQALSELRLAGV------DGPYSVLLSADVYTKVSETSDHGYPIREHLNRLVD
                                                                                                               SKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNIPGIEHCISSNEAFYLPEPPR
                                                                                                                                                    DS-DWEPVKEAAKKLAFVEDRTIFEGYSAAS-----IEGIRSA-SSNPALTLPEDPR 147
GDIIWA----PA----IDGAFVLTTRGG---DFDLQLGTDVAIGYASHDTDTB
                                                                                                                                                                                         MEHLRESAGFGWEFDRTTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSL
                                                                                                                                                                                                                                                                   EAAW-----NAATLYKKRVA---VIDVQMVHGPPFFSALGGTCVNVGCVPKKLMVTGAQY
                                                                                                                                                                                                                                                                                                                                           Conservative
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41;

Mismatches

96; Indels

82;

Gaps

18,

--KPLVRLRVPFTLSRNE-IDDVER---

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97

70 65

130

190

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A;Molecule type: DNA
A;Residues: 1-94, 'K',96-111,'E',113-155,'N',157-352,'N',354-401,'NI',404-440,'V',442-49
A;Residues: 1-94,'K',96-111,'E',113-155,'N',157-352,'N',354-401,'NI',404-440,'V',442-49
A;Crose-references: UNIPARC:UPI00001378PB; EMBL:M38051; NID:9162316; PIN:AAA63547.1; P
C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
C;Keywords: NADP; oxidoreductase; redox-active disulfide
F;9-468/Domain: dihydrolipoamide dehydrogenase homology
F;53-58/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                     A; Title: Cloning, sequencing, overproduction and purification A; Reference number: S30204; MUID:91187059; PMID:2011150 A; Accession: S30204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Borges, A.; Fairlamb, A. submitted to the EMBL Data Library, June 1992
A;Description: Mutagenesis of the redox-active cysteines in the trypanothione reductase
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A;Title: Site-directed mutagenesis of the redox-active cysteines
A;Reference number: S68968; MUID:95255281; PMID:7737173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Trypanosoma cruzi
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S68968; S24243; S30204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: I-111,'E',113-139,'A',141-155,'N',157-492
A;Cross-references: UNIPARC:UP100001720C2; EMBL:Z13958
R;Sullivan, F.X.; Walsh, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biochem. Parasitol. 44, 145-148, 1991
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      8.2%;
Score 111; UB .
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                                         DB 1;
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                                         Length 492;
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Data Library,
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January 1995
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A; Accession: E75395
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-467 <WHI>
A; Cross-references: UNIPROT: Q9Rt
A; Experimental source: strain R1
C; Genetics: A; Gene: DR1435
A; Map position: 1
C; Superfamily: uncharacterized of
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875395
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Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans (c;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004 C;Accession: E75395
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A; Reference number: A75250; MUID:20036896; PMID:10567266
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A; Residues: 1-390 < KAW>
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72639
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                                                                                                                                 Map position: 1
Superfamily: uncharacterized conserved protein
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Best Local
                                                    Query Match
Best Local (
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                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 VLLSAD--VYTKVSETSDHGY---PIREHLNR---LVDGDIIW----APAIDG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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Similarity 24.5%;
57; Conservative 3
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                           Conservative
                        7.8%; Score 105.5; DB 2; 26.1%; Pred. No. 1.3; tive 25; Mismatches 87;
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Pred. No. 1;
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                           Indels 115;
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C.; Ma
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid
                                                                                                     129 EGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGP---YSVLLSADVYTKVSETS 185
                                                                                                                                                                                                                                                                  56 GCGVMVGVKEGQVVATHGDMQAEVNRGLNCIKGYFLSKIMYGTDRLKTPLLRKRN-----
                                                                                                                                                                                                                                                                                                                 43 GGPVTAAVSTGRLI----DVKAPTNGVIAHLRA---SKPLV---RLRVPFTLSRNEIDDV 92
                                                                                                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
     DHGYPI - - - - -
                                                                                                                                                         GAFAKDGEFEPVSWDEAFDVMAEQAKKV--LKDKGPTAVGMFGSGQWTIFEGYAATKLMR 168
                                                                                                                                                                                                              ERGSKDSDWEPVK-----EAAKKLAFVEDR------TIFEGYSAASI--
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                           7.6%;
                                                    DPNARHCMASAAYAFMRTFGMDEPMGCYDDFEHADAFVLWGSNM 220
     -REHLN-------RLVDGDIIWAPAIDGAFVLTTRGGDF
                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                     Score 102.5; I
Pred. No. 5.1;
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 834;
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435 AĞTARHD 441
232 IGYASHD 238 
379 AÍTRHLGRTPDWVLLSNSKIEPÁVQRRYQQBGÁTYLTLDGAGRDLRGRVRFAPLIQ 434
190 PIREHLNRLUDGDIIWAPAIDGAFULTTRGGDFDLQLGTDVA 231
327 GPGSLFTSIIPALLIPD-IARAVRESPAPVVYVASLMTEPGETDGLSLSDHVN 378
149IPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGY 189
267 TTRPVTLVABLADGRTIRGESRFAEQIRPSRIERVRLEPENPSALTQVLEAVRDAEMIVL 326
115
213 ARLLIHRFGRGEGLEGHTFGNLLLATLSEERGGLGTAMQDIHEILKVRGRVYPA 266
76 VRLRVP
161 LTGLKTHSSNITAVVTVADDGGSSGRLREALDMVAPGDLTDCYAALSESPAL 212
21 LEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVIAHLRASKPL 75

C;Accession: B95346

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow, F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilou A;Reference number: A95262; MUID:21396509; PMID:11481432 NapA periplasmic nitrate reductase [imported] - Sinorhizobium meliloti (strain 1021) C;Species: Sinorhizobium meliloti (C;Species: Sinorhizobium meliloti (C;Date: 24-Aug-2001 #text\_change 09-Jul-2004 (C;Date: 24-Bug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004 (C;Date: 24-Bug-2001 #sequence\_revision 24-Aug-2001 #sequence\_re

99;

110

128

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cellulose synthase homolog T26B15.10 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) c;Pate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02553; D84734 C;Accession: T02553; D84734 B;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Jab, Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab, Jung, K.H.; Alam, M.; Freitas, T.

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
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B84311
B94311
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
A;Cross-references: UNIPROT:080891; UNIPARC:UPI00000485E0; EMBL:AC004681; NID:g3298532; A;Experimental source: cultivar Columbia A;Experimental source: cultivar Columbia R;Lin, X:, Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Venter, Vente
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A,Reference number: Z14678
A,Accession: T02553
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C; Genetics:
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A; Residues: 1-694 <S
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A;Title: Genome sequence of Halbacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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Best Local S
Matches 58
                                                                                                                                                                                                               Status: translated from
                                                                                                                                                      Residues: 1-755 <ROU>
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C;Superfamily:
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                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                         Similarity
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A;Accession: D84734
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-755 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402, 761-768, 1999
A; Title: Sequence and ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 88/2; 194/3; 236/3; 277/3; 344/3; 390/1; 450/3; 567/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: At 2g32540; T26B15.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI00000485E0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                         245 VGDEKEVPHVVYISREKRPNHFHHYKAGAMNFLVRVSGLMTNAPYMLNVDCDMYVNEADV
                                                                                                                                                                                                                                                                                                                185 EFSKDWEMTKREYEKLSOKVEDATGSSHWLDAEDDFEAFLNTKSNDHSTIVKVVWENKGG
                                                                                                                                                                                                                                                                                                                                                                    96 SKDSDWEPVKEAAKKLA-FVEDRTIFEGYSAA--SIEGIRSASSNPALTLPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PTNGVIAHL------RASK-----PL----VRLRVPFTLSRNBIDDVERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VTEAAWABIBLEAARTFKRHIAGR-----RVVDVSDP--GGPVTAAVSTGRLIDVKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
CFHTRRVMYGLSLDDLGDDGSLSSIA----TRKYLAEESLT
                                              VLTTRGGDFDL---QLGTDVAIGYASHDTDTERLYLQETLT 251
                                                                                                                                                                                                                                                             --DPREIPDVI------SQALSEL-RLAGV--DGPYSVLLSADVYTKVSET
                                                                                                                                                                                                                                                                                                                                                                                                                     PANKLACYVSDDGCSPLTYPSLKEASKFAKIWVPFCKKYNVRVRAPFMYFRNSPEAAEGS
                                                                                                    VRQAMCIFLQKSMDSNHCAFVQYPQDFYDSNVGELTVLQLYLGRGIAG--IQGPQYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITNIKWSPADY---KTYPERLDERVHELPPVDMFVTTADPVREPPLIVVNTVLSLLAVNY
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20.8%; Pred. No. 7.6;
                                                                                                                                                     SDH----GYP-----IREHLNRLVDGDIIWAPAIDGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                    144
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acetyl-coenzyme A synthetase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120
A;Notce: Nostoc sp. strain PCC 7120 is a symonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004 C;Accession: AB2338

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840 Iriguch

A;Accession: AB2338

A;Cross-references: UNIPROT:08YPE0; UNIPARC:UPI00000CEA81; GB:BA000019; PIDN:BAB75956.1 A;Experimental source: strain PCC 7120

acetate-CoA ligase; acetate-CoA ligase homology

멂

2;

Length 524;

149 IPDVISQALSELRLAGVDGPYSVLLSA------DVYTKVSETSDHGY-----PI MPMIPEAAIAMLACARIGAPHSVVPGGFSAEALRDRLIDAQAKVVVTADGGWRKDAIVPL REHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLG-----Conservative 7.2%; Score 96.5; Di 25.8%; Pred. No. 7.8; tive 25; Mismatches 46; Indels -TDVAIGYASHDTDTERLY 27; Gaps 205 191 245 6

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regulatory protein ppsR [imported] - Rhodobacter sphaeroides C;Species: Rhodobacter sphaeroides C;pate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_chan C;Accession: T50734 R;Choudhary, M.; Kaplan, S. Nucleic Acids Res. 28, 862-867, 2000 A;Title: DNA sequence analysis of the photosynthesis region o A;Reference number: Z25222; MUID:20115911; PMID:10648776 A;Accession: T50734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1489 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Description: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyketide synthase pksF - Mycobacterium N;Alternate names: L518 F1 8 protein C;Species: Mycobacterium leprae C;Date: 19-Mar-1997 #sequence_revision 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Reywords: carrier protein; phosphopantetheine; phosphoprotein; 26-436/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS2>;549-832/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>;934-1001/Domain: acyl carrier protein homology <ACP3>
;936-1001/Domain: acyl carrier protein homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S73015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Start codon: GTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                 LQETLTFLCYTARASVALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEVGPGGSLTGSAMRHPRWSSGHRAVRLMRHPLQNVDDHDTFLRALGELWSAGIEVDWAP 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNDPGNCVVAGPKDQIRAFSQRLDEVGIPVRRVRATHAFHTSSMEPMLREFSEFLSRQQL 763
                                                                                                                                                                                                                                                               EHPTLASLTAAVDASFASS
                                                                                                                                                                                                                                                                                                                                                                                                                    QRSVMPHL----VSLPGYPFARQRHWVEPRYTIWAQIPGASSGSPVDSSVDSATVEGVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLSADVYTKVSETSDHGYPIREHLNRLVDGDIIWA------PAIDGAFVLTTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGYSAASIEGI----RSASSNPALTLPEDPR---BIPDVISQALSELRLAGVDGPYSV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVPNTPLLSNLTGTWMSEQQVTDPB-----NW--TRQISSTIRFADBLDVVLSQSGRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVPFT-----LSRNBIDDVBRGSKDSDWBPVKBAAKKLAFVBD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDPGGPVTAA-----VSTGRLIDVKAPTNGVIA----HLRASKPLVR------L
                                                                                                                                                                                                                                                                                                                                          GESQTEATLQRIWSQCLGVSSVDRNANFFD--LGGDSLMAISISMAAANEGMTITPQDMY
                                                                                                                                                                                                                                                                                                                                                                                 GD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%;
ilarity 21.9%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $; Score 96.5;
$; Pred. No. 34;
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November 1993 cosmid L518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                      21-Jul-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-Apr-1997
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                                                                                                                                                                                                                                                                                                                                                                               FDLQLGTD----VAIGYASHD----TDTERLY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101;
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                                        of Rhodobacter sphaeroides
                                                                                                                          09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                          989
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S

LAPVTEAAWABIELEAARTFKRH---IAGRRVVDV--SDPGGPVTAAVSTGRLIDVKAPT 62

Matches Query Match

68

Conservative

31;

Pred. No. 11; 1; Mismatches Score 96; DB Pred. No. 11;

111; Indels

52;

Gaps

В

2;

Length 614;

Local

Similarity

7.1**%**; 26.0**%**;

```
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Coliveira, M.C.; de Oliveira, R.C.; Palmieri,
F.G.; Nunes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
M.B.; M.S.; M.S.; M.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision
C;Accession: G8230
R;anonymous, The Xylella fastidiosa Con
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
G82830
ATP-dependent RNA helicase XF0252 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: The genome sequence of the plant pathogen Xylella fastidiosa. A,Reference number: A82515; MUID:20365717; PMID:10910347 A,Note: for a complete list of authors see reference number A59328 below A,Accession: G82830
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                                                  A; Contents: annotation
                                                                        A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Cross-references: UNIPROT:Q9PGP6; UNIPARC:UPI00000C234B; GB:AE003878; GB:AE003849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Residues: 1-614 <SIM>
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XF0252
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A; Molecule type: DNA
A; Residues: 1-673 < XUA>
A; Cross-referan
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A;Status: preliminary A;Molecule type: DNA A;Residues: 658-673 <XUI>A;Coss-references: UNIPARC:UPI0000175098 A;Coss-references: UNIPARC:UPI0000175098 A;Note: sequence extracted from NCBI backbone (NCBIN:123409, NCB C;Superfamily: NADH dehydrogenase (ubiquinone) chain 11 C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P29915; UNIPARC:UPI000016FD3C; R;Xu, X.; Matsuno-Yagi, A.; Yagi, T. Biochemistry 32, 968-981, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Xu, X.; Matsuno-Yagi, A.; Yagi, T. Arch. Biochem. Blophys. 296, 40-48, 1992 A;Title: Structural features of the 66-kDa A;Reference number: S23946; MUID:92296779; A;Accession: S23948
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A45456
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO3 -
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Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                      214
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                                                                                                                                                                                                                                                                              61 PTNGVIAHLRASKPLVRLRVPPTLSRNBIDDVER----GSKDSDWBPVKGAAKKLAFVED 116
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                                      VLTTRGGD-FDLQLGTDVAIGYASHDTDTBRLYLQBTLTFLCYTABASV 261
                                                                                                                    AGVDGPYSVLLSADVYTKVSETSDHGYPIRE-----HLNRLVDGDIIWAPAIDGAF 213
                                                                                                                                                                                                       RTI-----FEGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRL 162
                                                                                                                                                                                                                                                                                                                               RENGRIRPASWPEALEAAARAMK----GKKIAGLIGDLVPAEAAFSLKQLVEGLGGKVEC 345
                                                                                                                                                                                                                                                                                                                                                                     RDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLID-----VKA 60
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VVYNLGADEVDIDQGPFVIYQGSHGDRGAHRDII---LPGACYTEESGL
                                                                                ARRDGE-AVLAHA---MKLAENSNSGLLILHTAAGRVGAMDVGAVTEGGLL--AAIDGAE
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ilarity 22.8%;
Conservative 4
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chain 11
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable nei protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B79982
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C;Superfamily:
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62; Conserv
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                                        ----IWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTDTERL
                                                                                  QRVLAGIGNVYCNELCFVSGVLPTAPVSAVADPRRLVTRARDMLWVNRFRWNRCTTGDTR
                                                                                                                           PREIPDVISQALSEL-RLAGVDGPYSVLLSADVYTKVSETSDHGYPIREHLNRLVDGDI-
                                                                                                                                                                     GAVVAHLGPDLLADDWDP-QRAAANLIVAPDRPIAE---
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Search completed: April 14, 2006, 17:34:23 Job time: 18.539 secs

RESULT 15

1

OM protein protein search, using sw model

Run April 14, 2006, 17:04:10 ; Search time 97.7763 Seconds (without alignments) 1912.171 Million cell updates/sec

Title: Perfect score: US-10-620-246-16 1348 1 MNNLYRDLAPVTBAAWABIB......LQBTLTFLCYTABASVALSH 265

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 et

summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

26 27 28 29 30 31	17 22 22 23 25	11 11 11 11 11 11 11 11 11 11	Result
101.5 101 101 101 101 100 99.5	108.5 106.5 105.5 105.5 104.5 104.5 103.5	1348 1341 1341 1184 1188 914.5 840 840 823 780.5 365.5 196.5 1196.5 1197.5 1122	Score
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241 TERLYLQETLTFLCYTABASVALSH 265

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181

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121 EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180

61 PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF 61 PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF 120

120

181 VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD

240 240

VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD

밁 δ

Query Match 100.0%; Score 1348; DB 2; Length; Best Local Similarity 100.0%; Pred. No. 1.2e-94; Matches 265; Conservative 0; Mismatches 0; Indels

Length 265;

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Gaps

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ENCE.  9; PubMed=95967  Rasmussen P.B.;  and characteri uberculosis cul ";  66:2728-2735(19  AA73350.1; -; G  AA73350.1; -; G  7544; Linocin M  Linocin M18; I  Linocin M8; I  AA; 28860 M8;	AINARY; irel. 0 irel. 0 irel. 2 irel. 2 irel. 2 irel. 3 irel. 2 irel. 3 irel. 3	755 588 762 762 271 2456 410 410 410 410 410 410 410 410 410 410
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DE 29 kDa A
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

EMBL; BX248336; CAD93683.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18; I.
Pfam; PF04454; Linocin_M18; I.
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
29 kDa ANTIGEN (FPD)
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O\[O\]181; Q\[O\]1997;
O\[O\]197 (TrEMBLrel. 04, Created)
O\[O\]1-1997 (TrEMBLrel. 04, Last sequence update)
O\[O\]1-1997 (TrEMBLrel. 04, Last sequence update)
O\[O\]2-SEP-2005 (TrEMBLrel. 31, Last annotation update)
O\[O\]2-SEP-NTIGEN (FPP29) (Bacteriotin CFP29).
Name=cfp29; OrderedLocusNames=MT0819, Rv0798c;
                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium;
Mycobacterium tuberculosis complex.
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NCBI_TaxID=1765;
     MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
                                 STRAIN=H37Rv;
                                                        NUCLEOTIDE SEQUENCE
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J. Bacteriol. 184.5479-5490(2002).
J. Bacteriol. 184.5479-5490(2002).
EMBL; BX842574; CAB09572.1; -; Genomic_DNA.
EMBL; AB000516; AAK45061.1; -; Genomic_DNA.
EPTR; B70520; B70520.
TIGR; MT0819; -.
TIGR; MT0819; -.
TubercuList; RV0798c; -.
Therror; IPR007544; Linocin_M18.
Pfam; PF04454; Linocin_M18; 1.
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Harris D.E., Gordon S.V., Biglmeier K., Gas S., Barry C.B. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy I.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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STRAIN-CDC 1551 / Obhkosh;

MEDLINE-22206494; PubMed=12218036;

MEDLINE-22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Pleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Owinn M.L., Ermolaeva M.D.,

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                  05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Hypothetical protein.
OrderedLocusMames=MAR96630c;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;

complex

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RESULT

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ID YPU3

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STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Pathkawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta Shikawa J., Yamashita Bequence of Nocardia farcinica IFM 10152.";
"The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
EMBL; AP006618; BAD59878.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18.
Pfam; PP04454; Linocin_M18; I.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Putative bacteriocin family protein.
OrderedLocusNames=nfa50260;
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InterPro; IPR007544; Linocin_M18.

Pfam; PF04454; Linocin_M18; I.

Complete proteome.

SEQUENCE 265 AA; 28618 MW; 6157F708A7DC98C9 CRC64.
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Corynebacterineae; Nocardiaceae; Nocardia.
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Pred. No. 1.9e-82
10; Mismatches 1
                                                                                                                                                       Score 914.5; DB 2;
Pred. No. 1.4e-61;
5; Mismatches 50;
                                                                                                                                                                                                                                                          D77C77B24F4F73FA CRC64;
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STRAIN=1282 / ATCC BAA-587;

STRAIN=12827 / ATCC BAA-587;

STRAIN=12827 / ATCC BAA-587;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Parris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Bakers S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Peltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

Onwin L., Whitehead S., Barrell B.G., Maskell D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007544; Linocin Pfam; PF04454; Linocin M18; I. Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative analysis of the genome sequences of Bordetella Bordetella parapertussis and Bordetella bronchiseptica."; Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella parapertussis.
Bacteria; Proteobacteria;
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STRAIN=12822 / ATCC
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Name=linM18; OrderedLocusNames=BPP1410;
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Last sequence update)
Last annotation update)
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Pred. No. 6.9e-56;
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X MEDLINB-22827954; PubMed-12910271; DOI=10.1038/ng1227;

X MEDLINB-22827954; PubMed-12910271; DOI=10.1038/ng1227;

X Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

X Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

X Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

X Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

X Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

X Feltwell T., Goble A., Hamlin N., Hauser H., Horvyd S., Jagels K.,

X Feltwell T., Goble A., Hamlin N., Hauser H., Horvyd S., Jagels K.,

X Heather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

X A Leather S., Moule S., Norberczak H., Squares S., Seger K.,

X A Leather S., Moule S., Norberczak H., Squares S., Stevens K.,

X Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

Y Comparative analysis of the genome sequences of Bordetella pertussis,

Y Tomparative analysis of the genome sequences of Bordetella pertussis,

Y Tomparative analysis of the genome sequences of Bordetella pertussis,

Y Tomparative B.S. 23-40(2003).

X Nat. Genet. 35:32-40(2003).

X Nat. Genet. 35:32-40(2003).

X Nat. BMSL BAK640444; CAB32973.1; -; Genomic_DNA.

PERMIL BAK640444; CAB32973.1; -; Genomic_DNA.
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Best Local S
Matches 165
13-SEP-2005
13-SEP-2005
Linocin_M18
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9 BURK
04LT19_9BURK PRELIMINARY;
04LT19;
04LT19;
13-SEP-2005 (Trembirel. 3
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bacteriocin.
Bacteriocin.
Mame=linM18; OrderedLocusNames=BB2479;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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  (TrEMBLrel. (TrEMBLrel. bacteriocin
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31, Creat
31, Last
31, Last
protein.
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Pred. No. 6.9e
31; Mismatches
                                                                                 Created)
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annotation updat
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Price C.,
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Best Local S
Matches 160
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                                                                                                                                                        01-NOV-1996
01-NOV-1996
01-MAR-2004
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
Valdes-Stauber N., Scherer S.;
"Nucleotide sequence and taxonomical
gene linM18 cloned from Brevibacteri
                                               NUCLEOTIDE
STRAIN=M18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames-Bcen2424DRAFT 4628;
Burkholderia cenocepacia HI2424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                             NCBI_TaxID=1703;
                                                                                                                                Linocin M18.
Name=linM18;
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Larimer F., Land M.,
"Annotation of the draft genome assembly
                                                                                                         Bacteria, Actinobacteria,
                                                                                                                      Brevibacterium linens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                               Micrococcineae;
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                                   MEDLINE=97077222; PubMed=8919789;
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  1 taxonomical distribution
Brevibacterium linens M18
                                                                                               Actinobacteridae; Actinomycetales; priaceae; Brevibacterium.
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Pred. No. 1.4e:
34; Mismatches
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Best Local Similarity
Matches 154; Conser
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MEDLINE-99287316; PubMede10360571; DOI=10.1038/20601;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,

Heidelberg J.F.; Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=TM0785;
Thermotoga maritima.
Bacteria; Thermotogae; Th
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                                                                                                                                                                                                                                                                                                                                      EMBL; AE001747; AAD35867.1; -; Genomic_DNA PIR; B72333; B72333.
                                                                                                                                                                                                                                                                                                                                                                                      genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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01-JUN-2003
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                                                                                                                                                                                                           Complete proteome. SEQUENCE 262 AA;
                                                                                                                                                                                                                                                    InterPro; IPR007544; Linocin M18. Pfam; PF04454; Linocin M18; 1.
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EMBL; X93588; CAA63787.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18.
InterPro; IPR000169; Pept_cyg_AS.
Pfam; PF04454; Linocin_M18; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 266 AA; 28597 MW; C33D960AC4C0529E
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                             MNNLYRDIAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVXA
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  MBFLKRSFAPLTEKQWQBIDNRARBIFKTQLYGRKFVDVEGPYGWBYAAHPLGB-VBVLS
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(TrEMBLrel. 24,
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llarity 36.2%;
Conservative 48
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                                                                                                 Score 384; DB 2;
Pred. No. 4.2e-21;
B; Mismatches 108
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Pred. No. 2.4e-51;
3; Mismatches 67;
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01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                                                                    Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence and analysis of Wolinella Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003). EMBL; BX571657; CAB09438.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100; Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O. Bandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Link Meyer F., Lederer H., Schuster S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINOCIN M18.
OrderedLocusNames=WS0287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7MSM9_WOLSU
                                                                                                                                                                                                                                                                                                                           InterPro; IPR007544; Linocin_M18. Pfam; PF04454; Linocin_M18; 1.
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Helicobacteraceae; Wolinella
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                                                                                                                                                                                                                                                                                                                proteome.
                                                                      V-SETSDHGYPIREHLNRLVDG-DIIWAPAI-DGAFVLTTRGGDFDLQLGTDVAIGYASH
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KSTNHELFFETLTFRINTPEASIAI
                                                LFGVAGNSGYPLTLKLAELLQGNNIIVAPALKSGALLVSLRGGDYELYSGMDIGVGYSEK
                                                                                                                                                 KLGEASVGVRMTPVIELKIPFSFPESEVEAILREANAFDISSIEKAAKKVCVAENELVF
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                                                                                                                                                                                                                                                                                                      266 AA;
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Last annotation updat
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RESULT 12 Q5L1H9\_GEOKA

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Best Local S
Matches 68
   NUCLEOTIDE SEQUENCE.

STRAIN=2CP-C;

STRAIN=2CP-C;

STRAIN=2CP-C;

STRAIN=2CP-C;

Copeland A., Lucas S., Lapidus A., Barry K., Deland A., Lucas S., Fitluck S., Richardson P.

Hammon N., Israni S., Pitluck S., Richardson P.

"Sequencing of the draft genome assembly of Ana
T dehalogenans 2CP-C.";

L Submitted (MAY-2005) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSLIH9_GEOKA PRELIMINARY;
QSLIH9;
QSLIH9;
01-FEB-2005 (TrEMBLrel. 29
01-FEB-2005 (TrEMBLrel. 29
01-FEB-2005 (TrEMBLrel. 29
91-FEB-2005 (TrEMBLrel 20)
Hypothetical conserved protorderedLocusNames=GK0916;
                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
similar to Uncharacterized protein linocin/CFP29 ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 32:6292-6303(2004).

EMBL; BA000043; BAD75201.1; -; Genomic_DNA.

InterPro; IPR0407544; Linocin_M18.

Pfam; PF04454; Linocin_M18; I.

Complete proteome; Hypothetical protein.

SEQUENCE 284 AA; 31836 MW; EFCDE94846619166 CRC64;
                                                                                                                                                                                 ORFNames=AdehDRAFT 1692;
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15576355; DOI=10.1093/nar/gkh970; Takami H., Takaki Y., Chee G.-J., Nishi S., Matsui S., Uchiyama I.;
                                                                                                                                                                                                                                                                                                  Q4NSX8_9DELT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Thermoadaptation trait revealed by the genome thermophilic Geobacillus kaustophilus."; Nucleic Acids Res. 32:6292-6303(2004).
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STRAIN=HTA426;
                                                                                                                                                  NCBI_TaxID=290397;
                                                                                                                                                                   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
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(TrEMBLrel. 29, Last sequence up)
(TrEMBLrel. 29, Last annotation
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                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 196.5; DB 2; Length Pred. No. 9.4e-07; 9; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             246
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                                                                   Query Match
Best Local S
Matches 63
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Best Local (
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067639;
01-AUG-1998 (
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                   MEDIINE=98196666; PubMed=9537320; DOI=10.1038/32831; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 27, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Hypothetical protein aq 1760.
OrderedLocusAmes=AQ_1760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CAUTION: The sequence shown here is der EMBL/GenBank/DDBJ whole genome shotgun preliminary data.
EMBL; AAHD01000020; EAL78653.1; -; Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-ORNL);

Larimer F., Land M.;

"Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aquifex aeolicus.
Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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STRAIN=2CP-C;
                                                                                                                                                                                                   Pfam; PF04454; Linocin_M18;
                                                                                                                                                                                                                                                 PIR; E70451; E70451.
                                                                                                                                                                                                                                                                        EMBL; AE000754; AAC07600.1; -;
                                                                                                                                                                                                                                                                                                                     aeolicus.
                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
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1 MNNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGG----
                                                                     63; Conserv
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281 AA;
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                                                                                                                                                                                                       IPR007544; Linocin M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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ilarity 24.2%;
Conservative 4
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28470 MW; 477948F0A22C0A49
                                                                                                                                                              31847
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                                                                   Score 142; DB 2;
Pred. No. 0.013;
1; Mismatches 120
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                                                                                                                                                                                                                                                                        Genomic_DNA
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RESULT 15
Q26970 TRYCR
Q26970; TRYCR PRELIMINARY;
AC Q25970;
AC Q25970;
DT 01-NOV-1996 (TrEMBLrel. 01,
DT 01-NOV-1996 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
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DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TrEMBLrel. 24,
DE Trypanosoma cruzi.
RR NICLEOTIDE SEQUENCE.
RR MEDLINES-6320199; PubMed=870
RR MEDLINES-6320199; PubMed=870
RR MEDLINES-6320199; PubMed=870
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RR MEDLINES-6320199; PubMed=870
RR MEDLINES-701 FR001320; PSL 14-53
DR G0; G0:0005137; C:cytoplasmi,
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G0; G0:0005136; F:GAD bindit
DR G0; G0:0005137; FAD byr_rec
DR InterPro; IPR001327; FAD byr_rec
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DR InterPro; IPR001409; Pyr_rec
DR InterPro; IPR001100; Pyr_rec
DR InterPro; IPR001100; Pyr_rec
DR InterPro; IPR001100; Pyr_rec
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Matches 76
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PDB; 18ZI; X-ray; A/B=1-453.

GO; GO:0005737; C:cyrcoplasm; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:FAD binding; IEA.

GO; GO:0050660; F:FAD binding; IEA.

GO; GO:005018; P:electron transport; IEA.

InterPro; IPR001327; FAD pyr redox.

InterPro; IPR001100; Pyr_redox.

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Pfam; PF02852; Pyr_redox_dim; 1.
PRINTS; PR00368; PADPNR.
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TIGREAMS; TIGR01423; trypano_reduc; 1.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
PRD; Flavoprotein; Oxidoreductase; Redox-active center.
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Am. J. Trop. Med. Hyg. 55:111-117(1996).
-I- SIMILARITY: Belongs to the class-I p
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Nozaki T., Engel J.C., Dvorak J.A.;
"Cellular and molecular biological analyses of nifurtimox resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Trypanothione reductase (Fragment).
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
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                                                                                          EAAW-----NAATLYKKRVA---VIDVQMVHGPPFFSALGGTCVNVGCVPKKLMVTGAQY 62
                                                                                                                                                      EAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDV-----KAPTNGV--
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                                                                                                                                                                                                                 Conservative
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25.8%;
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                                 GDIIWA-----PA-----IDGAFVLTTRGG---DFDLQLGTDVAIGYASHDTDTE 242
ANGIQILTKENPAKVELNADGSKSVTFESGKXMDFDLVM---MAIGRSPRTKDLQ
                                                                     RVLTVGGGFIS-VEFÄGIFNAYKPKDGQVTLCYRGEM---ILRGFDH--TLREELTKQLT
                                                                                                       EIPDVISQALSELRLAGV-----DGPYSVLLSADVYTKVSETSDHGYPIREHLNRLVD
                                                                                                                                          ESKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNIPGIEHCISSNEAFYLPEPPR
                                                                                                                                                                             DS-DWEPVKEAAKKLAFVEDRTIFEGYSAAS-----IEGIRSA-SSNPALTLPEDPR 147
                                                                                                                                                                                                                 MEHLRESAGFGWEFDRTTLRAEWKKLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSL
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Search completed: April 14, 2006, 17:32:09 Job time: 101.776 secs

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Result
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1348
1 MNNLYRDLAPVTEAA
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Gapop 10.0 ,
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/cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/H_COMB.pep:*
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/cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
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US-09-252-991A-20218
US-09-252-991A-20218
US-09-252-991A-20287
US-09-252-991A-29565
US-09-252-991A-29565
US-09-252-991A-29568
US-10-206-576-268
US-09-071-035-268
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\$ — \$ 8 — \$	NGVIAHLRA           GVIAHLRA	NLYRDLAPY          NLYRDLAPY	100. Similarity 100. 5; Conservative	9-16 6, Application US/ 6641814 FORMATION: 1 ANDERSEN, Peter 1 ORTITINGER, Thoma 2: RASMUSSEN, Peter 2: ROSENTRANDS, Ida 3: WELDINGH, Karin 1: FICHION: NUCLEIC INVENTION: NUCLEIC INVENTION: DERIVED RENCE: 670001-2002 PPLICATION NUMBER: 11LING DATE: 1997-0 PPLICATION NUMBER: 11LING DATE: 1997-1 11LING DATE: 1997-1 11LING DATE: 1997-1 11LING DATE: 1997-1 12LING DATE		
IEGIRSASSNPALTLP                 IEGIRSASSNPALTLP	SKPLVRI 	TEAAWAI	100.0% 100.0% tive	lon US/0: Peter Rikke Thomas Flomas Peter IS Flomas Rarin Floratio		1601 2 1287 2 330 2 2216 2 4572 2 297 2 313 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
PALTLPEDPREIPDVISQALSI 	LRVPFTLSRNEIDDVERGSKDS 	BIELEAARTFKRHIAGRRVVD 	; Score 1348; DB 2 ; Pred. No. 2.1e-14 0; Mismatches 0	CGMENTS AND TUBERCULOSIS	ALIGNMENTS	US-09-345-473E-40 US-09-862-027-40 US-09-862-027-40 US-09-252-991A-29606 US-09-583-110-3623 US-09-902-540-12221 US-10-042-665A-4 US-09-605-703B-296 US-09-605-703B-294 US-09-605-703B-294 US-09-489-039A-12219 US-09-489-039A-12219 US-09-902-540-16656 US-09-902-540-16656 US-09-902-540-16307 US-09-396-651B-1 US-09-328-335-30 US-09-328-352-7043
SNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 	PTNGVIAHLRASKPLVRLRVBPTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF 	mnilyrdlapyteanmabibleaartekrhiagrryvdysdeggpytaaystgrlidyka 	; Length 265; 1; Indels 0; Gaps	POLYPEPTIDE FRAGMENTS		Sequence 40, Sequence 2960 Sequence 1222 Sequence 1222 Sequence 296, Sequence 294, Sequence 1201 Sequence 1201 Sequence 1665 Sequence 1665 Sequence 1665 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167 Sequence 167
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US-09-050-739-23
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Patent No. 6641814
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
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Best Local Similarity
Matches 60; Conserv
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
RUMBER OF SEQ ID NOS: 16825
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, KARIN
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT FILING DATE: 1998-03-30
CURRENT FILING DATE: 1998-03-30
EARLIER APPLICATION NUMBER: 0376/97
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APPLICANT: RASMUSSEN, Peter Birk
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24.6%; Pred. No. 1.2e-07;
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   APPLICANT: YE, RICK W.
TITLE OF INVENTION: GENES ENCODING DENITRIFICATION REACTIONS
FILE REFERENCE: CL-1255
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APPLICANT: YE, RICK W.
TITLE OF INVENTION: GENES ENCODING DENITRIFICATION REFILE REFERENCE: CL-1255
CURRENT APPLICATION NUMBER: US/09/354,129
CURRENT FILING DATE: 1999-07-15
EARLIER APPLICATION NUMBER: 60/093,181
EARLIER FILING DATE: JULY 17, 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER PPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOPTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
                                                           RESULT 5
US-09-504-357-10
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US-09-354-129-10
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-23
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Sequence 10, Application US/09504357
Patent No. 6429003
GENERAL INFORMATION:
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ORGANISM: Pseudomonas
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Local Similarity 25.1%;
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100.0%; Pr/
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Pred. No. 0.5;
27; Mismatches
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US-09-252-991A-20218
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US-09-252-991A-20218
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CURRENT FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/093,181
EARLIER FILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Microsoft Office 97
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 57; Conserv
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SEQ ID NO 20218
LENGTH: 269
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APPLICANT: Marc J.
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
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184 TSDHGYPIR------FHLWRLVDGDIIWAPAIDGAFVLTTRGGD-------FDLQ 225
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                                                                                                                                             49
                                                                                                                                                                                                                                                                  30 HIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVIAHLRASKPLVRLRVPFTLSRNEI
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                                                                                                                                             DPMTDMPATAD-EPVRLLLVDDHPMMRKGVAQLLELEDDLSVVGEAGSGEEALRLAA---
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                                                               -----ELDPDMILLDLNMKGMNGLDTLRALREAGVDARIVVFTVSDDKGDVVNVLR 155
                                                                                                       ALTLPEDPREI-PDVI-----
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25.1%;
                                                                                                                                                                                                                                                                                                        6.9%; Score 93.5; DB 2; 22.7%; Pred. No. 0.096; tive 28; Mismatches 91;
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Pred. No. 0.5;
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                                                                                                     ---SQALSELRLAGVDGPYSVLLSAD---VYTKVSE 183
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US-09-252-991A-20287
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US-09-489-039A-8355
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8355
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 20287
                                                                               Matches
                                                                                                                  Query Match
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20287,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6551795
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                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                              LENGTH: 530
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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273 ABRDLEVPPVNASQALSGRGIQGEVEGRRL-----ALGNRRLLDEQELKPGAL
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                                    17 ABIBLE-----AARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVI 66
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                                                                                                   Similarity
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                                                                               Conservative
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                                                                                              6.7%;
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23.1%; Pred. No. 0.32;
tive 32; Mismatches 5
                                                                           32;
                                                                         Score 90; DB 2
Pred. No. 0.72;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS OR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                  Length 530;
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US-09-252-991A-18091
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US-09-252-991A-32791
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Sequence 18091, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARTUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: MAIC J. RUBENFIELD & al.

APPLICANT: MAIC J. RUBENFIELD & CID AMD AMINO ACID SEQUENCES RELATING 'ITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING 'ITTLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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LENGTH: 268
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29565
LENGTH: 744
TYPE: PRT
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US-09-252-991A-29565
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US-09-252-991A-29565
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LENGTH: 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29565, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                             Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                           188 ---GYPI----REHL-NRLVDGDIIWA----PAIDGAFVLTTRG----GDFDLQLG
                                                                                                                      184 ITKRPTDRLRGSMTVFTNIPESSKDGATRRANFSLSGPLTEALSFRAYGSANKTDSDDTD
                                                                                                                                                                                                           131 SSRNSVRYGWRGERDTRGDSNWVPPEE-----VERIEVLRGPAAARYGSGAAGGVVNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GAFVLTTRGGDFDLQLGTDVAI --- GYASHDTDTERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 GRIDGVLYHLGNHRLVEBLGLCSPALBERLDALBRQGKTVIALCDPQRVRALFAVADGVK
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                                                                                                                                                                                                                                               84 LSRNEIDDVERGSK----DSDWEPVKEAAKKLAFVEDRTIFEGYSAASI-EGIRSASSNP
                                                                                                                                                                                                                                                                                                 81 VNDLSEIRTMPGVNLTGNSSSGQRGNNRQIDIRGMGPENTLI--LVDGKPV-----
                                                                                                                                                                                                                                                                                                                                          36 VVDVSD-----PGGPVTAAVSTG-----RLIDVK--APTNGVIAHLRASKPLVRLRVPFT
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                                                                                                                                                                                                                                                                                                                                                                               h 6.6%; Score 88.5; D
Similarity 24.8%; Pred. No. 1.9;
64; Conservative 30; Mismatches
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                                  INLGHTVNPSRTVAGREGVRNRDLSGMLSWQVTPDQVVDFEAGFSRQGNIYAGDTQNNNG
                                                                                                                                                             ALTLPEDP-----REIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSET-SDH--
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-461-774-2
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Best Local (
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SEQ ID NO 2
LENGTH: 538
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Patent No. 6807481
GENERAL INFORMATION:
APPLICANT: CHAN, Lily
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APPLICANT: Gil H.
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APPLICANT: LIM, Renee Lay Hong
TITLE OP INVENTION: Bacterial-derived molecules
TITLE OP INVENTION: diagnostic uses therefor
FILE REFERENCE: 1781-0180P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/461,774
CURRENT FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 22
           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      STREET:
APPLICATION NUMBER:
                                                                                                                               COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AVIKVGAATDTALKERKESVEDAVAAAKAAVEEGIVPGGGASLIHQARKALTELRASLTG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 VKAPTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKDSDW--BPVKBAAKKLA---
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                                                                                                                                                                                    F: 9410 Key West Avenue
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                                                                                                                                                                                                                        Human Genome Sciences,
                                                                                                                                                                                                                                                                                                      H. Choi
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US/09/071,035
                                                                                      3.50 inch, 1.4Mb storage
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Pred. No. 1.4;
9; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6913907
GENERAL INFORMATION:
APPLICANT: Choi et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 268,
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 268:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TOPOLOGY: lir
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                                                   COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOPTMARBE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-UNI-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 TEK----ETLTALTTDTQGNVS 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLPAGVVTPGETITIISKDGAGNESQPATAVIPADVVLAAPTITKVEGNKANGYTVTGTA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESQP-ATATTPVD 197
                                                                                                                                                                                                                                                                   STATE: Maryland
                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                           ZIP: 20850
                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10206576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 86.5;
24.4%; Pred. No. 1
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US-09-071-035-258
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; SEQUENCE DESCRIPTION: SEQ ID NO: 268:
US-10-206-576-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 amino acids
                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                           COMPUTER: HP Vectra 466/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 20850
                   APPLICATION NUMBER: FILING DATE:
                                                                                                   FILING DATE:
                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 TEK----ETLTALTTDTQGNVS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 LATPTIDSI-TGNSSKGYBITGTABPKTTIDVRDADGTIIAATTA-----NETGQYTV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESQP-ATATTPVD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 LSRNEIDDVERGSKDSDWEPVKEAAKKLAF---VEDRTIFEGYSAASIEGIRSASSNPAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 VDVSDPGGPVTAAVSTG-----RLIDVKAPTNGVI-----AHLRASKPLVRLRVPFT
                                                                                                                                                                                                                                                                                                                                   T: 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERLYLOSTLIFICYTAEASVA 262
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                                                                                                                                                                                                                                                                                                                Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLPAGVVTPGETITIISKDGAGNESQPATAVIPADVVLAAPTITKVEGNKANGYTVTGTA
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FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09071035
                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                      MSDOS version 6.2
                                                                                                                         US/09/071,035
                                                                                                                                                                                                                             3.50 inch, 1.4Mb storage
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; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-258
Search completed: April 14, 2006, 17:37:52
Job time : 26.5038 secs
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Best Local Similarity 24.4%; Pred. No. 11;
Matches 64; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                          1355 DPNVTVQFYNSSEQL--LASGN------
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                                                                                                                                                                                                                                                                                                                                                     1243 LATPTIDSI-TGNSSKGYEITGTÄEPKTTIDVRDADGTIIAATTÄ-----NETGQYTV 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                            1184 VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESOP-ATATTPVD 1242
                                                                                                                                                                                                                      192 -----REHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD 240
                                                                                                                               241 TERLYLQETLTFLCYTAEASVA 262
                                                                                                                                                                                                                                                                                                          141 TLPE---DPREIPDVISQ--ALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPI---- 191
                                                                                                                                                                                                                                                                                                                                                                                              84 LSRNEIDDVERGSKDSDWEPVKEAAKKLAF---VEDRTIFEGYSAASIEGIRSASSNPAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 VDVSDPGGPVTAAVSTG-----RLIDVKAPTNGVI-----AHLRASKPLVRLRVPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1638 amino acids
                                                                                    BTLTALTTDTQGNVS
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Minimum
Maximum
                                                                                           Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                         Scoring table:
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Perfect score:
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DB
                                                                                                                                                                                  seq length: 0
seq length: 2000000000
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1348
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4 US-10-369-493-9172 4 US-10-369-493-9415	4 US-11-097-143-25428	6 US-11-097-143-25428 US-09-980-217-22	4 US-11-39-493-1/304 5 US-11-097-143-25428 3 US-09-980-217-22 5 US-10-732-923-20546 4 US-10-389-566-1442	4 US-11-097-143-17904 5 US-11-097-143-25428 3 US-09-980-217-22 5 US-10-733-923-20546 4 US-10-389-566-1542 4 US-10-425-114-54770	4 US-10-359-493-1/304 6 US-11-097-143-25428 3 US-09-980-217-22 5 US-10-732-923-20546 4 US-10-399-566-1542 4 US-10-425-114-54770 5 US-10-739-930-9412 6 US-10-739-930-9512	4 US-10-39-493-1/904 5 US-10-97-143-25428 3 US-09-980-217-22 5 US-10-732-923-20546 4 US-10-399-566-1542 4 US-10-425-114-54770 5 US-10-425-124-5256 4 US-10-282-1224-52256 4 US-10-389-493-18051	5 US-11-097-143-17904 5 US-11-097-143-25428 3 US-09-980-217-22 5 US-10-732-923-20546 4 US-10-389-566-1542 4 US-10-425-114-54770 5 US-10-739-930-9412 5 US-10-822-122A-52256 4 US-10-369-493-18051 5 US-10-369-493-18051	4 US-10-39-493-1/304 5 US-10-97-143-25428 3 US-09-980-217-22 5 US-10-732-923-20546 4 US-10-489-566-11542 4 US-10-425-114-54770 5 US-10-282-122A-52256 4 US-10-369-493-116051 5 US-10-450-763-54677 5 US-10-450-763-54677 6 US-10-369-493-11226
		9172, 9415, 17504, 25428, 22, AI	9172, 9415, 17504, 25428, 22, AF 20546, 1542,	9172, 9415, 17504, 25428, 25428, 22, AF 20546, 1542, 54770,	9172, 9415, 17504, 25428, 22, AE 20546, 1542, 9412, 9412,	9172, 9415, 17504, 25428, 225, AE 205,	9172, 9415, 17504, 25428, 22, AE 20546, 154770, 9412, 54677, 54677,	9172, 17508, 254208, 254208, 222, AE 20546, 15427, 54770, 54770, 54677, 18055, 18057, 71439,
		95 7.0 4038 3 US-09-980-217-22 Sequence 22, App	95 7.0 4038 3 US-09-980-217-22 Sequence 22 App 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 92.5 6.9 583 4 US-10-389-566-1542 Sequence 1542, 1	95 7.0 4038 3 US-09-980-217-22 Sequence 22, App 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 92.5 6.9 583 4 US-10-389-566-1542 Sequence 1542, J 92 6.8 728 4 US-10-425-114-54770 Sequence 54770,	95 7.0 4038 3 US-09-980-217-22 Sequence 22, App. 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 95 7.0 4038 5 US-10-732-923-20546 Sequence 1542, 7 92.5 6.9 583 4 US-10-389-565-1542 Sequence 1542, 7 92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 7 93 105-10-739-930-9412 Sequence 9412, 7 91 6.8 472 5 US-10-739-930-9412	95 7.0 4038 3 US-09-980-217-22 Sequence 22, Apy 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 92.5 6.9 583 4 US-10-389-560-1542 Sequence 54770, 92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 91 6.8 472 5 US-10-282-12256 Sequence 52256, 90.5 6.7 526 4 US-10-289-493-18051 Sequence 18051,	95 7.0 4038 3 US-09-980-217-22 Sequence 22, App. 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 95 6.9 583 4 US-10-389-566-1542 Sequence 1542, 1 92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 1 91 6.8 172 4 US-10-282-11224-5256 Sequence 2256, 90.5 6.7 526 4 US-10-369-493-18051 Sequence 18051, 90.5 6.7 1220 5 US-10-450-763-54677 Sequence 54677,	95 7.0 4038 3 US-09-980-217-22 95 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 3 92.5 6.9 583 4 US-10-389-56-1542 Sequence 1472, 3 92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 3 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 3 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 3 91 6.8 472 5 US-10-382-122A-52256 Sequence 52256, 3 91 6.8 472 5 US-10-389-493-18051 Sequence 18051, 3 90.5 6.7 526 4 US-10-389-493-18051 Sequence 18051, 3 90.5 6.7 1220 5 US-10-389-493-15296 Sequence 71439, 3 90 6.7 464 4 US-10-389-493-15296 Sequence 71439, 3 Sequence 71439, 3 Sequence 71439, 3 Sequence 71439, 3 Sequence 15296, 3
6 7.1 614 4 US-10-369-493-17504 Sequence 17504, 6 7.1 621 6 US-11-097-143-25428 Sequence 25428, 5 7.0 4038 3 US-09-980-217-22 Sequence 22. App. 5 7.0 4038 5 US-10-732-923-20546 Sequence 20546, 6 9 583 4 US-10-389-566-1542 Sequence 1542, 2 6 6.8 728 4 US-10-389-566-1542 Sequence 1542, 2 6 6.8 728 4 US-10-425-114-54770 Sequence 9412, 2 1 6 6 472 5 US-10-39-930-9412 Sequence 9412, 2 1 6 6 702 4 US-10-282-122A-5256 Sequence 52256, 6 7 1220 5 US-10-450-763-54677 Sequence 18051, 6 6 7 1220 5 US-10-450-763-54677 Sequence 71439, 6 6 7 328 4 US-10-282-122A-71439 Sequence 71439,	92.5 6.9 583 4 US-10-393-566-1542 92 6.8 728 4 US-10-39-566-1542 92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 91 6.8 702 4 US-10-282-122A-52256 Sequence 52256, 90.5 6.7 526 4 US-10-369-493-18051 Sequence 18051, 90.5 6.7 520 5 US-10-450-763-54677 Sequence 54677, 90.6.7 328 4 US-10-282-122A-71439 Sequence 74339,	92 6.8 728 4 US-10-425-114-54770 Sequence 54770, 91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 91 6.8 702 4 US-10-282-122A-52256 Sequence 52256, 90.5 6.7 526 4 US-10-369-493-18051 Sequence 18051, 90.5 6.7 1220 5 US-10-450-763-54677 Sequence 54677, 90 6.7 328 4 US-10-282-122A-71439 Sequence 71439,	91 6.8 472 5 US-10-739-930-9412 Sequence 9412, 91 6.8 702 4 US-10-282-122A-52256 Sequence 52256, 90.5 6.7 526 4 US-10-369-493-18051 Sequence 18051, 90.5 6.7 1220 5 US-10-450-763-54677 Sequence 54677, 90 6.7 328 4 US-10-282-122A-71439 Sequence 71439,	90.5 6.7 1220 5 US-10-282-122A-71439 Sequence 71439, 90.6 6.7 328 4 US-10-282-122A-71439 Sequence 71439,	90.5 6.7 1220 5 US-10-450-763-54677 Sequence 54677, 90 6.7 328 4 US-10-282-122A-71439 Sequence 71439,	90 6.7 328 4 US-10-282-122A-71439 Sequence 71439,		

90 6.7 792 3 US-09-815-242-11966 90 6.7 792 4 US-10-127-032-165 90 6.7 792 4 US-10-127-032-16574 89.5 6.6 415 4 US-10-369-493-4737 89.5 6.6 416 4 US-10-369-493-4737 89.5 6.6 416 4 US-10-369-493-4737 89.5 6.6 216 418 103-10-369-493-660 89 6.6 684 4 US-10-369-493-12042 88.5 6.6 229 3 US-09-738-626-4844 88.5 6.6 317 4 US-10-16-761-10897 88.5 6.6 342 5 US-10-494-836-112 88.5 6.6 765 4 US-10-19-833-5138-33 88.5 6.6 765 5 US-10-494-836-126 88.5 6.6 765 5 US-10-425-114-542293 88.5 6.6 810 4 US-10-425-114-542293 88.5 6.6 810 4 US-10-425-114-542293	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	
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3 US-09-815-242-11966 4 US-10-127-032-165 4 US-10-128-128-66574 4 US-10-437-963-174225 4 US-10-369-493-7496 4 US-10-369-493-7496 4 US-10-369-493-12042 3 US-10-369-493-12042 4 US-10-369-493-12042 5 US-10-369-493-12042 5 US-10-156-761-10897 5 US-10-494-836-112 5 US-10-156-761-8159 5 US-10-156-761-8159 5 US-10-732-923-7244 6 US-10-732-923-7244 7 US-10-425-115-322796 7 US-10-425-115-322796 7 US-10-425-115-322796	1185	810	767	765	751	498	342	317	299	684	309	416	416	415	792	792	792	
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	173561,	54293, 1	322796,	7244, Ap	8159, Ap	33, Appl	112, App		4484, Ap	12042, A	660, App	7496, Ap	4737, Ag	174225,	66574, I	165, App	11966, 1	10000

### ALIGNMENTS

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APPLICANT: WELDINGH, Karin

APPLICANT: PLORIO, Walter

TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1

CURRENT FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 03/050,739

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 1277/97

PRIOR PILING DATE: 1997-04-02

PRIOR FILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR PILING DATE: 1998-01-05
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-16
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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OSTTINGER, Thoma
APPLICANT: RASMUSSEN, Peter
APPLICANT: ROSENKRANDS, Ida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 16
                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1348; DB 3; Best Local Similarity 100.0%; Pred. No. 1.7e-124; Matches 265; Conservative 0; Mismatches 0;
121 EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180
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                                                                                                                                                                                             1 MNNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA
                                                                                                                                                                                                                      1 MNNLYRDLAPVTEAAWAEIBLEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA
                                                                                                 PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
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GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter
APPLICANT: OETTINGER, Thomas
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
ITILE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITILE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/50,739
PRIOR FILING DATE: 1998-03-30
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TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 265
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US-10-620-246-16
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/ ORGANISM: Mycobacterium tuberculosis
US-09-804-980-16

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US-09-804-980-16
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Best Local Similarity
Matches 265; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-205-032-16
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PRIOR FILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,894
PRIOR APPLICATION NUMBER: 09/415,894
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
                                                                         US-10-205-032-16
                                                                                        SOFTWARE: Patentin version 3.0

SEQ ID NO 16

SEQ ID NO 16

TYPE: PRT

TYPE: PRT

ORGANISM: micromonospora carbonacea subspecies aurantiaca
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/10205032 Publication No. US20030113874A1 GENERAL INFORMATION:
Best Local Similarity
                      Query Match
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                                                                                                                                                                                                                 APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
FILE REFERENCE: 3016-2US
CURRENT APPLICATION NUMBER: US/10/205,032
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 39
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
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Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
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SOPTWARE: PastSEQ for
SEQ ID NO 28128
LENGTH: 8805
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APPLICATION NUMBER: 60/173,383
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APPLICATION NUMBER: 60/175,693
FILING DATE: 2000-01-12
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                                                                                  1474 SQIQFNEIRTLKRSQQLGGHSVLDIAGIRDPRTGRVLTIGBAIQLRILDVRTGEMLVGDR 1533
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                                                                                                                                                                ABIBLEAARTFKR--HIAGRRVVDVSDPGGPVTAAVST-----GRLIDVK-----
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RESULT 7 US-10-991-347-21

Sequence 21, Application US/105
Publication No. US20050147627A:
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka

Application US/10991347 No. US20050147627A1

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; ORGANISM: E.
US-10-125-692-21
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Publication No. US20030044429A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.5%; Score 101; DB 4; I Best Local Similarity 22.9%; Pred. No. 1; Matches 67; Conservative 44; Mismatches 109;
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APPLICANT: Hayashi, Funitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
APPLICANT: Ozinsky, Adrian
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: P-IS 5155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
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229
                                       210 DGAFVLTTRGGDFDLQLGTDVAIGYASHDTDTERLYLQETLTFLCYTABASV 261
                                                                                                                                               172 LLSADVYTKVSETSDHGYPIREHLNRLVDG---------DIIWAPA-I 209
                                                                                                                                                                                                                                               116 DRTIFEGYSAASIEGIR--SASSNPALTLPEDPREIPDVISQALSELRLAG--VDGPYSV 171
                                                                                                                                                                                                                                                                                                 73 SVAQTTEGALSEINNNLQRIRELTVQATTGTNSDSDL----DSIQDEIKSRLDEIDRVS 127
                                                                                                                                                                                                                                                                                                                                                  57 DVKAPTNGVIAHLRASKPLVR-LRVPPTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVE 115
                                                                                                                                                                                                                                                                                                                                                                                                 16 NNINKNOSALSSSIERLSSGLRINSA---KODAAGOAIANRFTSNIKGLTQAARNANDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NNLYRD---LAPVTEAAWAEIELEAARTFKRHIAGRRVVD--VSDPGGPVTAAVSTGRLI
DGSKVSTB-----ADVGFGAAAPGTPVEYTYHKDTNT---YTASASV 267
                                                                                                                                                                                                GOTOFNGVNVLSKDGSMKIQVGANDGETITIDLKKIDS----DTLNLAGFNVNGE---
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                                                                                                -GÉTANTAATIKDMVGIKLÖNTGVTTAGVNRYIADKAVASSTÖILNAVÄGV
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APPLICANT: ROSENKANDS, IGA
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TOURRENT APPLICATION NUMBER: 09/050,739
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PRIOR DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-04-04
PRIOR FILING DATE: 1997-04-07
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: ANDERSEN, Rikke
APPLICANT: OFTINGER, Tho
APPLICANT: RASMUSSEN, Pet
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NUMBER OF SEQ ID NOS: 64
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 554
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Best Local Similarity
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APPLICANT: Underhill, David M.
APPLICANT: Underhill, David M.
APPLICANT: Ozinsky, Adrian
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: of Use
FILE REPERENCE: 66661-122
CURRENT APPLICATION NUMBER: US/10/991,347
CURRENT FILING DATE: 2004-11-16
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR APPLICATION NUMBER: US 60/285,477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 NNINKNOSALSSSIERLSSGLRINSA---KDDAAGQAIANRFTSNIKGLTQAARNANDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
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SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGAFVLTTRGGDFDLQLGTDVAIGYASHDTDTERLYLQETLTFLCYTAEASV 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSKVSTE-----ADVGFGAAAPGTPVEYTYHKDTNT---YTASASV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GÉTANTAATLKDMVGLKLDNTGVTTAGVNRYIADKAVASSTDÍLNÁVÁGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OETTINGER, Thomas RASMUSSEN, Peter Birk
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22.9%;
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Pred. No. 1;
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APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 67001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 19
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-804-980-23
APPLICANT: ROSENKEANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Walter
ITITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 10277/97
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
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; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-23
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/10620246 Publication No. US20040115211A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OETTINGER, Thou
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
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US-10-156-761-14324
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APPLICANT: IKEDA, HARUO
APPLICANT: ISTRAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT PILING DATE: 2002-05-29
CURRENT PILING DATE: 2002-05-29
CURRENT PILING DATE: 2002-05-29
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PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR FILLING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR FILLING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILLING DATE: 1998-10-08
PRIOR PILLING DATE: 1998-10-08
PRIOR FILLING DATE: 1998-10-08
PRIOR FILLING DATE: 1998-10-08
PRIOR PILLING DATE: 1998-10-08
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Best Local Similarity
Matches 57; Conserv
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SEQ ID NO 14324
LENGTH: 410
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Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.4%; Score 100; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 0.0075; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                      245 GKSVVRLKGGDPFVFGRG----
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  --LQLGTDVAIG 233
                                              VILMGVDKIGKIADTLVAHGKPAGTPVALVQEGTTAAQRRVDATLATVAETVRAQDVKPP 393
                                                                                          SVLLSADVYTKVSET-SDHGYPIREHLNRLVDGDIIWAPAIDGAFVL---TTRGGDFD-- 223
                                                                                                                                                                                                                                                                                    SKPLVRLR--VPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFEGYSAASIE 129
                                                                                                                                           GISSSISVPGAAGIPVTHRGVAHBPTVVSGHVAPDDERSLVD--WPALAKLR-----GTL 333
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llarity 22.6%;
Conservative 2:
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; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-369-493-9172
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US-10-732-923-1986
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US-10-732-923-1986
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Publication No. US20050108791A1
GENERAL INFORMATION:
Query Match
                                                                                                                                     SEQ ID NO 9172
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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Best Local Similarity
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PILING DATE: 2002-12-04
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                                                                                                               ENGTH: 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 SVILSADVYTKVSET-SDHGYPIREHLNRLVDGDIIWAPAIDGAFVL---TTRGGDFD-- 223
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22.6%; Pred. No. 1
7.1%;
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  Score 96;
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Length 565;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
INUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9415
LENGTH: 579
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US-10-369-493-9415
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US-10-369-493-9415
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                        y Match 7.1%; Score 96; DB 4; Length 579,
Local Similarity 26.0%; Pred. No. 3.4;
hes 68; Conservative 31; Mismatches 111; Indels
                                    223
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290
                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                              ATMPPQIRRI-----AQTYLQDPIE----VTIATKTTTAANIRQRYWWVSGLHKLDAL 229
                                                                                                                                                                                                                                                                                    NGVIAHL-RASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFE 121
                                                                                                                                                                                                       GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY 178
                                                                                                                                                                                                                                                                                                                                                                    LAPVTEAAWAEIELEAARTFKRH---IAGRRVVDV--SDPGGPVTAAVSTGRLIDVKAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAPTRELA----IQVAEAFQRYAASISGFRVLPVYGGQSYGQQLAALKRGVHVIVGTP-
DILVATDV----AARGLDVERI 307
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                                                                               TRILEVETFDAMIIFVRTKAATEELAEKLQARGLTAAAINGDMQQAQRERTIHQLKDGKL 289
                                                                                                                     TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF-----VLTTRGGDF 222
                                                                                                                                                                                                                                                GRVIDHLBRGTLDLSELK---TLVLDEADEMLRMGFIED---VEEVLRKLPASRQVALFS
                                                                                                                                                                                                                                                                                                                             LAPTRELA----IQVAEAFQRYAASISGERVLPVYGGQSYGQQLAALKRGVHVIVGTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILVATOV----AARGLDVERI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plolgrovalgyashdTDTERL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF-----VLTTRGGDF
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2006, 18:40:29

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Search completed: April 14, Job time: 95.095 secs
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US-10-369-493-17504
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SEQ ID NO 17504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17504, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
IITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 614
TYPE: PRT
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                                                                                                                                         223 DLQLGTDVAIGYASHDTDTERL 244
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                                                                                                                                                                                                                                                                                                                                                                                                        63 NGVIAHL-RASKPLVRLRVPFTLSRNBIDDVBRGSKDSDWBPVKBAAKKLAFVBDRTIFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 LAPTRELA-----IQVAEAFQRYAASISGFRVLFVYGGQSYGQQLAALKRGVHVIVGTP-
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                                                                                              DILVATOV----AARGLOVERI 323
                                                                                                                                                                                      TRILEVETFDAMIIFVRTKAATEELAEKLQARGLTAAAINGDMQQAQRERTIHQLKDGKL
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                                                                                                                                                                                                                                                                                ATMPPQIRRI-----AQTYLQDPIE----VTIATKTTTAANIRQRYWWVSGLHKLDAL
                                                                                                                                                                                                                                                                                                                        GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY 178
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Published Applications AA New:*

1: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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1 MNNLYRDLAPVTEA
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991.565 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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81.5	81.5	81.5	82	82	82	82	82	83.5	83.5	84	84	84	84	85.5	85.5	85.5	86	86.5	87	88.5	88.5	8	88.5	91	Score	
6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.4	6.4	6.5	6.6	6.6	6.6	6.6	6.8	Query	æ
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US-11-096-568A-33997	US-10-793-626-508	US-11-156-084-352	US-11-188-298-20429	US-11-096-568A-5491	US-11-096-568A-5492	US-10-506-454-808	US-10-793-626-3008	US-11-124-367A-446	US-11-091-936-1	US-10-453-372-1132	US-10-453-372-1142	US-11-079-463-6012	US-11-188-298-8396	US-11-024-959-436	US-11-096-568A-10907	US-11-096-568A-10908	US-10-506-454-238	US-11-087-099-8172	US-10-506-454-1639	US-11-201-916-18	US-11-188-298-18131	US-11-188-298-10005	US-10-506-454-493	US-10-506-454-1169	ID	
Sequence 33997, A	508,	Sequence 352, App	Sequence 20429, A	Sequence 5491, Ap	Sequence 5492, Ap	Sequence 808, App	3008,	Sequence 446, App	Sequence 1, Appli	Sequence 1132, Ap	1142,	Sequence 6012, Ap	Sequence 8396, Ap	Sequence 436, App	Sequence 10907, A	10908	238, 1	8172,	1639	Sequence 18, Appl	Sequence 18131, A	10005	Sequence 493, App	Sequence 1169, Ap	Description	

45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26
79	79	79	79.5	79.5	79.5	80	80	80	80.5	80.5	80.5	80.5	80.5	81	81	81	81	81.5	81.5
5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0
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US-11-188-298-13412	US-11-188-298-7003	US-11-188-298-5701	US-10-506-454-922	US-11-188-298-13516	US-11-087-099-5898	US-11-186-284-26	US-11-188-298-13272	US-10-793-626-1500	US-11-087-099-7521	US-10-714-995-18	US-10-506-454-1477	US-10-506-454-200	US-11-188-298-2003	US-11-188-298-17834	US-11-087-099-12330	US-11-096-568A-17914	US-11-096-568A-17915	US-11-096-568A-33996	US-11-201-916-28
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
13412, A	7003, Ap	5701, Ap	922, App	13516, A	5898, Ap	26, Appl	13272, A	1500, Ap	7521, Ap	18, Appl	1477, Ap	200, App	2003, Ap	17834, A	12330, A	17914, A	17915, A	33996, A	28, Appl

#### ALIGNMENTS

US-10-506-454-1169

GENERAL INFORMATION:

APPLICANT: Slesarev, Alexi I APPLICANT: Mezhevaya, Katja APPLICANT: Polushin, Nikolai

Mezhevaya, Katja V Polushin, Nikolai N

Sequence 1169, Application US/10506454 Publication No. US20060068386A1

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PILE REFERENCE: FID001

CURRENT APPLICATION NUMBER: US/10/506,454

CURRENT FILING DATE: 2004-08-31

PRIOR APPLICATION NUMBER: PCT/US03/06664

PRIOR FILING DATE: 2003-03-04

PRIOR APPLICATION NUMBER: 60/361,742

PRIOR FILING DATE: 2002-03-04

PRIOR FILING DATE: 2002-03-04

VIMBER OF SEQ ID NOS: 1722

SOPTWARE: PatentIn version 3.2

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APPLICANT: Shakhova, Vera V
APPLICANT: Malykh, Andrei G
APPLICANT: Malykh, Andrei G
APPLICANT: Kozyavkin, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophil
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OF INVENTION: and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 441
TYPE: PRT
ORGANISM: Methanopyrus kandleri
114
                                                                                       168 ----VPLYSPGDPRLEEFHDRVLEAWMECKGLGKKPPSPEMVAVTAILPTVTPILAMRKG 223
                                                                                                                                         134 ASSNPALTLPEDPR--EIPDVISQALSELRLAG--VDGPYSVLLSADVYT------KV 181
                                                                                                                                                                                                                                                    81 PFTLSRNEIDDVERG-----SKDSDWEPVKEAAKKLAFVEDRTIFEGYSAASIEGIRS 133
                                                                                                                                                                                                                                                                                                            60 FRRYL-GNOVELTPDAVILKGPGG--TRRIPVEDILDVEERESGVVV----LTKDLERVPM 113
                                                                                                                                                                                                                                                                                                                                                                27 FKRHIAGRRY-----VDVSDPGGPVTAAVSTGRLIDVKAPTNGVIAHLRASKPLVRLRV 80
                                                                                                                                                                                                   PP-----DSDRLRHGLRILLAHKKGSPGDAVVEAVRELGELPILEVVGGTVFARWRWLR- 167
                                -WAPAIDGAFVLTTRGGDFDLQLGTDVA 231
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Sequence 1005, Application US/11188298

publication No. US20060075522A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569

SEQ ID NO 10005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US03/0664
PRIOR FILING DATE: 2003-03-04
PRIOR PILING DATE: 2003-03-04
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
SOFTWARE: Patentin version 3.2
SEQ ID NO 493
LENGTH: 263
                                                                                                                                                                                                                                                                                    RESULT 3
US-11-188-298-10005
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US-10-506-454-493
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US-10-506-454-493
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KOZYAVKIN, Sergel A
TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: FIDD01
TIDE REFERENCE: FIDD01
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CURRENT FILING DATE: 2004-08-31
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APPLICANT: Mezhevaya, Katja
APPLICANT: Polushin, Nikolak
APPLICANT: Shcherbinina, Olç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 SIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 VYWAIARRVDSVPVPKSRI-KHATLTFLEYNA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                  HGYPIREHLNR-----TRGGDFDL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIGVVGPEVVDALVPLYRLREQLLDGEKAS-----IRDIGRSFGFVENMPL----- 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWAVLRIRGPEVEEAAEEIVEEFDTVRSLFDVS-PGD----VIYGRIVDLYRVGYGIYV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWA-----EIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVIA 67
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Polushin, Nikolai N
Shcherbinina, Olga V
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Malykh, Andrei G
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21.1%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abad, Mark S. et al.
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVI
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 18131
LENGTH: 315
TYPE: PRT
ORGANISM: Corynebacterium glutamicum ATCC 13032
US-11-188-298-18131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum ATCC 13032 US-11-188-298-10005
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US-11-188-298-18131
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 SASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 LGTDVAI--GYASH 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LPATKTVPKELL--PVVDT--PGIELIAAEAAELGATRLAIITAPNKAGVLAHFERSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LEAARTFKRHIAGRRYVDVSDPGGPVTAA----VSTGRLIDVKAPTN-GVIAHLRASKPL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
                                                       DAIDLLIDEGHPVH
                                                                                            LGTDVAI--GYASH 237
                                                                                                                                        BIEADTKOSOVKKVKGMVEKPAIEDAPSRLAATGRYLLDRKIFDALRRITPGAGGELQLT 242
                                                                                                                                                                                                                          DDDEDVVAVMLPDDLVLPTGVMERMAQVR-ABFGG--SVLCAVE----VSEADVSKYGIF 182
                                                                                                                                                                                                                                                                SASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIR 192
                                                                                                                                                                                                                                                                                                                                                      VRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAA---KKLAFVEDRTIFEGYSAASIEGIR 132
                                                                                                                                                                                                                                                                                                                                                                                                  LPATKTVPKELL--PVVDT--PGIELIAAEAAELGATRLAIITAPNKAGVLAHFERSSEL
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k; Pred. No. 2.1;
37; Mismatches
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RBSULT 6
US-10-506-454-1639
; Sequence 1639, Application US/10506454
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; Sequence 18, Application US/11201916
; Publication No. US20060039922A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 870109.408
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 31-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICANT: Wisniewski, Jan
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STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/1 FILING DATE: 11-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                            484
                                                                                                                                                                                      435
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                                                                                                                                                199 VDGDIIWAPAIDGAF--VLTTR 218
                                                                                                                                                                                                                                                                                                                                                                              58 VKAPTNGVIAHLRASKPLVRLRVPPTLSRNBIDDVERGSKDSDW--EPVKEAAKKLA--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DLAPVTEA-----AWASISLEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLID
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                                                                                                            SYGDL----AADGVIDPVKVTR
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                                                                                                                                                                                                                                                               AVIKVGAATETALKERKESVEDAVAAAKAAVEEGIVPGGGASLIHQARKALTELRASLTG 434
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                                                                                                                                                                                      DEVLGVDVFSEALAAPLFWIAANAGLDG-----SVVVVKKVSELPAGHGL----NVNTL 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 88.5; DI
25.2%; Pred. No. 4.8;
ative 20; Mismatches
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Sequence 8172, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 8172
LENGTH: 581

TYPE: PRT
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US-11-087-099-8172
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                                                                                        ; ORGANISM: Bradyrhizobium japonicum USDA 110 US-11-087-099-8172
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SOPTWARE: PatentIn version 3.2
SEQ ID NO 1639
Query Match 6.4
Best Local Similarity 28.3
Matches 57; Conservative
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Best Local :
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APPLICANT:
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APPLICANT: Mezhevaya, Katja
APPLICANT: Polushin, Nikolai
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PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR PILING DATE: 2002-03-04
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APPLICANT: Kozyavkin, Sergei A
TITLE OP INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophil
TITLE OP INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OP INVENTION: and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
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ORGANISM: Methanopyrus kandleri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.5%; Score 87; DB Local Similarity 24.5%; Pred. No. 2.8; Pred. No. 2.8; es 60; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 --ISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIREHLNRLVDGDIIW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 FVEDRTI------FEGYSAASIEGIRSASSNPALTLPEDPREIPDV----- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDW-----EPVK-----EAAKKLA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AELTLAGLLELGYEVEVTTLEGKSLPGRRRIELADE----VKGVVTGRYVEELLDSDRV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APVTEAAWAEI--ELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVSTREPSFTDLVVDLGAAPGGWSSFAAQMAENV--VAVDPA-RLEDRVRELENVHHLRI 196
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Polushin, Nikolai N
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Shakhova, Vera V
Malykh, Andrei G
6.4%; Score 86.5; ]
28.1%; Pred. No. 8.2,
tive 30; Mismatches
                                          DB 7;
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  77;
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                                             Length 581;
  39;
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  13
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Indels

Gaps

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CURRENT APPLICATION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/US03/06664
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2002-03-04
INUMBER OF SEQ ID NOS: 1722
SOPTWARE: PATENTIN VERSION 3.2
SEQ ID NO 238
LENGTH: 455
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US-10-506-454-238
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US-11-096-568A-10908
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US-10-506-454-238
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Best Local S
Matches 42
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238, Application US/10506454 Publication No. US20060068386A1 GENERAL INFORMATION:
                                                                                        Sequence 10908, Application US/11096568A Publication No. US20060048240A1
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APPLICANT:
APPLICANT:
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APPLICANT: Mezhevaya, Katja V
APPLICANT: Polushin, Nikolai N
APPLICANT: Shcherbinina, Olga V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOZYAVKÍN, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: FID001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                              345 QYYERALRARTWIRRRLLEALEGYDALL-----
                                                                                                                                                                                                                                                   102 BPVKEAAKKLAFVEDRTI--FEGYSAASIEGIRSASSNPALTLPEDPREIPDVIS 154
                                                                                                                                                                                                                                                                                      295 YYVINYVEFFSATRRFDGRRYGRRIEHVCGKEVLRRIVAGAAISRQEV----RG-----
                                                                                                                                                                                                                                                                                                                                                               248 LVREFLEVSEPEIAEVAKEAARALER-----
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                                                                                                                                                                                                                                                                                                                          63 NGV------IAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDW 101
                                                                                                                                                                                                                                                                                                                                                                                                  4 LYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGR-LIDVKAPT
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42; Conservative
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Malykh, Andrei G
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Pred. No. 6.4
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
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                                                                                                                                                                                                                ----GPTVPKPPHRIGEELS
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1 Monophyly
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10908
LENGTH: 390
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Ceres Seq. ID no. 1359745
US-11-096-568A-10908
                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10907
SEQ ID NO 10907
LENGTH: 436
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
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US-11-096-568A-10907
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; LOCATION: (1)..(436)
; OTHER INFORMATION: Ceres Seq. ID no.
US-11-096-568A-10907
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                                                                                                                                                                                                                  Query Match
Best Local 9
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Best Local S
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                                         113 DIVINHRCAED-----KDGRGIYCIFKGGGPEGLLDWGPGMICSDDTKF-SDGT---GYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 TTRG 219
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                                                                              81 PFTLSRNEIDDVERGSKDS----
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                                                                                                                                                                                            6.3%;
ilarity 24.2%;
Conservative 2
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llarity 24.2%; Pred. No. 5.7;
Conservative 27; Mismatches
       -SAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDG----PYSVLL
                                                                                                                                                                                            27;
                                                                                                                                                                                              Score 85.5; D
Pred. No. 6.7;
27; Mismatches
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165 SADVARTYVONTSPGFVVAEIWNSLSYDGDGKPAVNODGEROELVNWAKAVGGPAMAFDF
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                                                                                55 IAGAGVTHVWLP--PPTHSVSSQGYMPGRLYDLDASKYGTAVELRSLIAAFGAKGIKCVA 112
                                                                                                                    31 JAGRRYVDVSDPGGPVTAAVST-----GRLIDVKAPTNGVIAHLRA-----SKPLVRLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 DIVINHRCAED-----KDGRGIYCIFKGGGPEGLLDWGPGMICSDDTKF-SDGT---GYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 IAGRRVVDVSDPGGPVTAAVST-----GRLIDVKAPTNGVIAHLRA-----SKPLVRLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDG----PYSVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Fragments and
                                     DWEPVKEAAKKLAFVEDRTIFEGY-
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                                                                                                                                                                     79;
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163
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US-11-024-959-436
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                                                                                                                                                                                                                                                   RESULT 12
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TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 04446-3160
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION UNMBER: 60/533,036
PRIOR APPLICATION UNMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 792
SOFTWARE: Patentin version 3.3
SEQ ID NO 436
LENGTH: 539
TYPER: DET
                                                                                                                                                               Sequence 8396, Application US/11188298 Publication No. US20060075522A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.3%; Score 85.5; DB 7; Best Local Similarity 21.8%; Pred. No. 9.1; Matches 52; Conservative 38; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 436, Application US/11 Publication No. US20060010516A1 GENERAL INFORMATION:
               APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GERSK AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(5452)B
CURRENT APPLICATION NUMBER: US/11/186,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 DMVKTVSGMFGRMSPEEIQNMMKMSSTLSRQNPSTSSRFDDITRGHSNMDSSPQSVSVDN 395
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SEQ ID
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TTKG 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGFSRDSFQATNAPDGQMYAESLRNLTENPDMLRTMQSLMKNVDPDSLV--ALSGGKLSP 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNETT, MARIE B.
EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
  NOS: 22569
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APPLICANT: GATY L. Breton
ITITLE OF INVENTION: NUCLEST ACID AND AMINO ACID SEQUENCES RELITIVES OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
ITITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
ITITLE OF INVENTION. POR DIAGNOSTICS AND THERAPEUTICS
ITITLE OF INVENTION. POR DIAGNOSTICS AND THERAPEUTICS
ICURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-04-04
INUMBER OF SEQ ID NOS: 104444
SEQ ID NO 6012
LENGTH: 901
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US-11-079-463-6012
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US-11-079-463-6012
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Publication No. US20060073161A1
GENERAL INFORMATION:
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Matches
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LENGTH: 538
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Best Local Similarity
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                                                                108 LDAVTVVARKNIEGEKALLQERQKATLA---IENM-
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163 SIASAGQLIVRGLGDRÝSTTTLNGLPIÁSPNÉDNKLIFLDLFFASTVKNITVSKVYAÁGA
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                                                                                                                                                                                31 | AGRRVVDVSDPGGPVTAAVSTG-------RLIDVKAPTNGVI------
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                                                                                                                                                                                                                                        h 6.2%; Score 84; DB 7; Length 901; Similarity 23.0%; Pred. No. 26;
                                                                                                          ----AHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWE----PVKEAAKKLAFV 114
                                                                                                                                               G---LGFALPAAVGAAIAQPDR-----TVLCLLGDGS
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                               B------DRTIFEGYSAASIEGIRSASSNPALTL-PEDPREIPDVISQALSELRLAGV
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                                                                                                                                                                                                                      37; Mismatches
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; ORGANISM: Homo sapiens
US-10-453-372-1142
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US-10-453-372-1142
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.2%; Score 84; DB 6; Length 491
Best Local Similarity 21.4%; Pred. No. 2.9e+02;
Matches 66; Conservative 50; Mismatches 106; Indels
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PRIOR
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PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLBIC ACIDS ENCODING SAME, AND METHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21402-589 A
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FILING DATE: 2001-03-19
APPLICATION NUMBER: 60/199476
FILING DATE: 2000-03-25
APPLICATION NUMBER: 09/863776
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FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
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FILING DATE: 2000-03-10
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                                                                                                                                                                                                      2163 PYSVNVPENLGTLPRTILQTASPC----VRFASASKAYFTTIPEDAFTGTDVLLVNASDA 2210
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RESULT 15
US-10-453-372-1132
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PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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FILING DATE: 2001-03-19
APPLICATION NUMBER: 60/199476
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APPLICATION NUMBER: 60/195792
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Mycobacterium

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immunological; immunogen;

Mycobacterium tuberculosis antigen MPT51.

21-JAN-1999 AAW72899;

(first entry)

AAW72899 standard; protein; 299 AA.

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## ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                               01-APR-1998;
                                                                                                      08-OCT-1998.
                                                                                                             WO9844119-A1
                                                                                                                    Mycobacterium
                                                                      (STAT-)
                                                                                                                           infection
                                                                      STATENS SERUM INST.
                                                                                                                    tuberculosis.
                                                                             97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                               98WO-DK000132
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Andersen P, Oettinger T, Nielsen Florio E,70 Rosenkrands I, Weldingh K, Rasmussen PB;

N-PSDB; WPI; 1998-542705/46. AAV63923.

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. for

Claim 1; Page 151-152; 163pp; English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnos of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. povis diagnosis

Abb73462 Abu36126 Abu56407 Aaw18165 Aaw63033

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RESULT 2
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protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion to the tuberculosis complex. The invention provides a (1) fusion polypeptide fragment (1) and at least polypeptide comprising at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis; fusion polypeptide; pharmaceutical; vaccination; M. af CFP7B; CFP19; CFP27; CFP3OA; RD1-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-1998;
01-APR-1998;
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                                                                                                                               The invention
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                                                                                                      n describes a substantially pure immunogenic polypeptide from Mycobacterium tuberculosis that is able to evoke a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second CC different amino acid sequence from M. tuberculosis, and/or including a CC sequence which protects the first amino acid sequence from in vivo CC degradation or post-translational processing; (3) a nucleic acid fragment CC that encodes the above polypeptides. The polypeptides and nucleic acid core useful as pharmaceuticals, for diagnosis of and as antigens for CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or CC povis. The polypeptides are also useful for diagnosing ongoing or CC previous sensitization in an animal with bacteria belonging to the CC tuberculosis complex. The invention also describes the use of CFP7A or CC PT910A or a T-cell epitope of for the induction of a strong immune CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell celipope of for diagnosis of TB in a mammal by performing a DTH type skin CC test; use of CFP27, CFP30A, CFP16, CFP19, CFP23, CFP23B, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and CC for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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                                                                               GAIAAGMOOFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                                        GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                                                                                          SABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR
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Pred. No. 7.2e-121;
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ADR12610 standard; protein; 299
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(first

entry)

antimalarial; antitubercular; tuberculostatic; anti-HIV; antibacterial; haemostatic: protozoacide; antiinflammatory; neuroprotective; virucide; Gene vaccine protein #34.

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AC haemostatic; protozoacide; antiinflammatory; neuroprotective; virucide; gene vaccine; ubiquitin; antigen; intracellular parasite; protozoan parasite infection; antigen; tuberculosis; txxxplassmosis; trypanosomiasis; AIDS; cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis; Ebbla hemorrhagic fever; Trypanosoma; Chagas disease; Japanese encephalitis; influenza; rubeola; dengue virus; poliomyelitis; Herpes virus; severe acute respiratory syndrome.

12-AUG-2004.

30-JAN-2004; 2004WO-JP000975

31-JAN-2003; 2003JP-00023507

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene vaccine having nucleic acids encoding ubiquitin and antigen protein of intracellular parasite, useful for treating parasite infections such as malaria, tuberculosis, toxoplasmosis.
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                                                                                                                                                                                                                 vaccinating agent; protozoan; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 299
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                                                               Location/Qualifiers 34. .299
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                                                                                                                                                                                                                                              M.tuberculosis; pathogen; bacteria; virus;
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                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
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31-OCT-1995;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccines derived from M.tuberculosis major abundant extracellular proteins - are easy to prepare and less toxic than conventional killed attenuated vaccines, useful for protecting against or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 41; 193pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterial infections.
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241
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                     AMIGQTABAMGNSRMFYNQYRSVGGHNGHFDFÞASGDNGWGSWAPQLGAMSGDIVGAIR 299
                                                                                           GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                                                                                                     SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                                                                                                                                                    MKGRSALLRALWIAALSFGLGGVAVAARPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
                                                                                                                                             SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                                                                               AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                                                                                                                                                                                                                                                                             MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYBNLMVPSPSMGRDIPVAFLAGGPH
                                                                       GATAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                                                                                                                                                       AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                                                                                                                                                                                                                                                                                                                                                         Conservative
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95US-00545926.
95US-00551149.
95US-00568357.
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                                                                                                                                                                                                                                                                                                                                                                                        99.7%;
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                                                                                                                                                                                                                                                                                                                                                                       Score 1616; DB 2;
Pred. No. 1.8e-120;
0; Mismatches 1;
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                                                                                                                                                                                         Matches 298;
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccines against Mycobacterium containing major extracellular proteins used to, e.g. induce protective and therapeutic immune responses, and idetecting an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodominant epitope; inter opsonising humoral response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis; vaccination; extra immunodominant epitope; interleukin-12; MF59;
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                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                           MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
                     Saelpdwlaanrglapgghaavgaaqggygamalaafhpdregfagsmsgflypsntttn 180
                                                                                            AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 120
                                                                                                                          299 AA;
SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                         Conservative
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99.7%;
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                                                                                                                                                                                                        Score 1616; DB 2;
Pred. No. 1.8e-120;
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SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN

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Best Local (
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06-DEC-1995;
23-MAY-1996;
                                                                                                                                                           The invention relates to a novel nucleic acid encoding an abundant extracellular protein of Mycobacterium tuberculosis useful as vaccines for generating protective or therapeutic immune response against viral, bacterial, fungal and protozoal infections. They are also used as immunotherapeutic agents. The present sequence is M. tuberculosis straiserdman extracellular protein
                                                                                                                                                                                                                                                                         A nucleic acid encoding an abundant extracellular protein of Mycobacterium tuberculosis useful as vaccines for generating protective or therapeutic immune response against viral, bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; antibacterial; fungicide; protozoacide; virucide; therapy.
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                                                                                                                                      Sequence
                                                                                                                                                                                                                                           Example 2;
                                                                                                                                                                                                                                                                protozoal infections.
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23-MAY-1995;
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 19
                       13
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                                                                                                    Similarity
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AVYLLDAFNAGFDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                              MKGRSALLRALWIAALS FGLGGVAVAAEPTAKAAPYENLMVPS PSMGRDI PVAFLAGGPH
                                                          MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIGQTABAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR
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                                                                                                                                                                                                                                           Col 33-36; 82pp;
                                                                                           Conservative
                                                                                                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis.
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94US-00289667.
95US-00447398.
95US-00551149.
95US-00568357.
96US-00652842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular 24 KD protein.
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                                                                                                    99.7%;
99.7%;
                                                                                          Score 1616; D
Pred. No. 1.8e
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      Best Loc
Matches
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                                                                                                                                                                                                          A gene vaccine (I) comprises nucleic acid sequence encoding ubiquitin, and a nucleic acid sequence encoding the antigen protein of an intracellular parasite containing T-cell target sequence. (I) is useful for preventing or treating the disease resulting from intracellular protozoan parasite infection such as malaria, tuberculosis, toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection, achlamydia disease, infections caused by Rickettsia, leishmaniasis, achlamydia disease, infections caused by Rickettsia, leishmaniasis, achlamydia disease, Trypanosoma infections, Chagas disease, Japanes encephalitis, Herpes virus (alpha) infections, or severe acute poliomyelitis, Herpes virus (alpha) infections, or severe acute respiratory syndrome. This sequence represent a protein used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene vaccine having nucleic acids encoding ubiquitin and antigen protein of intracellular parasite, useful for treating parasite infections such as malaria, tuberculosis, toxoplasmosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimalarial; antitubercular; tuberculostatic; anti-HIV; antibacterial; haemostatic; protozoscide; antiinflammatory; neuroprotective; virucide; gene vaccine; ubiquitin; antigen; intracellular parasite; protozoan parasite infection; malaria; tuberculosis; toxoplasmosis; trypanosomiasis; AIDS; cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis; Ebola hemorrhagic fever; Trypanosoma; Rickettsia; laishmaniasis; Ebola hemorrhagic fever; Trypanosoma; Chagas disease; Japanese encephalitis; influenza; rubeola; dengue virus
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2003; 2003JP-00023507
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The present invention relates to a vaccinating agent for promoting an immune response in a mammalian host against an infectious Mycobacterium pathogen. The vaccinating agent comprises at least a portion or at least one immunodominant epitope of at least one majorly abundant extracellular product selected from M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 XD protein and their analogs, homologs, and subunits, and an II-12 or MF 59 adjuvant. The compositions of the present

New vaccinating agent i Mycobacterium pathogen extracellular products

for promoting an immune response against infectious and HIV infection using majorly abundant from Mycobacterium tuberculosis.

Example

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protozoa, virus
the HIV virus.
The invention relates to a novel method for the early detection of mycobacterial disease or infection in a subject. The method comprises assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies specific for
                                                                            Early detection of mycobacterial infection in a subject by assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies for early Mycobacterium tuberculosis antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amigqtaeamgnsrmfynqyrsvgghnghfdfþasgdngwgswapqlgamsgdivgair 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVYLLDAFNAGFDVSNWYTAGNAMYTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
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                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIGQAAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR
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                                                                                                                                                          Zolla-Pazner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are useful for stimulating a protective immune hosts against intracellular pathogens, such as viruses and fungus, particularly Mycobacterium irus. The present sequence is a M. tuberculosis
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                                                                                                                                                                                                                                                                                              tuberculosis.
                                                                                                                                                                                                                                                                                                                              disease; infection;
                                                                                                                                                                                                                                                                                                                                                     tuberculosis
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                                                                                                                                                                                                                                                                                                                                                     51
                                                       English
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bacteria,
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extracellular
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Best Local S
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                                                                                                                                                                                                                                                                                                                                               or more early Mycobacterium tuberculosis antigens. The invention furelates to: a kit for early detection of M. tuberculosis disease; are antigenic composition for early detection of the M. tuberculosis discor infection. The compositions of the invention have antibacterial activity. The method is useful for early detection of mycobacterial disease or infection in a subject and for preparing a vaccine against tuberculosis infection. This sequence represents a Mycobacterium tuberculosis MPT 51 protein of the invention.
                                                                                                                                                                                                                                                                                                                          Sequence
                         274
                                                    181
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                                                                                                                                                                                                                                                                                                                            266
              ASGDNGWGSWAPQLGAMSGDIVGAIR
                                                    VHASILAQNNTRVWVWSPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFP
                                                                                                        LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                                                                       LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                                                                                                             VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMA
                                                                                                                                                                           VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMA
 ASGDNGWGSWAPQLGAMSGDIVGAIR
                                                                                                                                                                                                                                                                     90.2%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                    Score 1462; DB 7;
Pred. No. 2.9e-108;
D; Mismatches 0;
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ADZ97846 standard; protein; 266 ₹

28-ЛП-2005 (first entry)

ADZ97846

Mycobacterium tuberculosis MPB51 protein -SEQ Ħ

vaccine; mycobacterium tuberculosis infection; antibacterial; MPB51

Mycobacterium tuberculosis.

JP2005130807-A.

31-OCT-2003; 2003JP-00372782

31-OCT-2003; 2003JP-00372782

(DOKU-) GYOSEI NICOH KAGAKU GIJUTSU HS

WPI; 2005-369245/38.

Novel MPT51 peptide having i for preparing anti-tubercle immune act e bacillus activity vaccine. with respect ដូ H cell, useful

Example 1; Ħ ĕ 4 gpp;

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AC for preparing a vacousequence represents invention comprises the amino acid sequence of Mycobacterium tuberculosis MPB51 protein. The preparing a vaccine against tuberculosis. The uence represents the Mycobacterium tuberculosis. d sequence of a C-terminal region of protein. The MPB51 peptide is useful culosis. The present amino acid tuberculosis MPB51 protein.

Sequence

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Best Local :
                                                                                                                                                                               of, or immunising a subject against Mycobacterium tuberculosis disease on infection. The composition of the invention contains a peptide from the M. tuberculosis GICB protein. The antigenic composition of the invention is useful for the early detection of, or immunising a subject against M. tuberculosis disease or infection. The present amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic composition, useful for early detection of, or subject against, Mycobacterium tuberculosis disease or in
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                       The invention comprises an antigenic composition for the early detection
                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
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secreted protein.
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                                                                                                                                                              represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UXNY )
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                                                                                                            256 AA;
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Score 1394; DB 7;
Pred. No. 7.3e-103;
0; Mismatches 0;
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Pred. No. 6.6e-107;
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The sequences given in AAB47555-57 show the protein subunits of the M. tuberculosis antigen 85 complex, Ag85A, Ag85B and Ag85C. Peptides of the invention derived from Ag85 can be recognized by a CD8 T-cell and may be used in the manufacture of agent for vaccinating prophylactically or therapeutically against infection by a mycobacterium by stimulating a CD8 T cell response. These peptides bind very strongly to HLA-B3501. Some of these peptides were able to induce cell mediated cytotoxicity using peptide-pulsed macrophages, and Ag85C(204-212) caused CD8 T cells to kill M. tuberculosis infected macrophages and induced intracellular IFN-gamma in activated CD8 cells. Ag85 derived polypeptides are useful for vaccinating a pre-selected host to stimulate a CD8 T cell response against a Mycobacterial infection. They are also useful for detecting in a population of T cells the presence or absence of CD8 T cells that recognize an epitope sequence, by contacting the population of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a polypeptide comprising CD8 T-cell groups derived from Mycobacterium tuberculosis antigen 85 in manufacture of a medicament vaccinating prophylactically or therapeutically against mycobacterial
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N-PSDB; AAH43503.
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RESULT 13
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ID AAM50
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XX AAM50
XX AAM50
XX Mtb;
XX Mtb;
XX Mtb;
XX Mtb;
XX Mycol
XX Mycol
XX Pept.
FT Pept.
FT Pept.
FT Prot
FT Prot
FT Prot
XX X
PN W020
XX 11-J
XX 10-J
XX 10-J
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Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising CD8 T-cells with the peptide in question and detecting whethe the CD8 T-cells recognize the peptide, by detecting the expression of a substance by the T cell which indicates that the T cell whave recognized the peptide or by detecting lysis by T cells of cells that present the peptide on their surface, the detection of lysis indicating that the T peptide on their surface, the detection of lysis indicating that the T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 340 AA;
                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells have recognized the peptide
                 WPI; 2002-164602/21
                                             Orme IM,
                                                                                                        10-JUL-2000; 2000US-0217646P
                                                                                                                                    10-JUL-2001; 2001WO-US021717
                                                                                                                                                                                                WO200204018-A2
                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM50731 standard; protein; 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPYWNEQLVAMKADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWYYCGNGTESDLGGDNIFAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFFFNGTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWVW----SPTNPGASD-PAAMI-GOTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SK-----OWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSAATTLPRRLAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVEYLQVPSASMGRDIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGSWAPQLGAMSGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                              Belisle JT;
                                                                                                                                                                                                                                                                                                                                                                 Ag85C; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                            COLORADO
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                     tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis immunodominant Mtb protein FbpC2 Ag85C.
                                                                                                                                                                                                                                            /label= Signal_peptide
/note= "SEC-dependent signal secretion
47...340
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                              /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%;
                                                                            STATE
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                                                                            RES
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                                                                                                                                                                                                                                                                                                                                                                 mycobacteria; immunisation; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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                                                                              FOUND
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S

문 S

Query Match

Score

DB 5;

Length

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Vaccine for boosting immunity to mycobacteria when administered life in a subject who has been vaccinated in childhood with Bac: Calmette-Guerrin, has purified proteins from mycobacterium tubes
                                                                                                                                                          tuberculosis.
                                                                                                                                                                ered in mid-
Bacillus
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Claim 8; Page 17; 61pp; English

strain H37Rv gene Rv0125c product, designated FbpC2 Ag85C. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAM50729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom protective immunity has waned. The vaccine compositions comprise 1 or more of the 31 purified immunogenic proteins. When used as immunogens, the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAM50759), the secreted product of the Rv3084v gene Sequence 340 present sequence ğ is that of the Mycobacterium tuberculosis (Mtb)

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                              251 IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS
                                                                                                                                 191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                  166
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                                                                                                                                                                                                                                                                                                                                                                                                     131;
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                                                                                                                                                                                                                                                                                                 53 AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG
                                                                                                                                                                                                                                                                                                                                                                  4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                               WGSWAPQLGAMSGDI
                                                                                            VWVW----SPINPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                         GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                 QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQPPYA
                                                                                                                                                                                                                                 SK-----QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
                                                                                                                                                                                                                                                             RSAATTLPRRLAIAAMGAVLVYĞLVGTFĞĞPATAGAFSRPGLPVEYLQVPSASMĞRDIKV
WPYWNEQLVAMKADI
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     34.8%;
                                 294
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No. 1.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                       119;
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25-MAR-2003
02-FEB-1993
                                                                        85-C.
            Protein
                                            Mycobacterium
                                                                                                                      AAR26167
                        Peptide
                                                          Immunise; antibody; vaccine;
                                                                                                                     standard; protein;
                                                                                      (first
                                                                                           (revised)
                                              tuberculosis
                               Location/Qualifiers
      /label= Mature_peptide
                  /label= Signal_peptide
                                                                                     entry)
                                                                                                                      340 AA.
                                                          PCR; antisera; amplify.
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Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; can respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis
                                                                                                                                                                                               AAY14857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 AA;
                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                          VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSNGQNYTYKWETELTREWPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFFYA
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Pred. No. 2.3e-36;
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23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
04-DEC-1998;
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                        GENESIS
 Watson
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97US-00997080.
97US-00997362.
98US-00095855.
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immune response ö an

Page 160; 243pp; English.

proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoldosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, allopecia areata, and skin cancers such as basal carcinoma, squamous ce M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The carcinoma and melanoma invention provides heat-killed Mycobacterium vaccae, or recombinant cell are

340 AA;

34.6%;

Score 561.5; DB 2 Pred. No. 2.3e-36;

2

Length

39;

Mismatches

119;

Indels

27;

Gaps

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WGSWAPQLGAMSGDI
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                                                                                                                              VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
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                                                                              IWVYCGNGTPSDLGGDNIPAKFLEGLT
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308 WPYWNEQLVAMKADI 322

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Search completed: April 14, 2006, 17:18:37 Job time : 117.851 secs

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1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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hypothetical glyci hypothetical glyci hypothetical prote	probable integral outer membrane pro	probable PPE prote tributyrin esteras	hypothetical glyci hupU protein - Rho	probable pntAA pro hypothetical glyci	fibroin - Chinese hypothetical prote	hypothetical glyci probable secreted

## ALIGNMENTS

fbpC1 protein precursor - Mycobacterium tuberculosis
N;Alternate names: major antigen MPT51
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: G70887; A60274

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9834230

A;Accession: G70887

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-299 <COL>

A;Cross-references: UNIPROT:Q48923; UNIPARC:UPI000012F437; GB:AL1022076; GB:AL123456; NI;A;Experimental source: strain H37RV
R;Experimental source: strain H37RV
R;Nagai, S.; Wiker, H.G.; Harbe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the cultur A;Reference number: A60274; MUID:91099889; PMID:1898899 A; Accession: A60274

Genetics:

A;Molecule type: protein A;Residues: 34-40,'Y',42-49;'K',51-58;59-76;77-78 <NAG> A;Cross-references: UNIPARC:UPI0000175922; UNIPARC:UPI00001794FC; UNIPARC:UPI00001794FD

A;Status: preliminary

A;Gene: fbpC1

C;Superfamily: Mycobacterium avium alpha-antigen
F;34-299/Product: fbpCl protein #status experimental <MAT>

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8 문 밁 S 片 8 Matches Query Match Best Local Similarity 121 121 SABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180 61 AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 120 μ 1 MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 120 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH Conservative 99.7**%**; 99.7**%**; Score 1616; DB 2; Length z: Pred. No. 2.4e-111; O: Mismatches 1; Indels Length 299; 0 Gaps 180 60

181 GAIAAGMQQFGGVDTNGMMGAPQLGRMXMHDPWVHASLLAQNNTRVMVMSPTNPGASDPA

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MPT51 protein - Mycobacterium leprae (fragment)
(;Species: Mycobacterium leprae
(;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
(;Accession: S32111
R;Rinke de Wit, T.F; Bekelie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, submitted to the EMBL Data Library, March 1993
A;Description: The M.leprae antigen 85 complex gene family: identification of the A;Reference number: S32107
A;Reference number: S32107
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-220 <RIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen 85C, mycolyltransferase (import C;Species: Mycobacterium legrae C;Date: 20-Apr-2001 #sequence_revision C;Accession: B86921 R;Cole, S.T.; Biglmeier, K.; Parkhill, R.; Davies, R.M.; Devlin, K.; Duthoy, Seam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <STO>
A;Cross-references: UNIPROT:Q05868; UNIPARC:UPI000012P4B7; GB:AL450380; NID:g13092480;
A;Cross-references: UNIPROT:Q05868; UNIPARC:UPI000012P4B7; GB:AL450380; NID:g13092480;
C;Genetics:
A;Gene: fbpc
A;Gene: fbpc
C;Superfamily: Mycobacterium avium alpha-antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B86921
      A; Cross-references:
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|Species: Mycobacterium leprae
|Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                           DIDAMIGQAVASMGSSREFYQQYRS
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      UNIPROT: Q05868;
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Duthoy, S.; I
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Pred. No. 1.4e-84;
3; Mismatches 41
      UNIPARC: UPI000016FB12;
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Fraser, 1
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      EMBL: Z21949; NID: g287923;
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Holroyd,
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A;Start codon:
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P31953; UNIPARC:UPI0000042501; GB:Z92770; GB:AL123456; NI A;Experimental source: strain H37Rv R;Content, J.; de la Cuvellerie, A.; De Wit, L.; Vincent-Levy-Frebault, V.; Ooms, J.; Infect. Immun. 59, 3205-3212, 1991
A;Title: The genes coding for the antigen 85 complexes of Mycobacterium tuberculosis n of the gene coding for antigen 85-C of Mycobacterium tuberculosis. A;Reference number: A43603; MUID:91348869; PMID:1715324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70615; A43603; S15504
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, R.; Davien, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
D70615
                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-20,'V',22-340 <CON>
A;Cross-references: UNIPARC:UPI000002DC31;
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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---QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
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Pred. No. 3.3
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genome

J.; D NID:

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RESULT 5

$32114

$32114

Sypotein - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: $32114

R;Rinke de Wit, T.F.; Bekelie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, J.E.

submitted to the EMBL Data Library, March 1993

A;Description: The M.leprae antigen 85 complex gene family: identification of the gene
A;Reference number: $32107

A;Accession: $32114

A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-333 <RIN>
A;Cross-references: UNIPROT:Q05862; UNIPARC;UPI0000125061; EMBL;Z21951; NID:g287921; P
C;Superfamily: Mycobacterium avium alpha-antigen
RESULT 6
$10326
$10326
alpha-antigen A, extracellular - Mycobacterium bovis
C,Species: Mycobacterium bovis
C,Species: Mycobacterium bovis
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: $10326; B41499
R,de Wit, L.; de la Cuvellarie, A.; Coms, J.; Content, J.
Nucleic Acids Res. 18, 3995, 1990
A,Fitle: Nucleotide sequence of the 32 kDa-protein gene (antigen A,Faccession: $10326
A,Faccession: $10326
A,Faccession: $10326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPTMIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FITQEMPSWIQANKNVLPTGNAAVGLSMSGSSALILASYYPQQPPYAASLSGFLNPSEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGLRAQEDYNGWDINTPAFEEYYHSGLSVIMPVGGQSSFYSNWYQPSQGNGQHYTYKWET 143
                                                                                                                                                                                                                                                                                                                                                                           GGDNIPAKFL--ESLTLSTNEIFQNTYAASGGRNGVFNFPPNGTHSWPYWNQQLVAMKPD
                                                                                                                                                                                                                                                                                                                                                                                                               GASD-PAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISABIPDWIAANRGIAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQ--DGSKQ-----WDT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIGTALLAGIVGVVGDTAIAVAFSKPGLPVBYLQVPSPSMGHDIKIQFQGGGQHAVYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPHAVYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGSWAPQLGAMSGDI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWVW-----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSNGQNYTYKWETPLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                                                                                                                                                                                                                                                                                                                    294
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Pred. No. 5.3e-33;
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A; Molecule type: DNA
A; Residues: 1-338 <WIT>
A; Residues: 1-338 <WIT>
A; Residues: 1-308 <WIT>
A; Cross-references: UNIPROT: P17944; UNIPARC: UPI000002CE66;
R; Wiker; H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A; Title: Evidence for three separate genes encoding the pro
A; Reference number: A41499; MUID: 90093478; PMID: 2403534
A; Accession: B41499
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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 324
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AL 325
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                                                                                        SDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVG
                                                                                                                                     TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                                                                                                                                          SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180
                                                                                                                                                                                                                                                                            LRAQDDFSGWDINTPAFEWYDQSGLSVVMPVGGQSSFYSDWYQPACGKAGCQTYKWETFL
                                                                                                                                                                                                                                                                                                                                                                                  AALSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDA
                                                                    NNLPAKFLEGFVRTSNIK-FQDAYNAGGGHNGVFDFPDSGTHSWEYWGAQLNAMKPDLQR
                                                                                                                                                                     GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
                                                                                                                                                                                                         TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
                                                                                                                                                                                                                                                                                                              FNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----SKQWDTFL
                                                                                                                                                                                                                                                                                                                                                AALVSGLVGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGANSPALYLLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium
                                    298
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     32.8%; Score 532; DB 2
40.1%; Pred. No. 8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         avium
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                                                                                                                                                                                                                                                                                                                                                                                                                      126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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32K antigen fbpA precursor - Mycobacterium tuberculosis (strain H37RV)
N;Alternate names: 30K native antigen; major protein antigen MPT45
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: H70887; A37024; C60274; A54318
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;

. : .; Gordon, Holroyd,

S

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 complete genome

A; Molecule type: DNA A; Status: nucleic acid sequence not shown; translation A; Reference number: A70500; A; Accession: H70887 10 10 shown

A;Residues: 1-338 <COL>
A;Cross-references: UNIPARC: UNIPARC: UPI000002CB66; GB:AL022076; GB:AL123456; A;Cross-references: UNIPARC: BTOOMS (GB:AL022076; GB:AL123456; A;Experimental source: strain H37Rv
R;Borremans, M.; De Wit, L.; Volckaert, G.; Ooms, J.; De Bruyn, J.; Huygen, K.; Van V Infect. Immun. 57, 3123-3130, 1989
A;Title: Cloning, sequence determination, and expression of a 32-kilodalton-protein gA;Reference number: A37024; MUID:89379378; PMID:2506131

Voo gen

Z

A;Molecule type: DNA
A;Residues: 1-23,25,"R',27-130,"R',132-291,"R',293-323,"HWVPRPTP'
A;Residues: UNIPARC:UPI00001794PB; GB:M27016; GB:X53898
A;Cross-references: UNIPARC:UPI00001794PB; GB:M27016; GB:X53898
R;Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991 A; Accession: A37024 ,332-333,335-338 **ABOR** 

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A;Accession: A54318
A;Status: preliminary
A;Molecule type: protein
A;Residues: 44-63 <SAL>
A;Cross-references: UNIPARC:UPI00000B9FC4
A;Experimental source: H37Ra
A;Note: sequence extracted from NCBI backbone (NCBIP:68909)
C;Genetics:
A;Gene: fbpA
C;Superfamily: Mycobacterium avium alpha-antigen
P;1-43/Domain: signal sequence #status predicted <SIG>
F;44-338/Product: 32K antigen fbpA #status experimental <MA
               A; Molecule type: DNA
A; Residues: 1-330 <STO>
A; Cross-references: UNIPROT: Q05861;
C; Genetics:
                                                                                                                                                                                                                  antigen 85A, mycolytransferase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: A86921 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Whee: R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, B.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin,
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                                                                                                         eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A86921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000015AA3B
R;Salata, R.A.; Sanson, A.J.; Malhotra, I.J.; Wiker, H.G.; Harboe,
J. Lab. Clin. Med. 118, 589-598, 1991
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A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A54318; MUID:92078747; PMID:1720803
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Best Local Simi
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 44-48 <NAG>
fbpA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSELPGWLQANRHYKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNLPAKFLEGFVRTSNIK-FODAYNAGGGHNGVFDFPDSGTHSWEYWGAQLNAMKPDLQR
                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>AALVSGLVGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGANSPALYLLDG</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 532,
Pred. No. 8
                                     UNIPARC: UPI0000125057; GB:AL450380; NID:g13092479;
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                                                                                                                                                                                                                            Thomson, N.R.; Wheeler, Fraser, A.; Hamlin, N.;
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Holroyd,
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A; Residues: 1-325 <WIT>
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A; Residues: 1-325 < COL>
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Best Local :
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                                                                                                                                                                                                            Superfamily:
                                                                                                                                                                                                                            Gene:
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                     79
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                                                                                             2
                   TAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----
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C; Superfamily: Mycobacterium avium alpha-antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
256 GKPTELGGNNLPAKLLEGLVRTSNIK-FODGYNAGGGHNAVFNFPDSGTHSWEYWGEOLN
                                                                                                                                                         173 YPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW---
                                                                                                                                                                                                                136 TYKWETFLTSELPQYLQSNKQIKPTGSAAVGLSMAGLSALTLAIYHPDQFIYVGSMSGLL
                                                                                                                                                                                                                                                               113 SKOMDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFL
                                                                                                                                                                                                                                                                                                                                                                               61 -AVYILDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    16 RRLVVEÁMGVÁLLSALIGVVGSÁPÁEAFSRPGLÞVEYLQVÞSÞSMGRÐIKVQFQNGGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RSALLRALWIAALS--FGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH-
                                                                                                         DPSNAMGPSLIGLAMGDAGGYKAADMWGPSTDPAWKRNDPTVNVGTLIANNTRIWMYCGN
                                                                                                                                                                                                                                                                                                                          PALYLLDGLRÄQDDFSGWDINTTÄFEWYYQSGISVVMFVGGQSSFYSDWYSPACGKAGCQ
                                                  -SPINDGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%; Score 521; DB 2
38.9%; Pred. No. 5e-31;
ative 39; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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A;Cross-references: UNIPROT:P31952;
A;Experimental source: strain H37Rv
R;de Wit, L.; Palou, M.; Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genon A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable fbpB protein - Mycobacterium tuberculosis (strain H37RV)
N;Alternate names; antigen 85-B precursor
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: C70516; S29664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S29663
A;Accession: S29664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;de Wit, L.; Palou, M.; Content, J submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                            Similarity
                                          GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDAFNAGPDVSNWV
GGAATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWD
                                                                                                                                                                                                                                                 Mycobacterium avium alpha-antiger
                                                                                                                        32.0%; Score 519; DB 2; llarity 38.7%; Pred. No. 6.9e-31; Conservative 39; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                   UNIPARC: UPI0000042500; EMBL: X62398; NID: g44563; PIDN: CAA44269.1;
                                                                                                                  Pred. No. 6.9e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             December 1991
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                                                                                                                                                                                      Length
                                                                                                                               Indels
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-SKQWDTFLSAELPDWLAAN

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RBSULT 11

A32348

A32348

A32348

A32348

A32348

Alpha-antigen B precursor, extracellular - Mycobacterium bovis alpha-antigen

C; Species: Mycobacterium bovis

C; Date: 21-May-1990 #sequence revision 21-May-1990 #text_chang

C; Accession: A32348; A41499; A60278

R; Mateuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Yamada, J. Bacteriol. 170, 3847-3854, 1988

A; Title: Cloning and expression of the Mycobacterium bovis BCG

A; Reference number: A32348; MUID:88314872; PMID:2842287

A; Accession: A32348

A; Molecule type: DNA

A; Residues: 1-323 - MA13

A; Residues: 1-323 - MA13

A; Residues: 1-323 - MA13
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A;Cross-references: UNIPROT:P12942; UNIPARC:UPI000012505B; R;Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M. Infect. Immun. 58, 272-274, 1990
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A; Residues: 1-325 <WIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRS -- SNLKFQDAYNAAGGHNAVFNFPPNGTHSWEYWGAQLNAMKGDLQSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAVKPTGSAAIGLSMAGSSAMILAAYHPQQPIYAGSLSALLDPSQGMGPSLIGLAMGDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDAFNAGPDVSNWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTN-PGASDPAAMIGQT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYKAADMWGPSSDPAWBRNDPTQQIPKLVANNTRLWVYCGNGTPNBLGGANIPABFLENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTPAPEWYYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWETLLTSELPQWLSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----SKQWDTFLSAELPDWLAAN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWD
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Pred. No. 1.9e-30;
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                                                                                                                                                                                                                        H.; Yamada,
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72

H--AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----

112

NSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSVIMPVGGQSSFYSDWYSPACGKAG 131 --SKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSG 170

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R;Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Terasaka, K.; Yamada, T. Infect. Immun. 58, 550-556, 1990
A;Title: Cloning and expression of the gene for the cross-reactive alpha antigen A;Reference number: A37185, MUID:90129315; PMID:2404875
A;Accession: A37185
                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-antigen precursor - Mycobacterium kansasii
C;Species: Mycobacterium kansasii
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A37185
                                            S
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A;Molecule type: DNA
A;Residues: 1-325 <MAT>
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R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium bovis
A;Reference number: A60278; MUID:91147217; PMID:1900061
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C;Superfamily: Mycobacterium avvum alpha-antigen
F;1-40/Domain: signal sequence #status predicted
F;41-323/Product: alpha antigen, extracellular #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Evidence for three separate genes encoding the proteins of A;Reference number: A41499; MUID:90093478; PMID:2403534 A;Accession: A41499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 41-59 < FIF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A60278
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                                                                                             Matches
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Similarity 38.7%;
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  GRRLLVGAAAAAALPGLVGLAGGAATAGAFSRPGLPVEYLQVPSAAMGRSIKVQFQSGGD
                                              GRSALLRALWIAALS--FGL-GGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEAMGNSRMFYNOYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAI 298
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                                                                                                Conservative
                                                                                                                                                                                                            UNIPROT: P21160; UNIPARC: UPI000012505D; GB:M53897
                                                                                           31.1%; Score 504.5; DB 2; 36.7%; Pred. No. 7.9e-30; 47. Mismatches 132;
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Pred. No. 2.2e-30;
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RESULT 13
JN0897
ANDREST TARREST pha-antigen - Mycobacterium avium C;Species: Mycobacterium avium C;Date: 06-Jan-1995 #sequence_revision C;Accession: S32773 R;Ohara, N.; Matsuo, K.; Yamaguchi, R.;
                                                                                                                                           RESULT 14
S32773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This protein is one of antigen 85.
C;Comment: This protein is an important stimulant of cellular C;Superfamily: Mycobacterium avium alpha-antigen E;1-40/Domain: signal sequence #status predicted <SIG>
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A;Title: Cloning, sequencing and expression of the gene
A;Reference number: JN0897; MUID:94071912; PMID:8250904
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A; Residues: 1-330 < KIT>
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     K.; Yamaguchi, R.; Yamazaki,
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Pred. No. 8.6
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eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonde, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen 85A, mycolyltransferase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #text_change 09-Jul-2004 C;Date: 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: G87162 C;Accession: G87162 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheel R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin,
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A; Accession: S32773
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-327 <STO>
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A;Description: Nucleotide sequence of the alpha-antigen gene of Mycobacterium
A;Reference number: 832773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-330 < OHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: G87162
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                                                                                           61 AVYLLDAFNAGPDVSNWVTAGNAMVTLAGKGISVVAPAGGAYSMYTNWEQDG-----S
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KQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLY
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                                                                                                                                                                                                                                                                                                                                            Mycobacterium avium alpha-antigen
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	311 AMKPDL 316	Db 311	
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AGGHNAVFNLNADGTHSWEYWGAQLN 310	253 TPSELGGTNVPABFLENFVHGSNLKFQDAYNGAGGHNAVFNLNADGTHSWEYWGAQLN 310	Db 253	
VGGHNGHFDFPASGDNGWGSWAPQLG 288	230 SPTNPGASD-PAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQIG 288	Qy 230	
QRNDPILQAGKLVANNTHLWVYCGNG 252	193 SSQGIEPQLIGLAMGDAGGYKAADMWGPPNDPAWQRNDPILQAGKLVANNTHLMVYCGNG 252	Db 193	
KWHDPWVHASLLAQNNTRVWVW 229	174 PSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW 229	Qy 174	
GSSALILAAYHPDQFIYAGSLSALMD 192		Db 133	

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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CDC 1531 / Oshkosh;

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DOI=10.1128/JB.184.19.5479-5490.2002;

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complete genome sequence.";
Nature 393:537-544(1998).
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POA4V6; O33176; Q48923;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
MPT51/MPB51 antigen precursor.
Name=mpt51; Synonyms=fbpD, mpb51; OrderedLocusNames=Rv3803c,
ORFNames=MTV026.08c;
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"Bvidence for the secreted protein MPT51 from
tuberculosis is a T-cell antigen.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAÎN-H37Rv;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae, Mycobacteriaceae; Mycobacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced t between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
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Name=fbpC1; OrderedLocusNames=MAP0217; Mycobacterium paratuberculosis. Bacteria; Actinobacteria; Actinobacter

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Mycobacteriaceae; Mycobacterium;

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R InterPro; IPR00801; Esterase_put.
R InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00756; Esterase; 1.
Pfam; PF00756; Esterase; 1.
Pfam; PF007178; AA_TRNA_LIGASE_I; UNKNOWN_1.
Complete proteome.
SEQUENCE 300 AA; 30929 MW; 11F27F49864427RD C
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Q05868; Q50207;
Q1-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
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Li L., Bann
                                                                                                            "Studies of MPT51 like I
Submitted (MAY-1995) to
[2]
                                                                                                                                                                                                                  Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B. Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamilholroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moul-
                                                     STRAIN=TN;
MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomso
                                                                                                                                                                                                                                                               MPT51 antigen precursor.
Name=mpt51; OrderedLocusNames=ML0098;
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STRAIN-Tha153;
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NCBI_TaxID=1769;
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Best Local S
Matches 234
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EMBL; AL583917; CAC29606.1; -
EMBL; Z21949; CAA79947.1; -; 0
PIR; B86921; B86921.1
PIR; S32111; S32111.
HSSP; P31953; 1DQZ.
SMR; Q05868; 36-301.
                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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MEDLINE-93366419; PubMed-8359887;
Rinke de Wit T.F., Bekelle S., Osland
Thole J.E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"Massive gene decay in the leprosy bacillus.";
"Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Acyltransferase;
SIGNAL 1
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                                                                                                                                                                                                                                                                                           Similarity
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                                                       DPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGA
                                                                                       TPLSSELPDWLATKRGLAPDGHAAVGASQGGYAALALAAPHPDRPGFAGSLSGFVYPSST
                                                                                                                                                 TFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNT
                                                                                                                                                                                     GPHAVYLLDAFNAALDVSNWVTAGNAMTTLGGRGISVVAPAGGAYSMYTNWENDGSKQWD
                                                                                                                                                                                                 GPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWD
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                                             DIDAMIGOAVASMGSSREFYQQYRS
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                      299
 301
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Belongs to the mycobacterial A85 antigen family.
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77.5%;
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-; Genomic_DNA.
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                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                             Score 1251; D
Pred. No. 1e-7
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                             mplete proteome; Signal; Transferase.
Potential.
MPT51 antigen.
S -> F (in Ref. 1).
S -> F (in Ref. 1).
APQLAAMSGDIVGAIR -> GAAVGCYVGRYRRHSLGRNQ
WHGRCCGDEPVSCMGRARMVSGEHRHRTPYVHRNLPRDLPI
                                                                                                                                                                                                                                                                                                                                       LLAGDPEWSRKCHVSATESSPGRLPCRWRPSWRWPLWLW (in Ref. 1).
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85A, 85C, and
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteriaceae; Mycobacterium;
Corynebacterium avium complex (MAC).
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MEDLINE=97427949; PubMed=9284137;
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Pfam; PF00756; Esterase; 1.
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   RVWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDN
                                                                                                                                                                                                                                                                                                                                     VQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEBFYQSGLSVIMPVGGQSSFYSNWYQP
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                                                                                                                                    AGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNT
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Fibronectin-binding.
Acyl-ester intermediate (By si
By similarity.
By similarity.
A29277CB650D60A4 CRC64;
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Pred. No. 1.1
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Q8KY58 MYCPA
ID Q8KY58 M
AC Q8KY58 7
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DT 01-QCT-2
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OS Mycobact
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Li L. Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AE017239; AASO6081.1; -; Genomic_DNA.
SMR; Q73U37; 49-326.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                        GWGSWAPQLGAMSGDI
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MUCLEOTIDE SEQUENCE.

MEDLINE=22481140; PubMed=12592709; DOI=10.1080/1042517021000019269;

MEDLINE=22481140; PubMed=12592709; DOI=10.1080/1042517021000019269;

Dheenadhayalan V., Shin K.S., Chang C.P., Chang S.J.,

McDonough S., McDonough P., Stehman S., Shin S., Torres A.,

Chang Y.P.;

"Cloning and characterization of the genes coding for antigen 85A,

and 85C of Mycobacterium avium subsp. paratuberculosis.";

DNA Seq. 13:287-294(2002).
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30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
Arransferase 85C) (RC 2.3.1.-) (Fibronectin-binding protein Name=EppC; Synonyme=mpt45; OrderedLocusNames=Mb0134c;
Mycobacterium bovis.
                                        NUCLEOTIDE SEQUENCE [LARGE
STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=1;
Garnier T., Eiglmeier K., (
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P0A4V5; P31953; P96806;
                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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    PubMed=12788972; DOI=10.1073/pnas.1130426100;
eier K., Camus J.-C., Medina N., Mansoor H.,
S., Grondin S., Lacroix C., Monsempe C., Simon
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ORFNames=MTCI5.03c; Mycobacterium tuberculosis Bacteria; Actinobacteria; /

Actinobacteridae; Actinomycetales;

MT0137;

\_MYCTU STANDARD; PRT; 340 AA.

ABSC MYCTU STANDARD; PRT; 340 AA.

POA4V4; P31953; P96806;

POA4V4; P31953; P96806;

10-JUL-1993 (Rel. 26, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

10-MAY-2005 (Rel. 47, Last annotation update)

Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)

transferase 85C) (RC 2.3.1.-) (Fibronectin-binding protein C

Name=fbpC; Synonyms=mpt45; OrderedLocusNames=Rv0129c, MT0137

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                                                                               VWVW----SPINPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
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Fibronectin-binding.
Acyl-ester intermediate (
By similarity.
By similarity.
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complete
Nature 39
[3]
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Harris D.B., Gordon S.V., Eiglmeler K., Gas S., Barry C.B. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davles R.M., Devlin K., Feltwell T., Gentles S., Hamlin
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.",
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                            potential targets for mycobacterial drugs and vaccines.";
Nat. Struct. Biol. 7:141-146 (2000).
-I- FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nece for maintaining cell wall integrity.
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: Belongs to the mycobacterial A85 antigen family.
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MEDLINS=2236494; PubMedd=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O. Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva Salzberg S.L., Delcher A., Utcerback T.R., Weidman J.F., Khouri Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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Infect.
[2]
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MEDLINE=20122630; PubMed=10655617; DOI=10.1038/72413;
Ronning D.R., Klabunde T., Besra G.S., Vissa V.D., Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
MCBI_TaxID=1773;
                                                                                                                                                                                                                                             use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
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MEDLINE=91348869; PubMed=1715324;
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BI; X57229; CAA40506.1; -; G
BI; BX842572; CAE55244.1; -;
BI; AE000516; PAK44361.1; AI;
R; D70615; D70615.
B; 1DQ2; X-ray; A=47-328.
B; 1DQ2; X-ray; A/B=49-328.
R; P0A4V4; 49-328.
R; P0A4V4; 49-328.
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Immun. 59:3205-3212(1991)
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Bioinformatics Institute. There are no
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    166 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
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              AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAFAGGAYSMYTNWEQDG
                                                   RSAATTLPRRLAIAAMGAVLVYĞLVGTFĞĞPATAGAFSRPGLPVEYLQVPSASMGRDIKV
                                                             RSA----LLRALWIAA----LSFGL-----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                                 QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
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Pred. No. 3.7e.
38; Mismatches
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RESULT
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01-FEB-1994
01-FEB-1994
10-MAY-2005
                                                                                                                                                                                                                                                                                      MEDLINE=1128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T. Biglmeier K., Parkhill J. James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B., Wheeler P.R., Basham D., Brown D., Chillingworth T., Connor R., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Hawlies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WXCLE
                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure necessor maintaining cell wall integrity (By similarity).
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01-FEB-1994 (Rel. 28, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein (Name=fbpC; Synonyms=fbpC2; OrderedLocusNames=ML2855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=93366419; PubMed=8359887;
MENTANE de Wit T.F., Bekelie S., Osland A.,
Thole J.E.R.;
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Barrell B.G.;
                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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European Bioinformatics Institute.
as long as its content is in no way
; Z21951; CAA79949.1; -; Genomic_DNA.; M90649; AAA91865.1; -; Genomic_DNA.; AL583926; CAC32187.1; -; Genomic_DN; S32114; S32114.

; P31953; 1DQY.
; Q05862; 49-328.
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RESULT 11
A85A_MYCBO
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PDAAV3; P17944; P17996;
01-NOV-1990 (Rel. 16, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A)
transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A
Name=fbpA; Synonyms=mpt44; OrderedLocusNames=Mb3834c;
                                                                                                                                                                               NUCLEOTIDE SEQUENCE.

STRAIN-BCG / Paris 1173 P2;

MEDLINE-90326531; PubMed-2197602;

de Wit L., de la Cuvellerie A., Ooms J., Content
"Nucleotide sequence of the 32 kDa-protein gene |
Mycobacterium boyis BCG.";
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Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G. "The complete genome sequence of Mycobacterium bovis.";
                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                              STRAIN=AF2122/97
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InterPro; IPR000801; Esterase put.
Pfam; PR00756; Esterase; 1.
                                                                                             MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
                                                                                                                                                                     Nucleic
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1765;
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Fibronectin-binding.

Acyl-ester intermediate (

By similarity.

By similarity.
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Query Match
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Matches 121
              A85A WYCTU STANDARD; PRT; 338 AA.
P044V2; P17944; P17996;
01-NOV-1990 (Rel. 16, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A)
Antigen 85-A precursor (85A) (Fibronectin-binding protein A
transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A
Name=fbpA; Synonyms=mpt44; OrderedLocusNames=Rv3804c, MT3911
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-I- FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nece for maintaining cell wall integrity.

-I- SUBCELIULAR LOCATION: Secreted.
-I- PTM: Contains one disulfide bridge.
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X53034; CAA37206.1; -; Genomic_DNA.
BX248347; CAD96020.1; -; Genomic_DN
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PF00756; Esterase;
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Fibronectin-binding.

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By similarity.

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CRC64;
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Pred. No. 6.
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MEDLINE-88295987; PubMed-9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R. Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-CDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M. Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harth G., Lee B.Y., Wang J., Clemens D.L., Horwitz M. "Novel insights into the genetics, biochemistry, and immunocytochemistry of the 30-kilodalton major extrac of Mycobacterium tuberculosis.";
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              Nature
[5]
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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MEDLINE=96333337; PubMed=8757831;
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                                                                rot entry is copyright. It is produced Swiss Institute of Bioinformatics and Bioinformatics Institute. There are
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Lee C.F., Chang S.Y., Yu D.S.;
Submitted (DEC-2002) to the EMBL/Ge:
EMBL; AY207395; AA062004.1; -; Geno
MSSP; P31952; 1F0N.
SMR; O847N5; 43-330.
InterPro; IPR000801; Esterase_put.
Pfam; PP00756; Esterase; 1.
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EMBL; AR000516; AAK48;
PIR; H70887; H70887.
HSSP; P31952; LPON.
SMR; P0A4V2; 43-330.
TIGR; MT3911;
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By similarity.
By similarity.
GAA -> AR (in Ref. 1).
G -> R (in Ref. 1).
G -> R (in Ref. 1).
ALGATPNTGPA -> HWVPRPTPGP (in Ref. 1).
STB1CF95D07D52C0 CRC64;
                                                                               EMBL/GenBank/DDBJ
-; Genomic_DNA.
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Last sequence update)
Last annotation updat
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Pred. No. 6.5e-
37; Mismatches
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05-JUL-2004 (TrEME
05-JUL-2004 (TrEME
05-JUL-2004 (TrEME
Secreted antigen (
                                                                                                                                                                                                                                                                                                                                                                                          Liu F., Yu S., Chen Q., Nie J., Ru:
Jiang X., Li Z.;
Submitted (MAR-2004) to the EMBL/G.
EMBL; AY577803; AAS89650.1; -; Gen
SMR; Q6PUJ6; 43-330.
InterPro; IPR000801; Esterase_put.
                                                                                                                                                                                                                                                                                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium bovis BCG.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=D2;
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                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00756; Bsterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=fbpA;
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                                                                                                                                                  14 AALSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDA
                                                                                                                                                                                                               121;
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SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                FNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
                                       LRAQDDFSGWDINTPAFEWYDQSGLSVVMPVGGQSSFYSDWYQPACGKAGCQTYKWETFL
                                                                                                                          AALVSGLVGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGANSPALYLLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          목교원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDPAAMIGQTABAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRAQDDFSGWDINTPAFEWYDQSGLSVVMPVGGQSSFYSDWYQPACGKAGCQTYKWETFL
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TIEMBLrel. 27, Created)
(TIEMBLrel. 27, Last sequence up
(TIEMBLrel. 27, Last annotation
:igen 85A precursor.
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                                                                                                                                                                                                       Score 532; DB
Pred. No. 6.5e.
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
-; Genomic_DNA.
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Pred. No. 6.5e-29;
                                                                                                                                                                                                                                                                                          Potential.
secreted antigen 8:
; 57B1CF95D07D52C0
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.5e-29;
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                                                                                -SKQWDTFL
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180
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RESULT 15

A85A MYCLE
ID A85A MYCLE
AC Q0567;
DT 01-WN-1994
DT 01-WN-1994
DT 01-WN-2005
DE Antigen 85-J
DE transferase
GN Mycobacteria; A
OCC Bacteria; A
OCC STRALMSThail
RC COTYNEBACTE;
RN [1]
RA Yin Y.;
RT 1Eprae and
RL Kansenshoga;
RN [2]
RP NUCLEOTIDE;
RA Yin Y.;
RT MOLECULAR
RT LEPRAE and
RL KANSENSHOSA;
RN [2]
RP NUCLEOTIDE;
RA Ge Mendonca
RL Submitted ()
RN [3]
RP NUCLEOTIDE;
RA MEDLINE=211
RA GLEST,
RA GLEST,
RA HOLTOYD S.;
RA MEDLINE=211
RA COLE S.T.,
RA MUCLEOTIDE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 143-330.
MEDLINE=93366419; PubMed=9359887;
Rinke de Wit T.F., Bekelie S., Osland
Thole J.B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-A precursor (85A) (Antigen 85 complex A)
transferase 85A) (EC 2.3.1.-) (Fibronectin-binding I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=Thai53;
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[2]
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Bacteria; Actinobacteria;
                                                                                                                                                                                                                                         "The Mycobacterium identification of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95130993; PubMed=7829901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=fbpA; OrderedLocusNames=ML0097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendonca-Lima
  FUNCTION: Proteins of the antigen 85 complex are responsible for the high affinity of mycobacteria to fibromectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure necessfor maintaining cell wall integrity (By similarity). SUBCELLULAR LOCATION: Secreted.

PTM: Contains one disulfide bridge (By similarity).
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its over production in Escherichia coli.";
aku Zasshi 68:1330-1337(1994).
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EMBL; AL583917; CAC29605.1; -; Genomic_DNA.
EMBL; Z21950; CAA79948.1; -; Genomic_DNA.
PIR; A86921; A86921, A86921.
PIR; S32107; S32107.
HSSP; P31952; 1PON.
SMR; O05861; 42-328.
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                                                                                                                                                                     SKQWDTFLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAWALAAFHPDRFGFAGSMSGFL
                                                                                                                                                                                                           PALYLLDGLRAQDDFSGWDINTTAFEWYYQSGISVVMPVGGQSSFYSDWYSPACGKAGCQ
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                                                                         -SPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHPDFPASGDNGWGSWAPQLG
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Fibronectin-binding.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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US-08-997-362-37
US-09-205-426-37
US-09-205-426-37
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US-09-295-820-31
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US-08-997-362-36
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	523	523	532	532	532	532	532	532	532	532	532	532	532	532	532	532	532	532
	32.3	32.3	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8
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	٢	<b>-</b>	N	N	N	N	N	N	N	N	N	N	N	N	Ŋ	N	۲	۲
ALIGNMENTS	US-08-997-362-30	US-08-997-080-30	US-09-295-820-28	US-09-342-673-39	US-09-200-643-34	US-09-200-643-32	US-09-205-426-34	US-09-205-426-32	US-09-324-542-34	US-09-324-542-32	US-08-705-347A-34	US-08-705-347A-32	US-09-095-855-34	US-09-095-855-32	US-08-873-970-34	US-08-873-970-32	US-08-997-362-34	US-08-997-362-32
	-	Sequence 30, Appl	-	Sequence 39, Appl	-	-	-	-	-	-	-	-				-	-	-

## APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter Birk APPLICANT: ROSENKRANDS, Ida APPLICANT: ROSENKRANDS, Ida APPLICANT: FLORIO, Walter TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS FILE REFERENCE: 670001-2002.1 CURRENT FILING DATE: 1996-03-30 CURRENT FILING DATE: 1996-03-30 EARLIER APPLICATION NUMBER: 0376/97 EARLIER APPLICATION NUMBER: 1277/97 EARLIER FILING DATE: 1997-04-02 EARLIER FILING DATE: 1997-04-02 EARLIER FILING DATE: 1997-04-02 EARLIER FILING DATE: 1997-04-08 EARLIER PILING DATE: 1997-04-18 EARLIER PILING DATE: 1997-04-18 EARLIER PILING DATE: 1997-04-18 ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-050-739-42 US-09-050-739-42 ; NUMBER OF SEQ ID NO: ; SOFTWARE: PatentIn V ; SEQ ID NO 42 ; LENGTH: 299 Query Match Best Local Simi Matches 299; GENERAL INFORMATION: sequence 42, Application US/09050739 Patent No. 6641814 EARLIER APPLICATION NUMBER: 60/070,488 EARLIER FILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOFTWARE: Patentin Ver. 2.0 Similarity Conservative 100.0%; ۰, Score 1621; DB 2; Pred. No. 2.7e-136; ); Mismatches 0; Indels Length 0, Gaps

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61 AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL

120

MKGRSALLRALMIAALSEGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH AVYLLDAFNAGPDVSNMVTAGNAMNTLAGKGISVVAPAGGAYSMYTNMEQDGSKQWDTFL

61

<u>بــ</u>

1 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH

181 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA

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US-08-107-676-3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 612-332-5300
TELEPAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/107,676
FILING DATE: 04-OCT-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 9
FILING DATE: 14-FEB-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DeBruyn, Jacqueline
TITLE OF INVENTION: Mycobacteri
TITLE OF INVENTION: Acids Encoc
TITLE OF INVENTION: Tuberculosi
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                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                         y Match 34.6%; Score 561.5; DB 1; Local Similarity 41.3%; Pred. No. 6.4e-42; hes 130; Conservative 39; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3100 No. CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/EF92/00268 FILING DATE: 07-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Merchant & Gould STREET: 3100 No. 5955356west Center
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131 QSNGQNYTYKWETFITREMPAWIQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA 190

    Application US/08107676
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                      SK-----QMDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                            AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                                                 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
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                                                                                    QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
                                                                                                                                                                         RSAATTLPRRVAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVEYLQVPSASMGRDIKV 70
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DeWit, Lucas
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                                                                                                                                                                                                                                                                                                     Length 340;
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RESULT 3
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SOPTMARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/107,676
FILING DATE: 04-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00268
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400388.4
APPLICATION NUMBER: EP 91400388.4
APPLICATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 3676.89USWO
TELEPHONE: 612-332-5300
                                                              Query Match 34.6%;
Best Local Similarity 41.3%;
Matches 130; Conservative 3
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Patent No. 5955356
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5955356west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DeWit, Lucas
APPLICANT: DeBruyn, Jacqueline
TITLE OP INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OP INVENTION: Acids Encoding Them for Diagnosis and Control
TITLE OP INVENTION: Tuberculosis
NUMBER OF SEQUENCES: 38
                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: Protein sequence from antigen 85C from M.
CLONE: tuberculosis
                                                                                                                                                                                                                                        MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
4 RSA---LIRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
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                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                   340 amino acids
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                                                                                                                                                                                                                                                                                                           linear
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                                                                ; Score 561.5; DB 1;
; Pred. No. 6.4e-42;
39; Mismatches 119;
                                                                     Indels
                                                                                                             Length 340;
                                                                     27;
                                                                     Gaps
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; Sequence:
; Patent No. 596052.
; Patent No. 596052.
; Patent No. 596052.
; GENERAL INFORMATION: JAMES D.
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                ; LENGTH: 340 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-080-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-997-080-37
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                                                                  Query Match
Best Local Similarity
                                               Matches 130;
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                        TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
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          4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7, Application US/08997080 
5968524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SK-----QWDTFLSAELPDWLAANRGLAPGGHAAYGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS 130
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                                                 Conservative
                                                                  34.6%;
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                                               39;
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                                               Score 561.5; DB 1;
Pred. No. 6.4e-42;
9; Mismatches 119;
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                                               27;
                                               Gaps
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US-08-997-362-37
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APPLICANT: Tan, P.
                                                                                                             INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                      APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970 FILLING DATE: June 12, 1997 APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 1996 ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet
                                                                                                                                                                         REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                         SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
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                                            TYPE: amino acids
                             STRANDEDNESS:
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        TOPOLOGY:
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Visser, Elizabeth
Skinner, Margot
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US-08-873-970-37
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATE: 08/705,347
APPLICATION UNMER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W.
STREET: 2601 Elliott Avenue, Suit
                 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASUSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: TREATMENT
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                                                    NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
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                                                                                                                                                                                                                                                                                                                                                         98121
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Visser, Elizabeth
 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skinner, Margot
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Pred. No. 6.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 n W. Speckman
Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
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US-09-095-855-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Tan, Pa
APPLICANT: Visser,
APPLICANT: Skinner
APPLICANT: Prestid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37, Application US/09095855 Patent No. 6160093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sin Matches 130;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                     OPERATING SYSTEM: DOS
SOPTWARE: PastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
APPLICATION NUMBER: 08/70:
FILING DATE: 29-AUG-196
APPLICATION NUMBER: 08/87:
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 98121
                                                                                                                                  FILING DATE:
                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 QSNGQNYTYKWETFLTREMPAMLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 SK-----OWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFBEYYQSGLSVIMPVGGQSSFYTDWYQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RSAATTLPRRVAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVBYLQVPSASMGRDIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                                                                                                                                                                                                                                                                                                                      Seattle: WA
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                                                                                                                                                                                                                                                                                                                                                           2601 Elliott Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tan, Paul
Visser, Elizabeth
Skinner, Margot
                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                 Diskette
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   08/997,362
                                      08/873,970
                                                                         08/705,347
                                                                                                                                                     US/09/095,855
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Pred. No. 6.4e-42;
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307

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US-08-705-347A-37
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Best Local Similarity 41.3%;
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tan, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 55
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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 APPLICATION NUMBER:
                                                                                                                                                                                                                ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 340 amino acids
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                                                                                                                                                                              Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLSGFLNPSBGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSA---LLRALWIAA----LSFGL----GGVAVAABPTAKAAPYENLMVPSPSMGRDIPV 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSAATTLPRRVAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVBYLQVPSASMGRDIKV 70
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                                                                                                                                                                                           B: Speckman Picard PLLC
2601 Elliott Avenue, Su
                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                Tan, Paul
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US/08/705,347A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 561.5; DB 2
Pred. No. 6.4e-42;
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                                                                                                                                                                                                                                                                     AND METHODS FOR TREATMENT AND OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                 Suite 4185
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APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Testidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-324-542-37
; Sequence 37, A
                                                                                             US-09-324-542-37
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Query Match
Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 632897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206.269.0565
TELEPHAX: 206.269.0563
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                ORGANISM: Mycobacterium tuberculosis
                                                                                                                                        LENGTH: 340
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Similarity 41.3%; Pred. No. 6.4e-42;
30; Conservative 39; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS 307
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34.6%; Score 561.5; DB 2
41.3%; Pred. No. 6.4e-42;
tive 39; Mismatches 119
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                                           DB 2;
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Conservative

Indels

27;

Gaps

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TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT FILING DATE: 1998-12-04

EARLIER FILING DATE: 1998-06-11

EARLIER FILING DATE: 1999-06-11

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER APPLICATION NUMBER: 08/873,970

EARLIER APPLICATION NUMBER: 08/705,347

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOPTMARE: PASTSEQ for Windows Version 3.0

TYDE: DEFT
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Best Local S
Matches 130
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                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis -09-205-426-37
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                           GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWXWHDPWVHASLLAQNNTR
                                                                                                                          QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS 130
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ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                       SK-----QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
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; Pred. No. 6.4e-42;
39; Mismatches 119;
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RESULT 12
US-09-295-820-3
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US-09-200-643-37
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 37
LENGTH: 340
TYPE: PRT
                                                                                                                                Sequence 3, Application Patent No. 6638511 GENERAL INFORMATION:
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Best Local (
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APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
ITIE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002CON
CURRENT FILING APPLICATION NUMBER: US/09/200,643
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
 NUMBER
                                                         TITLE
                                                                                                              APPLICANT: Content,
                                                                                                                                                                                                                                                                                                                                                                               226
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               DeBruyn, Jacqueline
INVENTION: Mycobacterium Polypeptides and Nucleic
Acids Encoding Them for Diagnosis and Control
Tuberculosis
SEQUENCES:
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Pred. No. 6.4e-42;
9; Mismatches 119
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TOPOLOGY: Inear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID
US-09-295-820-3
                                                                                                       RESULT 13
US-09-295-820-31
Sequence 31, Application US/09295820
Patent No. 6638511
GENERAL INFORMATION:
APPLICANT: Content, Jean
DeWit, Lucas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: BP 91400388.4
FILING DATE: 14-PEB-1991
ATTORNEY/ACENT INFORMATION:
NAME: Kowalchyk, Katherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,820
FILING DATE: 21-App-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6638511west
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,676
FILING DATE: <Unknown>
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                WGSWAPQLGAMSGDI 294
                                                                                                                                                                                                                                                                                                                                                           ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                               GSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SK-----QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSAATTLPRRVAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVBYLQVPSASMGRDIKV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSA---LLRALWIAA----LSFGL----GGVAVAABPTAKAAPYENLMVPSPSMGRDIPV
                                                                                                                                                                                         WPYWNEQLVAMKADI 322
                                                                                                                                                                                                                                                                       IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 6.4e-42;
9; Mismatches 119
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Best Local (
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INFORMATION FOR SEQ ID NO: 31:
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FILING DATE: <Unbrown>
APPLICATION NUMBER: EP 91400388.4
FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,820
FILING DATE: 21-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis IMMEDIATE SOURCE:
CLONE: Protein sequence from antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
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ADDRESSE: Merchant & Gould
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TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
Acids Encoding Them for Diagnosis and (
Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
  280 WGSWAPQLGAMSGDI
                                                                                                       226 VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                            166 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                                131 QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                                                                                                                                                                                                                                                         113
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                                                                IWVYCGNGTPSDLGGDNIPAKPLEGLT---LRTNQTPRDTYAADGGRNGVFNFPPNGTHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RSA---LIRALWIAA----LSFGL----GGVAVAABPTAKAAPYENLMVPSPSMGRDIPV
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Pred. No. 6.4e-42;
9; Mismatches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE: ORGANISM: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/508,761B
FILING DATE: 31-UUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
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                                                                                                                                                                                                                                                                                 Local Similarity
nes 123; Conserv
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TOPOLOGY: 11
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REFERENCE/DOCKET NUMBER: P58525NA
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                                                                                          ELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTNGA
                                 IAAGMOOFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGASD 238
                                                                      EMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYAASLSGFLNPSEGWWPTL 185
                                                                                                                                        AQDDYNGWDINTPAFEBYYQSGLSVIMPVGGQSSFYTDWYQPSQSNGQNYTYKWETFLTR 125
                                                                                                                                                                         AGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSK-----QWDTFLSA 122
                                                                                                                                                                                                              AVLVYGLVGTFGGPÄTÄGAFSRPGLPVEYLQVPSASMGRDIKVQFQGGGPHÄVYLLDGLR 65
IGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTRIWVYCGNGTPSDLGGDN
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400 Seventh St. N.W.
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Pred. No. 6.3e-42;
B; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                     Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY AGENT INFORMATION:
ATME: Sleath, Janet
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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COUNTRY: US
ZIP: 98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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235 GASD-PAAMIGQTAHAMGNSRMFYNQYRSVGGHNGHFDFFASGDNGWGSWAPQLGAMSGD
                                                                                                     204 WPTMİGLAMNDSĞĞYNANSMÜĞPSTDPAÜKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
                                                                                                                                                                                                                                               144
                                                                                                                                                                                                                                                                                                          119 FLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTT 178
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                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                66 DAFNAGEDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQ--DGSKQ-----WDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AVIGTALLAGIVGVVGDTAIAVAFSKPGLEVEYLQVESESMGHDIKIQFQGGGQHAVYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPHAVYLL
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Search completed: April 14, 2006, 17:37:57 Job time : 28.6477 secs	322 i 322	294 I 294	264 GGDNIPAKFLESLTLSTNBIFQNTYAASGGRNGVFNFPBNGTHSWPYWNQQLVAMKPD 321

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Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2006 Biocceleration
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US-10-9810-505-37
US-09-880-505-36
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RESULT 1		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
RESULT 1		506	506	506	512	512	512.5	513	513	514.5	514.5	514.5	518	518	518	519	519	519	519
3		31.2	31.2	31.2	31.6	31.6	31.6	31.6	31.6	31.7	31.7	31.7	32.0	32.0	32.0	32.0	32.0	32.0	32.0
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	ALIGNMENTS	US-09-804-980-173	US-09-805-427A-4	US-09-791-171-173	US-10-051-643-35	US-09-880-505-35	US-10-369-983-18	US-10-329-087-43	US-10-332-512A-31	US-10-205-979-31	US-10-051-643-45	US-09-880-505-45	US-10-205-979-29	US-10-051-643-43	US-09-880-505-43	US-10-695-155-161	US-10-332-512A-2	US-10-689-921-14	US-10-051-643-33
		Sequence 173	Sequence 4,	Sequence 173		Sequence 35	Sequence 18							Sequence 43,	Sequence 43,	Sequence 16	Sequence 2,	Sequence 14	Sequence 33,
		73, App	Appli	73, App	•	•	, Appl						, Appl			161, App	Appli		

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUMBER: 03/09/791,171
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 03/050,739
PRIOR APPLICATION NUMBER: 037/97
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 299
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-791-171-42
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1998-01-05
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                     121 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAPHPDRFGFAGSMSGFLYPSNTTTN
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SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                              AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                                                                                   AVYLLDAFNAGPDVSNWVTAGNAMVTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
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180
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APPLICANT: WELDINGH, Karin

APPLICANT: FLORIO, Walter

TITLE OF INVENTION: UUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1A

CURRENT APPLICATION NUMBER: US/10/620,246

CURRENT FILING DATE: 2003-07-15

PRIOR APPLICATION NUMBER: 09/50,739

PRIOR FILING DATE: 1998-03-30

PRIOR FILING DATE: 1998-03-30

PRIOR FILING DATE: 1997-04-02

PRIOR PRIOR DATE: 1997-04-02

PRIOR PRIOR DATE: 1997-04-02

PRIOR PRIOR DATE: 1997-04-08

PRIOR PRILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05
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US-10-620-246-42
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SEQ ID NO 42
LENGTH: 299
TYPE: PRT
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PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                                                                        y Match 100.0%; Score 1621; DB 4; Local Similarity 100.0%; Pred. No. 2.2e-130; hes 299; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-01-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/116,673
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GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                          SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180
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                                                                 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
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TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
FILE OF INVENTION: AND USE
FILE REPERENCE: 51326-00004
CURRENT APPLICATION NUMBER: US/10/695,155
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: 08/652,842
PRIOR APPLICATION NUMBER: 08/652,842
PRIOR FILING DATE: 1996-03-23
PRIOR APPLICATION NUMBER: 08/568,357
PRIOR APPLICATION NUMBER: 08/51,149
PRIOR FILING DATE: 1995-10-31
PRIOR APPLICATION NUMBER: 08/447,398
PRIOR FILING DATE: 1995-05-23
PRIOR APPLICATION NUMBER: 08/447,398
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR REPLING DATE: 1995-05-23
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR REPLICATION NUMBER: 08/289,667
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: 08/25,358
PRIOR APPLICATION NUMBER: 08/55,358
PRIOR APPLICATION NUMBER: 08/545,926
PRIOR FILING DATE: 1995-10-20
PRIOR FILING DATE: 1995-10-20
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US-10-695-155-166
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 166
LENGTH: 299
TYPE: PRT
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APPLICANT: HARTH, GUNTER
APPLICANT: LEE, BAI-YU
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                    241 AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
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                                                                              GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
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o. US20040228873A1
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Pred. No. 5.9e-130;
0; Mismatches 1;
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RESULT 4
US-09-804-980-42
; Sequence 42, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:

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; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 298
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US-10-481-563A-14
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US-10-481-563A-14
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Best Local
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 252
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Best Local (
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TITLE OF INVENTION: MYCOBACTERIAL PROTEINS AS
FILE REFERENCE: 32004-173355
CURRENT APPLICATION NUMBER: US/10/481,563A
CURRENT FILING DATE: 2003-12-22
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/212,048 PRIOR FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                   TYPE: PRT
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              LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                              VVAPAGGAYSMYTNWEQDGSKQWDTFLSABLFDWLAANRGLAFGGHAAVGAAQGGYGAMA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
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                                                            VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANR-----
                                                                                                                       APYENLMVPSPSMGRDIPVAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNA-NTLAGKGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGR-IPVAFLAGGPH

    - AAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW

                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                  94.7%;
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Pred. No. 5.7e-129;
0; Mismatches 0;
                                                                                                                                                                                     0;
                                                                                                                                                                                  Score 1335; DB 5;
Pred. No. 5.4e-106;
0; Mismatches 0;
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US-10-332-512A-3
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FILE REFERENCE: 11000.1007c2
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RESULT 7
(WS-09-880-505-37)
; Sequence 37, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Of Inmunologically-Mediated Skin Disorders
; TITLE OF INVENTION: Of Inmunologically-Mediated Skin Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-332-512A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.8%; Score 564.5; DB 4; Best Local Similarity 41.6%; Pred. No. 6.9e-40; Matches 131; Conservative 38; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ORME, IAN M.
APPLICANT: BELISLE, John T.
APPLICANT: BELISLE, John T.
TITLE OF INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMM
FILE REFERENCE: 38861-186292
CURRENT APPLICATION NUMBER: U$/10/332,512A
CURRENT FILING DATE: 2003-01-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
ONUMBER OF SEQ ID NOS: 31
SOFTMARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 WGSWAPQLGAMSGDI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWXWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RSAATTLPRRLAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVBYLQVPSASMGRDIKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS 130
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CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR PILING DATE: 1999-06-02
PRIOR PILING DATE: 1999-06-02
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARR: FREUSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 340
                                                                                                                                                                                               APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: System using Mycobacterium Vaccae FILE REFERENCE: 11000.1008c2

CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US09/156,181

PRIOR APPLICATION NUMBER: US09/156,181

PRIOR APPLICATION NUMBER: US09/56,624

PRIOR APPLICATION NUMBER: US09/56,624

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208
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US-10-051-643-37
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                                                                                                   ; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 37; LENGTH: 340; TYPE: PRT; ORGANISM: Mycobacterium tuberculosis US-10-051-643-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/10051643 Publication No. US20020197265A1
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Best Local
                                  Matches 130;
                                                  Query Match
Best Local Similarity
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 4 RSA---LIRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
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                                  Conservative
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                                                  34.6%;
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                               ; Score 561.5; DB 4; ; Pred. No. 1.2e-39; 39; Mismatches 119;
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Pred. No. 1.2e-39;
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LENGTH: 333
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Sequence 36, Application US/09880505

| Publication No. US20030007976A1
| GENERAL INFORMATION:
| APPLICANT: Watson, James D.
| APPLICANT: Watson, James D.
| APPLICANT: Tan, Paul L.J.
| APPLICANT: Tran, Paul L.J.
| APPLICANT: Prestidge, Ross
| TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders | FILE REFERENCE: 11000.1007c2
| CURRENT APPLICATION NUMBER: US/09/880,505
| CURRENT FILING DATE: 2001-06-13
| PRIOR APPLICATION NUMBER: US 09/324,542
| PRIOR APPLICATION NUMBER: US 09/97,080
| PRIOR FILING DATE: 1997-06-02
| PRIOR FILING DATE: 1997-012-23
| NUMBER OF SEQ ID NOS: 194
| SOFTMARE: PastSEQ for Windows Version 3.0
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US-09-880-505-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNEPPNGTHS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
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GGDNIPAKFL--ESLTLSTNEIFQNTYAASGGRNGVFNFPPNGTHSWPYWNQQLVAMKPD
                                           GASD-PAAMIGOTAEAMGNSRMFYNOYRSVGGHNGHFDFPASGDNGWGSWAPOLGAMSGD
                                                                                                 WPTMIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
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; Sequence 36, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of th
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008C2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US/9156,181
; PRIOR APPLICATION NUMBER: US/996,624
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US/996,624
; PRIOR FILING DATE: 1998-09-17
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US-10-282-122A-64050
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 333
; TYPE: PAT
; ORGANISM: Mycobacterium leprae
US-10-051-643-36
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US-10-051-643-36
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                             Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohleen, Kari
Zyskind, Judith
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLIQEMPSWLQANKAVILPIGNAAVGLSMSGSSALILASYYPQQFPYAASLSGFLNPSEGW 203
             Wall, Daniel
Trawick, John
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                                         US-09-800-505-32

US-09-800-505-32

; Sequence 32, Application US/09880505

; Publication No. US20030007976A1

; GENERAL INFORMATION:
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Best Local S
Matches 118
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
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OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR FILING DATE: 2000-09-06
OR FILING DATE: 2000-09-06
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
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33.8%; Score 548; DB 4;
Local Similarity 39.2%; Pred. No. 1.7e-38;
hes 118; Conservative 41; Mismatches 128
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APPLICANT: Watson, James D. APPLICANT: Tan, Paul L.J. APPLICANT: Prestidge, Ross

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CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
PRIOR PELICATION NUMBER: US 08/997,080
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOPTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 338
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; Sequence 34, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
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                                                               US-09-880-505-34
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR PILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Skin Disor
FILE REFERENCE: 11000.1007c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, APPLICANT: Tan, P. APPLICANT: Presti
                                                                    TYPE: PRT
ORGANISM: Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
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32.8%;
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Pred. No. 4.1e-37;
Score 532; DB 3;
Pred. No. 4.1e-37;
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                      Length 338;
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APPLICANT: Watson, James D.
APPLICANT: Watson, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Resp
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REPERENCS: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 1908-09-17
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
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// ORGANISM: Mycobacterium tuberculosis
US-10-051-643-32

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Publication No. US20020197265A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 121; Conservative
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Best Local Similarity 40.1%;
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                                                                   TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                                                                                                          TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 532; DB 4;
; Pred. No. 4.1e-37;
37; Mismatches 126
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APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: OF Immunologically-Mediated Diseases of the Respiratory
FILLE OF INVENTION: 000: 202
FULLE REFERENCE: 11000.10082
CURRENT APPLICATION NUMBER: US/9/156,181
PRIOR APPLICATION NUMBER: US/9/156,181
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1997-12-23
INUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 338
TYPE: PRI
ORGANISM: Mycobacterium bovis
US-10-051-643-34
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US-10-051-643-34
; Sequence 34, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
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Search completed: April 14, 2006, 18:40:37 Job time : 106.026 secs
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                                                                                                                                                                                                                                                                                                 205 TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG 264
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                                                                                                                                                                                                                                                                                                                                                                                                 145 TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP 204
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Published Applications AA New:*

1: /SIDS5/ptcdata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDS5/ptcdata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDS5/ptcdata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDS5/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDS5/ptcdata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDS5/ptcdata/2/pubpaa/USO3_NEW_PUB.pep:*

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Sequence 318, App Sequence 144, App	138,	Sequence 154, App	4274,	12200	Sequence 133, App	160,	Sequence 166, App	Sequence 13202, A	Sequence 4262, Ap	150, /		17488	542,	162,	Sequence 172, App	Sequence 11858, A		Sequence 163, App	Sequence 19912, A	11967	157,	Sequence 68, Appl	Sequence 9174, Ap	Description

RESULT 2
US-11-082-389-68
; Sequence 68, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
92.5	93	93	93	93.5	93.5	93.5	94	94.5	94.5	95	95	95	95.5	96.5	96.5	96.5	97	97.5	98
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7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
US-11-188-298-14874	US-11-052-554A-148	US-11-188-298-9414	US-11-130-821-1	US-11-052-554A-135	US-11-096-568A-12717	US-11-096-568A-12718	US-11-222-451-2	US-11-052-554A-146	US-11-052-554A-165	US-11-052-554A-141	US-11-052-554A-152	US-11-188-298-8416	US-11-172-740-539	US-11-052-554A-142	US-11-188-298-21964	US-11-188-298-2825	US-11-052-554A-159	US-11-052-554A-140	US-11-052-554A-139
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
14874, A	148, App	9414, Ap	1, Appli	135, App	12717, A	12718, A	<ol><li>Appli</li></ol>	146, App	165, App	141, App	152, App	8416, Ap	539, App	142, App	21964, A	2825, Ap	159, App	140, App	139, App

### ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR PILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9174
LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-11-079-463-9174
; Sequence 9174, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.9%; Score 176.5; DB 7; Best Local Similarity 30.2%; Pred. No. 2.8e-07; Matches 64; Conservative 35; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOO-03DIV2
                                         169
                                                                                      164 NPAYRYETFVSSELVNYIDRNYKTIADRKGRAITGLSMGGHGAMMLGIRHKDVFGAAGST 223
                                                                                                                                                                                      107 LGKNÄAACPVLYLLHGY--GGHAKTWIQIKPNLPEIÄDEKGIIFVCP-DGKDSWYWDSPK 163
224
                                                                                                                                    111 DGSKQWDTFLSABLPDWLAAN-RGLAP-GGHAAVGAAQGGYGAMALAAFHPDRFGFAGSM 168
                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                               57 GGPHA-----VYLLDAFNAGPDVSNWVTAGNAMNTLAG-KGISVVAPAGGAYSMYTNWEQ 110
                                                                                                                                                                                                                                                                                                                             1 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAF----LA 56
                        SGPL----YPSNTTTNGAIAAGMQQFGGVDTN 196
                                                                                                                                                                                                                                                                              SGGVDIRPFPKNWSMN-----KQLGELASN 248
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RESULT 3
US-11-052-554A-157
; Sequence 157, Applicat
; Publication No. US200:
; Publication No. US200:
; GENERAL INFORMATION:
                                 PRIOR APPLICATION NUMBER: US 6/589,227
PRIOR APPLICATION NUMBER: US 6/589,227
PRIOR APPLICATION NUMBER: US 6/589,227
PRIOR APPLICATION NUMBER: US 6/589,227
PRIOR APPLICATION NUMBER: UN 173/DEL/2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-08-31
Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 446
SEQ ID NO 68
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HABETHAUET, GREGOT
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
SOFTWARE: PatentIn version 3.3
                      NUMBER OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US 60/143262
OR FILING DATE: 1999-07-09
OR APPLICATION NUMBER: US 60/151281
OR FILING DATE: 1999-08-27
OR APPLICATION NUMBER: DE 19930487.4
OR FILING DATE: 1999-07-01
OR APPLICATION NUMBER: DE 19930489.0
OR APPLICATION NUMBER: DE 19930489.0
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FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932134.5
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-07-01
APPLICATION NUMBER: DE 19931549.3
FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                             116 TSTRIWEAKAR-LOGLNPTADYPMYGIHGWAQFNSQLERTQGRVLDVMNA 164
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                                                                                                                                                                                                                                                                                Application US/11052554A o. US20050288866A1
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                                                                                                                                                                                                IDENTIFYING ADHESIN POTENTIAL
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                                                                                    문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 11967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11967, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR
FILE REFERENCE: 38-21(53452)B
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LENGTH: 783
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CURRENT FILING DATE: 2005-07-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 RP---LIGNGANGAPGTGANGAPGGWLLGNGGAGGSAAAGSGLPGGAAGLFGTGGAG
                                            159 PDR--FG----FAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDP 212
                                                                                                                               104 MY-----TNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFH 158
                                                                                                                                                                         77 -LWLLVATILVIFMNAG---FAMVEAGMCRQKNAVNILA-KNLFVFALAVTAYWFVGYSF
                                                                                                                                                                                                                    61 AVYLLDA-----FNAGPDVSNWVTAG-----NAMNTLAGKGISVVAPAGGAY-----S
                                                                                                                                                                                                                                                              31 IRGFSSNRAMTWLACAPLALMGLGIFT-LSAKA---EEL------PDLNAAFLANN--
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                                                                                                                                                                                                                                                                                                      1 MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH 60
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    AERIKFGEFVVFALILTAFIY
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                                                                                    MYGDAAIDGWLYFGGLFFDPTVTAE----TISDAGLVPTVDFLFQAAFAGTAATIVSGLV
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Pred. No. 0.14;
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RESULT 6
US-11-052-554A-163
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US-11-188-298-19912
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-02-06
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                                                                                                                                                                                                         Sequence 163, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
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SEQ ID NO 19912
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TITLE OF INVENTION: GERES AND USBS FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
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                                                                                                                                                                                                                                                                                                                                                                                            IPGHNMSIATLGALILWIGWYGFNPGSQLAMDQWVPYVAVTTTLGA-AGGAIGA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVHASLLAQ-----NNTRVWVWSPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLNSVGNABFIDFAGSSIVHSVGAW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GHFDFPASGDNGWGSWAP-----QLGAMSGDIVGA 297
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                                                                                                                                                              IDENTIFYING ADHESIN AND ADHESIN-LIKE POTENTIAL
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                   Matches
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SEQ ID NO 151
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sachdeva, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                        y Match 6.6%; Score 107.5; Local Similarity 23.0%; Pred. No. 0.5
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                                                    196 GIPALAGGPTAINLGIANVGGGNV-----GNANNGLANIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 QDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMS 169
                                                                                            51 PVAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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       DGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMS- 169
                                                                                                                                                                                      ALLRALWIAALS-----FGLGGVAVAARPTAKAAPYENLM------VPSPSMGRDI 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTGQAGGPGGLLYGNGGNGG----SGGVGQAGGAGGSAGLIGIGGTGGAGGAGAVGGVGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVAFLAGGPHAVYLLDAFNAGPDVSNWV-TAGNAMNTLAGKGISVVAPAGGAYSMYTNWE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAÄAFHERFIQALSTAAG--ÄYGSAEAANÄSPLQQALNVINAPTQTLLGRPLIGNGTNGA 125
                                                                                                                                           ATYEQMWAADVSAMSAYHAGASAIASALSPFSK--PLQNLAGLPAWLASGAPAAAMTAAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G----NAYLFGSGGAGGQ--GGMGAAGADGV-----
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Pred. No. 0.29;
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                             DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
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                                                                                                                                                                                                                                   92;
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Matches

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Sequence 11858, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 00/592,978

PRIOR APPLICATION NUMBER: 00/592,978

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569
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RESULT 9
US-11-052-554A-172
; Sequence 172, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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US-11-188-298-11858
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 11858
LENGTH: 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                   YGAMALAAFHPDR--FG---FAGSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                GVGNLGNLNT---GFANTGLGNFGFGNTGNNNIGIGLTGNNOIG------
                                                                                                                                             VGA 297
                                                                                                                                                                          GKFVGGKAQAIPGHNMSIATLGALILWIGWYGFNPGSQLAMDQWVPYVAVTTTLAAAGGA 320
                                                                                                                                                                                                                                                                                                     TAATIVSGLVAERVKFGEFVVFSLVLTGFIYF------ÍÁ-
                                                                                                                                                                                                                                                                                                                                                                    SSYWFIGYSLMYGDPVSAGWLYFNGLFFDPAVTPE----LISEAGLVPSVDFLFQAAFAG 178
                                                                                                                                                                                                                                                                                                                                                                                                 GAY-----SMY-----TNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEGPMLLLRSIRGFSSNRSLTWLACVPLALFGLGLF-----NLSAHAAEM-PEL
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                                                                                                                                                                                                           SRMFYNQYRSVGGHN-----
                                                                                                                                                                                                                                        --GSWEWNGGWLNTAFGEGVEFIDFAGSSIVHSVGAW------AGLVGAMLLGPRI 260
                                                                                                                                                                                                                                                                      QLGRWKWHDPWVHASL-----LAQNNT--RVWVWSPTNPGASDPAAMIGQTAEAMGN 252
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21.2%;
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Pred. No. 0.28;
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID;
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PO'
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
FRIOR APPLICATION NUMBER: US 60/589,227
FRIOR APPLICATION NUMBER: US 60/589,227
FRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOPTWARE: Patentin version 3.3
SOPTWARE: Patentin version 3.3
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US-11-052-554A-162
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; ORGANISM: Rickettsia
US-11-052-554A-172
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                                   S
                                                                                                                                                              US-11-052-554A-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 162, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 172
                                                                               Matches
                                                                                                                    Query Match
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL FILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR PRIOR DATE: 2004-07-20 PRIOR APPLICATION NUMBER: IN 173/DEL/2004 PRIOR FILING DATE: 2004-02-06 NUMBER: OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sachdeva,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sachdeva, et al.
                                                                                                                                                                                                  LENGTH: 543
TYPE: PRT
                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 1643
                                                                                                    Local
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  280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 VTGTLGGNLKGIIELNTAAVÁGKLISQGGAÁNÁVIGTDNGAGRAÁGFIVSVDN-GNÁATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 GLGSITFÄÅAPSVLEFNLINPTTQEÄPLTLGANSKIVNGGNGTLNITNGFIQVSDNTFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PHAVYLLDA----FNAGPDVSNWV---TAGNAM--NTLAGKGISVVAPAGGAYSMYTNWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GLGGVAVAA-----EPTAKAAPY---ENLMVPSPSMGR-DIPVAFLA-----GG
                                       16 LSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPHAVYLLDAFNAGPDVS 75
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                                                                               72;
                                                                                                    Similarity
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  LFLGLGGDGGAGG----
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prowazekii
                                                                                                  6.5%;
24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%;
                                                                             ; Score 106; DB 7;
; Pred. No. 0.34;
24; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 106.5;
Pred. No. 1.1;
    TSNNNGGDGGAGGTAGG-----RLFSLGGDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFYING ADHESIN POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                   121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND ADHESIN-LIKE
                                                                                 Gaps
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CURRENT APPLICATION NUMBER: US/11/172,740
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,621
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,829
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR PILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 542
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-172-740-542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROVER, VYACHESIAV
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2750-1602PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature LOCATION: (1)...(292)
                                                                                                                                                                                                                                                                                                                        LOCATION:
OTHER INFORMATION: Utility:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1). (292)
OTHER INFORMATION: Public GI no.
                              LOCATION:
OTHER INFORMATION: Utility:
                                                                                                                                                                                                                                         FEATURE:
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OTHER INFORMATION: Utility:
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
OTHER INFORMATION: Utility:
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                                                                     NAME/KEY: misc_feature
                                                                                                           OTHER INFORMATION: Utility:
                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                    FEATURE:
                                                                                                                                                                                  OTHER INFORMATION: Utility: Useful
                                                                                                                                                                                                                    NAME/KBY: misc_feature
                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-----GMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPAAMIGQTAEA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAVLIGTGVGGFGGLGGGS---NGTGGAGGAGG----TGATLIGLGAGGGGGIGGFAV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NG-GAGTAIGSNAGDG-----GAGGDSSALIGYAQGGSGGLGGF-----GESTGGDGGLG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGGNGGDGGDGGLFSIGVGGDGGNAGNGAMPANGGNGGNAGVIANGSFAPSFVGFGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEXANDROV,
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                                                                                                           plants with
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                                                                                                           increased biomass
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FITTLE OF INVENTION: GENES AND USES FOR PLANT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION UNMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 17488
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US-11-188-298-17488
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US-11-188-298-17488
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                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17488, Application US/11188298 Publication No. US20060075522A1
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abad, Mark S. et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Utility: Useful FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                     Local Similarity
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246
                            201
                                                         186
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                                                                                                                                                  103
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                                                                                                                   130 YSLMYGGSVADGWLYFGGLFFDPTVTAD----MVTDAGLVPTVDFLFQSAFAGTAATIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                              77 N---LWLLIATILVIFMNAG---FAMVBAGMCRSKNAVNILA-KNLFVFALAVTSYWFIG 129
                                                                                                                                                                                                                                           32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                           58 GPHAVYLLDA-----FNAGPDVSNWVTAG----NAMNTLAGKGISVVAPAGGAY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 LNIEGEADSWDFGVGAGFYLNATNEKWKNWRWYDYVVKELPKVLSDNFEQLNTSRASIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 PSMGRDIPVAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAP-----
                                                                                                                                                                                                                                                                       1 MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIP----VAFLAG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                            -----APQLGRWKWHDPWV---HASLLAQNNTRV-WV-WSPTNPGA 236
                                                          GLVAERVKFGEFVVFAIVLTAFIYFIAGSWKWNGGWLDSLGFVDFAGSSIVHSVGAWAGL
                                                                                       AFHPDR--FG---FAGSMSGFLYP--SNTTTNGA--IAAGMQQFGG---VDTNGMWG--
                                                                                                                                                                                                                                            IRGPSSNRSMLWLATVPLALFGLGI-FNLSAHAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGAMLLGPRIGKYSDGKPQAMPGHNMAIATLGALILWIGWYGFNPGS
                                                                                                                                                -----SMYTNWEQDGSKQWDTFLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSMGGHGALTIYLKNTDKYKSVSAFSPVVNPINCP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----APQLGRWKWHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AGGAYSMYTNWEQDGSKQWD--TFLSAELPDWLAANRGLAPGGHAAV-G 143
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                     6.5%;
25.1%;
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                                                                                                                                                                                                                                                                                                     Score 105.5; D
Pred. No. 0.33;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105.5; D
Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                            DLPBLNAAFLAN 76
                                                                                                                                                                                                                                                                                                       77;
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RESULT 13

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US-11-052-554A-150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-188-298-8448
                                                                                                                                                                         US-11-052-554A-150
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 763
SOPTWARE: PatentIn version 3.3
SEQ ID NO 150
LENGTH: 618
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 150, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 8448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8448, Application US/11188298 Publication No. US20060075522A1
                                                                                                       Query Match
Best Local
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Best Local (
                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
PRIOR FILING DATE: 2004-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 6.5%;
Local Similarity 25.1%;
nes 72; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIP----VAFLAG
                                   MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYE--NLMVPSPSMGRDIPVAFLAGG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFHPDR--FG----FAGSMSGFLYP--SNTTTNGA--IAAGMQQFGG---VDTNGMWG--
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  LSAQAAMFHEQFVRÄLAAGGNSYÄVÄEAATÄQSVQQDLLNLI-----NAPTQALLGR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLVAERVKFGEFVVFAIVLTAFIYPIAGSWKWNGGWLDSLGFVDFAGSSIVHSVGAWAGL 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----APQLGRWKWHDPWV---HASLLAQNNTRV-WV-WSPTNPGA
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                                                                                     Conservative
                                                                                                    22.24;
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                                                                                 Score 105; DB Pred. No. 0.48; Mismatches
                                                                                                                          DB 7;
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Search completed: April 14, Job time: 13.8124 secs
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US-11-087-099-4262
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US-11-087-099-4262
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(33450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4262
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                            SSPS
                                                                                                                MGNS
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                                                                                                                                                    PPPAAGHGNASL---
                                                                                                                                                                                                                          GPTVATLYPSWPTMRPPAPAGAGAGAVAIGGPQFYSGIGSIAQPINGSPLLTAAGLWRGP 234
                                                                                                                                                                                                                                                             GSMSGFLYPSNTTTN-----GAIAAGMQQF-GGVDT--NGMWGAPQL---GRWKWH 210
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                                                                            286
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24.0%; Pred. No. 0.33;
vative 29; Mismatches 108
                      2006, 18:42:15
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                                                                                                                                                                                                                                                                                                                                   -----AAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -ĠVGGPGGSGGASALAFGSGGV-----GGAGGLGGPTD
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Minimum
Maximum
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A Geneseq_21:*
1: geneseqp1980
2: geneseqp2001
3: geneseqp2001
4: geneseqp2002
6: geneseqp2003
7: geneseqp2003
8: geneseqp2004
9: geneseqp2004
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1192
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                                                                                                                                                                            Maximum Match 100%
Listing first 45 sv
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1133.996 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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U	8.4			9.2	9.2	9.2	9.3	9.4			10.5	10.7	10.8	12.0	12.0	12.2	12.2	12.2	12.2	12.7	12.9	13.4	100.0	•		Query
		313	255	375	288	288	106	274	295	335	270	293	331	302	211	278	278	278	278	278	292	280	228	228		
ID  AAW72909  AAY21926  AAG92764  ADS15066  AAR8733271  AAW69403  AAB18558  AAW79403  AAB18588  AAB79143  AAB79143  AAG97188  AAB79177  ABO72188  AAB79177  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  AAB7917  ABO72188  ABO7317  ABO72188		7	9	4	œ	4	G	σ	7	7	7	σ	7	w	4	w	N	N	N	8	σ	4	ν	N		
		ABO71801	AEA04518	ABG22460	ADQ30600	AAM78698	ABP04085	ABJ37463	ADF06706	AB078267	AB072188	ABM67317	ABO73240	AAY95035	AAB79143	AAB18558	AAW69403	AAW31306	AAR87535	ADS15066	ADA33271	AAG92764	AAY21926	AAW72909		

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived me. The complex can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosi of or vaccination against tuberculosis caused by M. tuberculosis, M.

diagnosis

africanum or M.

povie

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 177-178; 163pp; English.

WPI; 1998-542705/46. N-PSDB; AAV63933.

Andersen P, Oettinger T,

Nielsen Florio

E,70

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

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45	44	43	42	41	40	39	38	37	36	35	34	U U	32	31	30	29	28	27	26	25
92	92	92	92	92	92	92	92	92.5	92.5	92.5	93	94	94.5	95	96.5	96.5	97.5	99	99	100.5
7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.9	7.9	8.0	8.1	8.1	8.2	8.3	8.3	8.4
1517	1509	1488	1482	327	315	315	281	6043	5674	3808	326	279	271	1107	518	513	282	284	217	485
w	ω	w	w	œ	œ	œ	œ	æ	œ	œ	7	8	7	σ	7	σ	v	œ	4	0
AAY84726	AAY84728	AAY84725	AAY84727	ADS23140	ADX78415	ADX74285	ADS44582	ADU47673	ADU47676	ADK16029	AB073278	ADS22855	ADF04061	ABU31207	ADF06351	ABU41093	ABB48896	ADS44848	ABG22462	ABM50627
Aay84726	Aay84728	Aay84725	Aay84727	Ads23140	Adx78415	Adx74285	Ads44582	Adu47673	Adu47676	Adk16029	Abo73278	Ads22855	Adf04061	Abu31207	Adf06351	Abu41093	Abb48896	Ads44848	Abg22462	Abm50627
Amino aci	Amino aci	Amino aci	Amino aci	Bacterial	Plant ful	Plant ful	Bacterial	S. cyaneo	S. cyaneo	Streptomy	Pseudomon	Bacterial	Bacterial	Protein e	Bacterial	Protein e	Listeria	Bacterial	Novel hum	Propionib

# ALIGNMENTS

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RESULT 1
AAW72909
ID AAW7
02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                               Mycobacterium infection.
                                                                                                                                                                                                                                                         AAW72909;
                                                                                                                                                                                                                                                                    AAW72909 standard; protein;
                                                                                                                                                               01-APR-1998;
                                                                                                                                                                           08-OCT-1998.
                                                                                                                                                                                       WO9844119-A1
                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen CFP25A.
                                                                                                                                                                                                                                            21-JAN-1999
                                                                                                                      (STAT-)
                                                                                                                      STATENS SERUM INST.
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                                                                   tuberculosis.
                                                                                                                                                                                                                     tuberculosis; antigen; vaccine;
                                                                                                                                                               98WO-DK000132
                                                                                                                                                                                                                                                                     228 AA.
                                                                                                                                                                                                                     immunological; immunogen;
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RESULT 2
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Matches 228;
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05-JAN-1998;
01-APR-1998;
The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP7B; CFP39; CFP39, CFP30A; RDI-ORF; CFP10A; CFP16; CFP19; CFP23; CFP25A; CFP30B; CFP30B.
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                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP30A or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MFT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-ORP2, RD1-ORP3, RD1-ORP3, RD1-ORP5, MFT59-ESAT6, ESAT6-MPT59, CFP30A, CFP30A, RD1-ORP3, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, CFP30B, C
                                                                                                                                                                                                                                   Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium; amino organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium
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                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2001.
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DB; AAH67983.
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                                                                                                                                                                                                                               Mizoguchi
Senoh A,
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2000JP-00159162.
2000JP-00280988.
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Ikeda M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 6518
                                                                                                                                                                                                                                   S, Hayashi
Ozaki A;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Anti-HIV; Antimicrobial; Immunosuppressive; quorum sensing signalling; bacterium; quorum sensing controlled gene; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SELPFÄGHPTIGTAYALLEAGLVKAKEGQLVQQCAAGLVTLTVNDSNHISFELPTPKITP 132
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Pred. No. 6.2e-07;
8; Mismatches 80
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Identifying a modulator of quorum sensing signaling in bacteria, for treating a biofilm-associated disorder, comprises contacting

the cell

WPI; 2004-709932/69

FFX#X5505050505050505050

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AC AAR8
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Best Local Similarity
Matches 62; Conser
    Ligon J,
                                                                                                                                                30-MAY-1995;
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15-OCT-1995
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                                                   (CIBA ) CIBA GEIGY AG.
                                                                                                 08-JUN-1994;
                                                                                                                                                                                                                                        W09533818-A2
                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HWRSRMFSPAYGVVEDAATGSAAGPLAIHLARHRQIPYGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
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ilarity 28.1%;
Conservative 26
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(first entry)
                                                                                                 94US-00258261
                                                                                                                                                95WO-IB000414
                                                                                                                                                                                                                                                                                                               Location/Qualifiers 210
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    Beck JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 151.5; DB 8
Pred. No. 9.3e-07;
6; Mismatches 88
       H111
    DS,
    Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
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    Gaffney
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       TD;
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Query Match
                                20-AUG-1990;
02-JUL-1992;
31-AUG-1992;
01-JUL-1993;
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene cluster may be express expressed in a transgenic portage of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the standardise of the s
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12-MAR-1998
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pyrrolnitrin and soraphen, useful for disease control in plants
08-JUN-1994
                                                                                                                                                                                                                                 01-JUN-1995;
                                                                                                                                                                                                                                                                                                             02-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytopathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW31306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW31306 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-040226/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phenazine; biosynthesis; antibiotic; antipathogenic; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aureofaciens phenazine phz3 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 KALGISD-STFFIEIYHNGFRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFAGAGRR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 DALAAADPADFPDDIAH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                90US-00570184.
92US-00908284.
92US-00937648.
93US-00087636.
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94US-00258261
                                                                                                                                                                                                                                 95US-00457342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product= "phz3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phz3 encoded by the phenazine gene cluster ORF3. expressed recombinantly to produce phenazine, or sgenic plant for disease- resistance. (Updated on dise OS field)
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Pred. No. 3.9e-06;
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Best Local &
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Transgenic plants containing such antipathogens (Updated on 17-OCT-2003 enhanced resistance to attack by phytopathogens. (Updated on 17-OCT-2003)
                                                                                                                                                                                                                                                                                                                                                            Pyrrolnitrin; biosynthetic pathway; pathogen protection; phenazine; plant antipathogenic substance production; anti-fungal antibiotic; fungal respiratory electron transport inhibitor; lipoprotein damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protecting plants against pathogens with genetically transformed biological control agent - which expresses all polypeptide(s) in pyrrolnitrin biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW69403;
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N-PSDB; AAT89957.
                                09-OCT-1996;
                                                                                    06-OCT-1998.
                                                                                                                                            US5817502-A.
                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phenazine gene cluster protein phz3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW69403 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 18; Col 149-150; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CIBA ) CIBA GEIGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALGISD-STFPIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFAGAGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DALAAADPADFPDDIAH-----AGS--- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGTDIALGAR-TONHRLFLETQMGTIAFELERQNGSVIAASMDQPIPTWTALGRDAELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEPAI-HDLDSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hill DS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                96US-00729214
                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                 /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%;
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Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                     damage
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CC enzyme required in the biosynthetic pathway of pyrrolnitrin. The DNA and CC transgenic plants with protection against phytopathogens. The enzymes are CC transgenic plants with protection against phytopathogens. The enzymes are CC (APS). The compound ultimately produced by the pathway, pyrrolnitrin, is C a broad range, anti-fungal antibiotic. It inhibits fungal respiratory CC electron transport and causes general lipoprotein damage. The transformed CC cells can additionally be used in compositions to be applied to plants to CC provide resistance, as can purified APS produced by them. Transgene CC dependent resistance eliminates the need to spray crops with chemical CC based pesticides and antibiotics, which is expensive and time consuming, CC and in addition, especially in the case of antibiotics, their over use CC overcomes problems of applying micro-organisms which can be slow growing CC and isolated in their growth areas. (Updated on 17-OCT-2003 to
 Matches
                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                               This sequence is encoded by the phenazine gene cluster, ison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes encoding enzymes of the biosynthetic pathway of pyrrolnitrin useful for producing transgenic plants which can produce pyrrolnitr
                                                                   Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aureofaciens. This sequence was used to isolate the pyrrolnitrin gene region of the invention, that encodes at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1994;
30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 18; Col 161-162; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-556391/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-pathogenic
 62; Conservative
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                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00258261.
95WO-IB000414.
                12.2%; Score 145.5;
28.3%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hill DS,
   33;
   Mismatches
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5; DB 2;
3.9e-06;
1es 83;
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                                 Length
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   isolated
                                   278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pyrrolnitrin as
   41;
   Gaps
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194
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WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIBFGQ
                                    LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                                                            KALGISD-STFPIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFAGAGRR
                                                                                                                                                                                            TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL 131
                                                                                                                                                                                                                                                                         GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP 77
                                                                                                                                                     LLGTDIALGAR-TDNHRLFLETOMGTIAFELERQNGSVIAASMDOPIPTWTALGRDAELL
                                                                                                                                                                                                                                  GNPVAVFFDADDLSAEQMQRIAREMNLSETTFV-LKPRNCGDALIRIFTPVNELPFAGHP
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### RESULT 9

AAB18558 standard; protein; 278 8

AAB18558;

12-SEP-2003 15-JAN-2001 (revised) (first entry)

Protein phz3 encoded by a phenazine gene region

\*\*\*\*\*\*\*\*\*\*\* Pyrrolnitrin; PrnA; PrnB; PrnC; PrnD; antibiotic; biocontrol; fungal respiratory electron transport inhibitor; transgenic pla antipathogenic substance; biosynthetic gene; fungal resistance; plant;

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Query Match
Best Local S
Matches 62
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30-MAY-1995;
09-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prnD enzyme catalyses the conversion of aminopyrrolnitrin to pyrrolnitrin. Pyrrolnitrin has antibiotic activity, and inhibits a broad range of fungi. It is a fungal respiratory electron transport inhibitor. The genes are useful for developing a host as a biocontrol agent, for protecting plants against a pathogen and for producing large, uniform amounts of pyrrolnitrin. The genes are also useful for producing transgenic plants that express antipathogenic substance (APS) biosynthetic genes. The genes and enzymes are useful for increasing the resistance of host plants to disease caused by phytopathogens, e.g. fungi, bacteria or nematodes. The microbial hosts are useful for controlling or inhibiting the growth of a phytopathogen. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hill D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene region. The specification describes pyrrolnitrin gene regions. This region encodes enzymes required in the biosynthetic pathway of pyrrolnitrin. The PrnA enzyme catalyses the conversion of tryptophan to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrrolnitrin biosynthesis genes and enzymes, useful for producing pyrrolnitrin for increasing plant resistance to phytopathogens, e. fungi or nematodes, and for developing microbial hosts useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -chlorotryptophan. The PrnB enzyme catalyses the conversion chlorotryptophan to monodechloroaminopyrrolnitrin. PrnC enzy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biocontrol agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conversion of monodechloroaminopyrrolnitrin to aminopyrrolnitrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-593649/56.
DB; AAA75304.
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                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                 LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18556-59 are encoded by a Pseudomonas aureofaciens phenazine ion. The specification describes pyrrolnitrin gene regions. This
                                                                                      KALGISD-STFPIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFÄGAGRR
                                                                                                                                        DALAAADPADFPDDIAH
                                                                                                                                                                                          LLGTDIALGAR-TDNHRLFLETQMGTIAFELERQNGSVIAASMDQPIPTWTALGRDAELL
                                                                                                                                                                                                                                               TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL
                                                                                                                                                                                                                                                                                                    GNPVAVFFDADDLSAEQMQRIAREMNLSETTFV-LKPRNCGDALIRIFTPVNELPFAGHP
                                                                                                                                                                                                                                                                                                                                                         GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
     Lam
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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95WO-IB000414.
96US-00729214.
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  12.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 145.5; DB : Pred. No. 3.9e-06 8: 3; Mismatches 8:
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                                                                                                                                                                                                                                                                                                                                                                                                              83;
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  RESULT 10
AB79143
ID 79143
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum hom and adaptation (HA) proteins given in AAB79023 to AAB79242. Th glutamicum HA genes (I) can be used in vectors for expression cells and production of fine chemicals, such as, an organic ac
                                                                                                                                                                                                                   New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins
                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                N-PSDB;
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2001-061974/07.

AAF71258.

Page 464-465; 712pp; English

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14-JUL-1999;
14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum; incheriacid; proteinogenic amino acid; proteinogenic amino acid; purine base; pyrimidine base; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; enzyme; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
                                                                             14-JUL-1999;
14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brevibacterium;
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 glutamicum.
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3-01041390.
3-01041391.
3-01042088.
                                                                                            3-01032935.
3-01032973.
3-01033002.
3-01033003.
                                       8-01041378.
8-01041379.
                                                                 E-01033005.
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RESULT 11
AAY95035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans.
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   Claim 3; Page 19-20; 133pp; English
                                                             immunocompromized subjects,
                                                                                         Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
                                                                                                                                                                              WPI; 2000-258614/23
                                                                                                                                                                                                                                         Contreras RH,
Logghe MG;
                                                                                                                                                                                                                                                                                                                               (JANC ) JANSSEN
                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
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                                                                                                                                                                                                                                                                    Nelissen B,
                                                                                                                                                                                                                                                                                                                                                                                   98GB-00017796
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                                                                                                                                                                                                                                                                                                                            PHARM NV.
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                                                       e.g., AIDS
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Pred. No. 4.3e-06;
Pred. No. 4.3e-06;
                                                                                                                                                                                                                                                                    De Backer MD,
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a polypeptide that is critical for the survival and growth of Candida albicans. The C. albicans nucleic acid molecules encoding the polypeptides of the invention may be used as probes and primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.albicans associated diseases, especially in AIDS patients and to treat vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for
                         WPI; 2003-615309/58.
N-PSDB; ABD06811.
                                                                                                                                                                                                                                  US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                             ABO73240 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302
                                                                      Rubenfield MJ,
                                                                                                                              18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                         18-FEB-1999;
                                                                                                                                                                                                     22-APR-2003.
                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                         Bacterial infection;
                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa polypeptide #5415.
                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                  ABO73240;
                                                                                                  (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lmmunocompromised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                  GENOMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNXDLAQIERLSLENGWTGIGVPGKHNENGDSVELRNIAPAVGVAEDPACGSGSGAIGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPDDIAHYL-----WTWT-----DRSAGSLRARMFAANLGVTEDEATGAAAIRITDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFELPYFKFHEIDDKVIBELQHSWNGTNIIGKPVLIDAGPKWAVFQLGS-----GKEVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNELPFAGHPTLGTAFALLEDGKIKPNDNGQIIQECGAGLVKISVEKTPNNNSNELPFLL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTEIPFAGHPTVGASWWLRERG--TPINTLQV----PAGIVQVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LANHVFNEKEKFTIDISQGK 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
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                                                                                                                              98US-0074788P.
98US-0094190P.
                                                                                                  THERAPEUTICS
                                                                                                                                                                          99US-00252991
                                                                      Nolling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patients, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.0%;
                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa infection; antibacterial
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                                                                                                  CORP.
                                                                                                                                                                                                                                                                                                                                                                                                              331 AA
                                                                      Deloughery
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Pred. No. 7.8e-06;
""matches 85;
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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

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ABM67317
ID ABM67317
XX ABM67317
XX ABM677
XX ABM67
XX Photo
XX Antib
KW Antib
KW detec
KW Antib
KW whoop
XX whoop
XX Whoto
XX Photo
XX OP-PE
XX WO200
XX YO7-PE
XX X (INSI
PA (CNRK
XX X
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and the therefore the state of the sequences are useful in diagnosis and the treatment of pathological conditions as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa derives, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences are other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                       Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful as molecular targets for diagnostics, prophylaxis and treatment pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                   Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM67317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 331 AA;
                                                                           07-FEB-2001; 2001FR-00001659
                                                                                                                 07-FEB-2002; 2002WO-IB003040.
                                                                                                                                                                                             WO200294867-A2
                                                                                                                                                                                                                                                                       whooping cough
                                                                                                                                                                                                                                                                                                                                                                  Photorhabdus luminescens protein sequence #414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM67317 standard; protein; 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html
                   (INSP ) INST PASTBUR.
(CNRS ) CNRS CENT NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNAVAVVIGADRLSSROMLEFAAWTQLSETTFLLRPTVAEADYRVRIFTPLRELPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRRIESGLGLSPGQVRGS-----QWVDNGPGWVAVRL-----ATRDE---VLAIR-PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLGSCQVWLNQGGGNAADEIVQECLAGLIRIRRKGALLSFA----APPLLRGGAVEDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVGA-SWWLRERG---TPINTLQVPAGIVQVSYHGDLTAISARSEWAPEF----AIHD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 21986; 455pp; English.
                     CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Pred. No. 0.00024;
4; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibictics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibicterials useful as insecticides, bactericides and fungicides. The
                                                                                                                                                                                                                                                                                                                  genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                            Sequence 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sources of probes and primers for detecting the genome of P. luand related species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duchaud E,
Buchrieser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of genes and their encoded
128 LDS-----
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                                                                                                                    19
                                                                                                                                                                                             62;
                                                                                                                                                        19 GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAH-ATIHTPRTEIPFAGH
                                                                             PTVGASWWLRERGTPINTLQVPAG-IVQVSYHGDLTA-ISARSEW-----APEFAIHD
                                       PTIGTAHALLEAG----LIQAREGRIVQECGAGLITLNVTERDEGQKLITFELPEPTITP
                                                                                                                  GNPVAVVMDAQELSSIQMQGIANWTNLSETTPI-LPABNPLADYRVRIFTPGSELPFAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taourit C;
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                    10.7%;
22.7%;
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                                                                                                                                                                                             39;
----LDALAAADPADFPDDIAH---
                                                                                                                                                                                                                    Score 127.5; DB 6
Pred. No. 0.00029;
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                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                 Gaps
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RESULT 14
ABO72188
SSXEXEXEXSX
SXSXEXEXEX
SXSX
                                     Pseudomonas
                                                    29-JUL-2004
                                                                   AB072188;
                                                                                 ABO72188 standard; protein; 270
                                    aeruginosa polypeptide #4363.
                                                    (first
                                                    entry)
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193 149 134

MNITGVCLYGAYHEGAEADIEVRSFAPSCGVNEDPVCGSGNGSVAAFM-RHHKVAMIDDK 251

----YLWTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGKGS LSSEQIDRLESILDCPLDRALTPALIDVGARWIVAHTTGAEAVLATKP-DYARLLEHDTQ

201

148 133 127 77

13

IVHSSQGKKLGRQGSVWLSHSDGKIFVGGSAVT 284 LIHTT-----W--SPEGWVRVAGRVVS 221 Ś

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Bacterial infection; Pseudomonas aeruginosa infection; antibacterial

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RESULT 15
AB078267
ID AB078
XX
AC AB078
XX
AC AB078
XX
AC A90-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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   29-JUL-2004
                                   AB078267;
                                                                    AB078267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6551795-B1
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                                                                                                                                                                                                                                                                                          129
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                                                                                                                                                      246
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                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                              HATIHTPRTEIPPAGHPTVGASWWLRER---GTPINTLQVPAGIVQVSYHGDLTAISARS 117
                                                                                                                                                                                                                                                                                          K-RPEPCATPDGLLEALGIAEAEVLKTD--DYLVVVDDEKTIAALAPDPARLKGLPCRGV
                                                                                                                                                                                                                                                                                                                          EWAPEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEVSVLRVFTDSDGNF-GNPLGVINASK-VEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
                                                                                                                                                                                      IHTTWSPEGWVRVAGRVVSDGVAQL
                                                                                                                                                                                                                      AVTARSQRFDFVSRWFGPNVGVNEDPVTGSAHTSLAPYWAQRLGKTRLSAEQGGARKGRL
                                                                                                                                                                                                                                                         --SAGSLR----ARMFAANLGVTEDBATGAAAIRITDYLSRDLTIT-----QG---KGSL
                                                                                                                                                                                                                                                                                                                                                           RLRWFTPQVEVDLCGHATLATAWVLIHKLDDASPVLRFATRSGELSVRREGDSLAMDFPA 128
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                                                                  protein; 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125; DB 7; I
Pred. No. 0.00047;
33; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-cerived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 27013; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                                         MFAA-----
                                                                                                         GTCRWFAEAFSL----SANDLSGHPPRVVSTGLPYLLLPVTAEALGRARQVNDLQEALDK
                                                                                                                                           ARSEW-APEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRA-----R
                                                                                                                                                                             LLGAAALLHHLRGGDNEQHWTLHLASKSVALRSVRAG---SGFYAEMDQGRAEFGATPDA
                                       LGAAFVYLLDVDGREGRTWDSLGLVEDVATGSAAGPVAAYLVEYGLAARGEPFVLHQGRF
                                                                                                                                                                                                           TVGAS-----
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     -TTWSPEGWVRVAGRV
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                                                                                                                                                                                                           -----WWLRERGTPINTLQVPAGIVQVSYHGDL-----TAIS
                                                                       -----NIGVTEDEATGAAAIRITDYLSRDLTITQGKGSLIH----
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Pred. No. 0.0033;
4; Mismatches 98
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301

LERPSRLDVQVATDGSVRVGGHV

Search completed: April 14, 2006, 17:18:29 Job time : 91.341 secs

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Minimum
Maximum
                                                                                              Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
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PIR 80:*
1: pir1:*
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1192
1 MAIEVSVLRVPTDS
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                                                                                                                                                                                                                                           283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                          MAIEVSVLRVFTDSDGNFGN......PEGWVRVAGRVVSDGVAQLD
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45 gt
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Re

ry ch Length DB ID  288 297532 1 214 2 T50577 2 314 2 S75237 2 314 2 S75237 2 305 2 AB3742 2 1 333 2 A95723 2 A95723 2 A93330 2 546781 2 294 2 S46781 2 1 281 2 H31330 2 1 281 2 H31330 2 2 546781 2 301 2 H83119 2 302 2 H98120 2 303 2 C69800 2 2 5499205 2 2 638293 2 2 638293 2 2 648992 2 3 2 648992 2 3 2 648992 2 4 297 2 C90887 2 4 297 2 C90887 2 4 297 2 C90887 2 4 297 2 C90887 2 4 297 2 C90887
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DB ID  2 G70532 2 T50577 2 R375237 2 R37481 2 R473234 2 S46781 2 R43330 2 R43481 2 P43330 2 R43487 2 P43687 2 G69800 2 G69800 2 G69800 2 G7983056 2 G69807 2 P63056 2 G79887 2 P63056 2 G79887 2 P63056 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887 2 P63556 2 G79887
ID  G70532 T50577 S75237 AB2742 A97523 AB3481 AR3284 S467234 S467234 S46723 AB3119 B83119 B83119 B831205 G955273 F83893 F83893 F83893 F83897 F83997 F85730 E879323 AF15285 F82733 AF15285 AF15330 AF15330
Descr hypot hypot hypot hypot hypot hypot n-met proba phena hypot conse hypot conse hypot

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88.5	89	90.5	91	91	91	91.5	94.5	95	95	95	95.5	96.5	97.5	99	100.5
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572	3413	2591	15281	1145	728	297	321	294	273	261	776	275	282	284	308
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
JC7833	T17467	T30288	841309	S37136	AF3299	AF0671	T24410	D85036	AB2049	<b>B83199</b>	T29064	C87648	AB1173	F70024	E75409
kumamolysin precur	rifamycin polyketi	pristinamycin I sy	cyclosporin synthe	structural polypro	malate synthase (E	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hyaluronate lyase	phenazine biosynth	conserved hypothet	diaminopimelate ep	probable antibioti

# ALIGNMENTS

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70532 A;Molecule type: DNA
A;Residues: 1-228 <COL>
A;Residues: 1-228 <COL>
A;Cross-references: UNIPROT:007215; UNIPARC:UPI000013BF5B; GB:Z96072; GB:AL123456; NID:
A;Experimental source: strain H37Rv
A;Experimental source: J.W.
B;Patkl, A.H.; Dale, J.W.
submitted to the EMBL Data Library, April 1991
A;Reference number: S21832 hypothetical protein Rv2716 - Mycobacterium tuberculosis (strain H37RV)
N;Alternate names: thymidylate synthase (EC 2.1.1.45) [misidentification]
C;Species: Mycobacterium tuberculosis
C;Date: 17-Unl-1998 #sequence revision 17-Unl-1998 #text\_change 09-Jul-2004
C;Accession: G70532; S21832 A;Accession: S21832 A;Molecule type: DNA A;Residues: 'MSAGVIKOVNIVERLASLEMGSEAMALLE','LPLVLPAVQIAGRIVGQGHRYHQLGARPAQ','CAAHFGRE RCASPGWRR','TIVIGSADIRVAVLNAIGSNERSATLITIG','SVRALPQVVQSGHG',3-228 <PAT> A;Cross-references: UNIPARC:UPI000016FBC6; EMBL:X59273; NID:944681; PIDN:CAA41963.1; PI 밁 S δ ঠ 밁 밁 A;Gene: Rv2716 A;Status: nucleic acid sequence not shown; translation not shown Query Match 100.0%; Score 1192; DB 2; Best Local Similarity 100.0%; Pred. No. 2.1e-97; Matches 228; Conservative 0; Mismatches 0; 181 181 AAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVVSDGVAQLD 121 121 PEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGA 180 ដ 61 HATIHTPRTEIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA 120 H 1 MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA 60 PEFAIHDLDSLDALAAADPADFFDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGA HATTHTPRTBIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA Indels Length 228; 228 228 0 the complete 180 60 120 0 Holroyd, S genome

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hypothetical protein - Synechocystis sp. (strain PCC 6803)
hypothetical protein - Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S75237
C;Accession: S75237
R;KAneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mio, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                   A; Note: the nucleotide C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-214 <RED>
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A;Title: A set of ordered cosmids and a detailed genetic and physical map for the A;Reference number: Z20556; MUID:97000351; PMID:8843436

A;Accession: T50577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein SCC75A.14c [imported] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50577 C;Accession: T50577 R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kina R;Redenbach, M.; Kieser, H.M.; Denapaite, D.;
                                                                                                                    S
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A; Residues: 1-314 < KAN>
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                                                                                                                                                                                                                                                  A;Start
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                         Cross-references: UNIPARC:UPI0000164C3D; EMBL:D90904; GB:AB001339; NID:g1652225; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                   Reference number:
                                                                                                                                                               Query Match
Best Local Similarity
Matches 89; Conserv
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                   PRTEIPFAGHPTVGASW--WLRERGTPINT----LQVFAGIVQVSYH---GDL------
                                                                                                                    LRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRV
LDVFTDQLFG-GNPLAVFPDAEGLTDGQMQKIAAEINYSETVFVLPPVTETGNFRLRIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRTLRQYAAVAEVDDLAVPPKGEWV-----YAWAWEDEAAGRVRARAFPGRDDGIDEDEA
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                                                                                                                                                            17.2%; Score 205.5; DB 2 29.9%; Pred. No. 1.6e-10; tive 37; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 407; DB 2
Pred. No. 2e-28;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                   PMID:8905231
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                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:AL133220; PIDN:CAB61714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyanobacterium
                                                                                                                                                               79;
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                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y.; Miyajima, N.;
Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
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8

101 IVQVSYHGDLTAISAR-----

SEWAPEFAIHD------LDSLDA 133

-RSAGSLRARMFAANLGVTED

234

178

134

LAAADPADFPDDIAHYLWTWTD-----

IAAVRDMDFDAN----LWLRTAPLVEGLLAAAYIYCRGGVNHAAKFHARMFSPEMGIAED

120 AVSFA-EFDLPRKSSRVELPLNHAALADALGVSEGHLGFENHVPSIWTAGVPFLLVPMHN

ঠ 문 S 문

PATGSAAAALSGAIHHFDGLTDGHYPLL EATGAAAIRITDYLSRDLTITQGKGSLI

262

A97523

hypothetical protein AGR\_C\_2485 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep\_2001 #sequence\_revision 30-Sep\_2001 #text\_change 09-Jul-C;Accession: A97523 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001

A;Title: Genome

Sequence

읁

Plant

Pathogen and

Biotechnology

Agent

Agrobacterium

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Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;

B.; Goldm Markelz,

Goldman,

09-Jul-2004

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C;Accession; AB2742
C;Accession; AB2742
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Clerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kut; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.;
                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-305 <KUR>
A;Residues: 1-305 <KUR>
A;Cross-references: UNIPROT:Q8UFQ1; UNIPARC:UPI00001645D4; GB:AE008688; PIDN:AAL42352.
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AB2742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Atu1346 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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AB2742
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A; Map position: circular
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                                                                                                                                                        Matches
                                                                                                                                                                                          Query Match
                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AQLPQTKDSAPSCEDLALLLGLSIDQLQQGEYEPQAYSCGLPFLFIPLINEEALNRISFN 194
  60
                                      60
                                                                                                                                                 71;
                                                                             _
                                                                                                                 1 MAIEVSVLRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTT
                                                                                                                                                                          Similarity
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  ASLRIFTPSGELPFÄGHPTVGÄAVAIAERNRGEGDDDIDMVCVLEEKVGPVRCAVKMRÄG
                                      AHATIHTPRIEIPFAGHPTVGASWWLRERGT------
                                                                           MALNYDIYDVFTEAK-MAGNPLAVNYDADDLSQDTMQAIAREMNLSETVFINRSTNPSHA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLDDRLDTPGSHHWQIEQGKALGRPSQLQLTVVKDGQGIRAVKVAGRSVLVSEGFMNL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSVWQNLLAGQWADCVYCLAPGDPSLGLSDNKLIHGRWFAPGLGIAEDPATGSGVAALGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PADFPDDIAH-----YLWTWTDRSAG-----SLRARMFAANLGVTEDEATGAAAIRITD
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SRDLTITQGKG----SLIHTTWSPEGW----VRVAGR--VVSDGVAQL 227
                                                                                                                                                                                                                                   chromosome
                                                                                                                                                                          15.5%;
                                                                                                                                                   34;
                                                                                                                                                                          Score 184.5; DB 2
Pred. No. 1.1e-08;
                                                                                                                                                        Mismatches
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; Kutyavin, T
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                                      PIN-TLQVPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   tumefaciens
  119
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A;Molecule type: DNA
A;Residues: 1-276 < KUR>
A;Cross-references: UNIPF
A;Experimental source: st
C;Genetics:
A;Gene: BMEI1835
A;Map position: I
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AB3481

R. DelVecchio, V.G., Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Force. Natl. Acad. Sci. U.S.A. 99, 43-448, 2002

A; Reference mumber: AD3252; PMID:11756688

RESULT: 6

Brucella melitensis

C; Accession: AE3481

REDEVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: I-333 <KUR>
A;Cross-references: UNIPROT:QBUPQ1; UNIPARC:UPI00000D1B12; GB:AE007869; C;Genetics:
A;Gene: AGR C 2485
A;Map positTon: circular chromosome
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A;Accession: A97523
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: UNIPROT:Q8YEP3; UNIPROT:Q8G339; UNIPARC:UPI000005820E; GB:AE008917;
;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
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Best Local |
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                                                                                                                                                                                                                                    75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 70; Conserv
                                                                                                                                                                                                                                                      Similarity
                                                                                                 RYPAPEMEVPFCGHATIALGAALAMRE-GDGRFALRLNHDBISVEGRKEGELFAASLQSP 116
                                                                                                                                                                                                  VSVLRVFTDSDGN-FGNPLGVINASKV-EHRDRQQLAAQSGYSETIFVDLPSPGSTTAHA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAAADPADFPDDIAHYLWTWTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVSFA-EFDLPRKSSRVELPLNHAALADALGVSEGHLGFENHVPSIWTAGVPFLLVPMHN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VALNYDIYDVFTEAK-MAGNPLAVMYDADDLSQDTMQAIAREMNLSETVFINRSTNPSHA
                                                                 WAPEFAIHDLDSLDALAAADPADFPDDIAH-----YLWTWTDRSAGSLRARMFAANL--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATGSAAAALSGAIHHFDGLTDGHYPLL
                                RTRNRAATEAEIGQALALFNYE--PDDLAHGISPALIHAGADHIVLPLRSREKLASMHYD
                                                                                                                                TIHTPRTBIPPAGHPTV--GASWWLRERGTPINTLQVPAGIVQVS--YHGDLTAISARSE 118
                                                                                                                                                                  MDVLRTAAFSQGDKGGNPAGVMTADRLPSPQDMQKIAKDVGFSETAFA---APDGESWRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATGAAAIRITDYLSRDLTITQGKGSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAAVRDMDFDAN----LWLRTAPLVEGLLAAAYIYCRGGVNHAAKFHARMFSPEMGIAED
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ilarity 26.1%;
Conservative 3
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                                                                                                                                                                                                                                 Score 161.5; DB
Pred. No. 1e-06;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 180.5; DB 2;
Pred. No. 2.8e-08;
5; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290
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                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                   96;
 GVTEDEATGAAAIRITDYLSRD--
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                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                    276;
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 192
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                                                                                                                                                                                                                                 RESULT
S46781
C;Genetics:
A;Gene: MIPS:YHR029c
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, 7; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, Ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobact A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                      A;Description: The sequence of A;Reference number: $46773 A;Accession: $46781
                            A; Molecule type: DNA
A; Residues: 1-294 < DUZ>
                                                                                                                                                       submitted to the EMBL Data Library, June A;Description: The sequence of S. cerevis
                                                                                                                                                                                                                                                 hypothetical protein YHR029c - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Bate: 28-Oct-1994 #sequence_revision 28-Oct-1994 #C;Accession: S46781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8U679; UNIPARC:UPI0000D2765; GB:AE008690; PIDN:AAL46292.1
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source:
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;Cross-references: UNIPROT:P38765; UNIPARC:UPI000013B267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 NLRNNELVIEQGTKMGRRSILHIRLKPEPELSGTGIVVLRGVIRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAPLRISDALSDVAPLADALGIGIGDIISEPAPRPADTGAAHIMVRVRNAGTVDEARPDA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAP---BEAIHDLDSL-DALA-----AADPADEPDD--IAH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASGAEVFGAGHNALGAWLWLGEHGNLGSLTTARTLQQEIGQDVLPIELELIAGRVHGRML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SRDLTITQ----GKGSLIHTTWSPEGWVRVAGRVVSDGVAQL
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                                                                                                                                                          cerevisiae
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EMBL:U10399; NID:g500689;
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probable phenazine biosynthesis protein PA4215 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: B83119; B83408 C;Accession: B83119; B83408 R,Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Larbig, S.; Lury, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic paragraphy.
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C;Genetics:
A;Gene: PA4215; PA1904
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A;Cross-references: UNIPROT:069754;
A;Experimental source: strain PAO1
A;Accession: B83408
A;Status: preliminary
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Best Local S
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GSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
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                                                       ALGLKGSTFPIEVYRNGPRHVFVGLESVAÄLSALHPDHRALCDFP-DLAVNCFAGAGR--
                                                                                                                                 LLGTAIALGAETDKDRLFLETRMGTVPFALERQDGKVVACSMQQPIPTWEHFSRPAELLA
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                                                                                             APEFAIHDLDSLDALAAADP-----ADFPDDIAHYLWTWTDRSA 158
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                                                                                                                                                                                                                                                                                         26; Mismatches
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Pred. No. 4.6e-06;
8; Mismatches 88
                                                                                                                                                                                                                                                                                                           Score 151.5; DB 2
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIPARC: UPI0000131A7B; GB: AE004838;
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                                                                                                                                                                                                             R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Jung, K.H.; Alam, M.; Fresttas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhar A;Tille: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-301 <S
                                                                                                                                                                                           A; Reference number: A84160; A; Accession: H84192
                                                                                                               A; Cross-references:
                                                                                                                                                                         A; Status: preliminary
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Query Match Best Local S Matches 77

Similarity

12.2%; Score 145; DB 2; 26.8%; Pred. No. 3.2e-05; 2ive 32; Mismatches 96;

Length 301;

Indels

82;

Gaps

17;

Conservative

VNG0332C

1-301 <STO>

UNIPROT: Q9HS99; UNIPARC: UPI00000635E1; GB: AE004437; NID: g10579960;

Ebhardt, H.; Lowe, T.M.;

D. W. ;

Shukla, Maddocks,

H.D.;

U . ດ : Lasky, & G., Jable

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RESULT 11
H84192
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Pazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letest Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitent A;Reference number: AD3252; PMID:11756688
A;Accession: AH3330
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                        hypothetical protein Vng0332c (imported) - Halobacterium sp. C_7Species: Halobacterium sp. NRC-1
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 01-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                    247
                                                                                                                                                                                                                185 ITDYLSRDLTITQGKGSLIHTTWSPEGWV 213
                                                                                                                                                                                                                                                                                                              138 ----DPADFPDDIAH------YLW-TWTDRSAGSLRARMFAANLGVTEDEATGAAAIR 184
                                                                                                                                                                                                                                                                                                                                                          132 PRLPEQVDVKIEREEAAAAIGLGTHEIGFENHVPGVWSAGTPCLLVPVHNL----IAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 TPRTEIPFAGHPTVGASWWLRERGTP-----INTLQVPAGIVQVS-YHGDLTAIS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 TPAYELPFAGHPTVGAAVSLARRQKTGDETDRLVTLEEKVGIVRCGVILGENSAFAEFDL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VFDVFADK-ALAGNFLAIVHDCEGLTDACMQAIAREFNLSETVFIHAPANPAHEASVRIF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VLRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
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ilarity 24.5%;
Conservative 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 148.5; DB 2
Pred. No. 1.6e-05;
1; Mismatches 95
                                                                                                                                                                  -SSQWWI
                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                        -----IHDLDSLDALAAA 137
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                                                      NRC-1
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RESULT 12
AI3080
AI3080
phenazine biosynthesis protein [imported] - Agrobacterium tumefaciens (strain co., phenazine biosynthesis protein [imported] - Agrobacterium tumefaciens (strain co., phenazine biosynthesis protein 11-Jan-2002 #text_change 09-Jul-2004 C; Accession: AI3080
R; Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; l; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Science 294, Zand, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Marthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon C. Mar
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A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: phzC
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A13080
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 < KUR>
A;Rosidues: 1-281 < KUR>
A;Cross-references: UNIPROT:Q8U830; UNIPARC:UPI00001648FC; GB:AB008689; PIDN:A
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAIEVSVLRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                          ASLAQWLFATGMVAADYVA 242
                                                                                                                                                                                                                                                                                                                                                                                                                       RRAQGRISFA---APPLIRSGAPTPAELEEALQLLGIEAHDVVDAAWIDNGPGWLGVRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARSEWAPEFAIHDLDSLDALAAADPADFPDDI-----AHYL--WTWTDRSAGSLRARMF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRVRIFSLDREMPFAGHPTLGSCHAWLSADGSPKNETAIIQECGAGLVPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHATIHTPRTBIPPAGHPTVGASW-WLRERGTPINTLQV----PAGIVQVSYHGDLTAIS
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                                                                                                                                                                                                        WSPEGWVRVAGRVVSDGVA
                                                                                                                                                                                                                                                                                SAEKVLSIDPVRSWPGRIDVGVVGPHAEGGEAAFEVRAFFSDHLGAIAEDPVTGSL----N
                                                                                                                                                                                                                                                                                                                                                     AA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDIAH---YLWTW--TDRSAGSLRARMFAANLGVTEDEATGAAAIRITDYLSR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYH-----GDLTAISARSEWAP-----EFAIHDLDSLDALAAADPADF-----P 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVDLCGHATIASHAHLYDDGALAAGEHTLETNVGVLDIEVAEDGTVWMAQNPPTVREVEL 128
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                                                                                                                                                                                                                                                                                                                                                  ·NLGVTEDEATGA-AAIRITDYLSRDL-TITQG--KGSLIHTT
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Pred. No. 3.3e-05;
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K; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, I.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Ye Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9887.

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: G95273
                                              A;Cross-references: UNLIPROT:0930U9; UNIPARC:UPI00000CAF97; GB:AE006469; PIDN:AAK64753.1 A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein SMa0180 [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95273
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G95273
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A;Molecule type: DNA
A;Residues: 1-290 <KUR>
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R;Goodner, B; Hinkle, G; Gattung,
A; Liu, F; Wollam, C; Allinger,
Science 294, 2323-2328, 2001
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                            A; Contents: annotation
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A; Residues: 1-290 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: H98205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AGR_L_1187 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Gene: AGR_L_1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 12.1%;
Similarity 27.4%;
71; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLAQWLFATGMVAADYVA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRVRIFSLDREMPFAGHPTLGSCHAWLSADGSPKNETAIIQECGAGLVPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHATIHTPRTEIPFAGHPTVGASW-WLRERGTPINTLOV----PAGIVOVSYHGDLTAIS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear chromosome
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Pred. No. 3.4e-05;
2; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIPARC: UPI00000D24DF;
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Markelz,
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kelz, B.
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A;Gene: SMa0180

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hypothetical protein BH1950 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: F83893 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: F83893
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F83893
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A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1950
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Search completed: April 14, 2006, Job time : 14.3694 Becs
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A; Residues: 1-295 <STO>
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Best Local Similarity
Matches 55; Conserv
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                                                                                           197
                                                                                                                               147 AHYLWTWTDRSAGSLRARMFAANL-GVTEDEATGAAA 182
                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 TITQ----GKGSLIHTTWSPEGWVRVAGRVVSDGVAQL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 VAPLADALGLDPRDILPEPPARPADTGATHLMVRVLNVDSVDRALPVADKLLAVLEKTPA 197
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                                                                                                                                                                                                                                                                                                             78 TVGASWWLRERGTPIN----TLQVPAGIVQVSYHGD------LTAIS-ARS 117
                                                                                                                                                                                                                                                                                                                                                          19 GNPAGIVLDGKGLTDSDROKIAKEVGFNETAF-PLPSE-RADVNIRFFTPGHEINLCGHA 76
                                                                                                                                                                                                                                                                                                                                                                                 19 GNPLGVINASK-VEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIFFAGHP
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                                                                                                                                                                                                                                                                    TMATIYALKTKGLLPDRDEITIETKÄĞİLPIRLSIDVDRSMMITMKQAAPQLRAFSGSRS
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                                                                                                                                                                               ELAASLALEEKOLHEELPVVYGSTGTWTLLIPIKKLDAFKRMOPNNOHFPHILOEMPRAS 196
                                                                                        VHPFCLETYDQEADMHARHFSSPYSGTVEDPVTGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 131.5; DB 2; ilarity 25.3%; Pred. No. 0.00048; Conservative 26; Mismatches 81;
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                                                                                                                                                                     MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H., Fryor M., Duthoy S., Grondin S., Los, Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Mycobacterium tuberculosis complex.
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SEQUENCE
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STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino Shiba T., Hattori M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Corynebacterineae; Nocardiaceae; Nocardia. NCBI_TaxID=37329;
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OrderedLocusNames=nfa37910;
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215 AA; 23024 MW;
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Nat. Blotechnol. 21:526-531(2003)
EMBL; BA000030; BAC73641.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
GO; GO:0009058; F:biosynthesis; TEA.
InterPro; IPR003719; PhzC PhzF;
PANTHER; PTHR13774; PhzC PhzF;
Pfam; PF02567; PhzC-PhzF; 1.
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MEDLINE-21477403; pubmedei-11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary."
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OrderedLocusNames=SAV5929;
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SEQUENCE
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Sakaki Y., Hattori M., Omura S.;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINB-22608306; PubMed=12692562; DOI=10.1038/nbt820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
NUCLEOTIDE SEQUENCE.
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proteome; Hypothetical protein.
214 AA; 23077 MW; 0ED571AD9BFD7D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                          EFAIHDLDS---LDALAAADPADFPDDIAHYLWTWTDRSAGSLRARWF-AANLGVTEDEA
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3 (TrEMBLrel. 24,
3 (TrEMBLrel. 25,
) (TrEMBLrel. 13, C:
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) protein SCO2268.
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                                                                                                                  PRELIMINARY;
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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil

Rabbinowitsch B., Rajandram M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill
NUCLEOTIDE SEQUENCE.
STRAIN-CGA009 / ATCC BAA-98;
STRAIN-CGA009 / DOI=10.1038/nbt923;
PubMedc14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S.,
Land M.L., Pelletter D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres
Harrison F.H., Gibson J., Harwood C.S.;
                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last samotation update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Phenazine biosynthesis PhzC/PhzF protein.
Name=phzF; OrderedLocusNames=RPA3182;
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Q6N501;
                                                                                                                                                                                                                          Bradyrhizobiaceae;
NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                             Rhodopseudomonas palustris. Bacteria; Proteobacteria; P
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GO; GO:000958; P:biosynthesis; IEA.
InterPro; IPR003719; PhzC PhzF;
PANTHER; PTHR13774; PhzC PhzF; 1.
Pfam; PF02567; PhzC-PhzF; 1.
Complete proteome; Hypothetical protein.
Complete 214 AA; 23321 MW; A5A53BF5EF9E9C07
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Nature 417:141-147(2002).
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RHOPA
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No. 1.4e-26;
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M. GO; GO:0003824; F:catalytic activity; TEA.

M. GO; GO:0003824; F:catalytic activity; TEA.

M. GO; GO:0003824; F:catalytic activity; TEA.

M. GO; GO:0003719; phzC phzF.

M. Interpro; JPR003719; phzC phzF.

PANTHER, PTHR13774; phzC phzF; 1.

Pfam; PF02567; PhzC phzF; 1.

Pfam; PF02567; PhzC phzF; 1.

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PF4am; PF02567; PhzC phzF; 1.

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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR003719; PhzC_PhzF.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein SMc03984.
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Q92M77;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Pfam; PF02567; PhzC-PhzP; 1.
TIGREAMS; TIGR00654; PhzP family; 1.
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                                                                                            EMBL; BA000022; BAA17151.1; ALT_INIT; Genomic_DNA.
InterPro; IRR003719; Phac_Phap.
PANTHER; PTHR13774; Phac_Phap.
Pfam; PF02567; Phac-Phap.
TIGRPAMs; TIGR00654; Phap-Family; 1.
TIGRPAMs; TIGR00654; Phap-Family; 1.
Complete proteome; Hypothetical protein; Oxidoredu.
SEQUENCE 306 AA; 33181 MW; EB8708EC5A779A41 CR
                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
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                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] MEDLINE=97061201; PubMed=8905231;
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Bacteria; Cyanobacteria; Chroococcales;
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LDVFTDQLFG-GNPLAVFPDAEGLTDGQMQKIAAEINYSETVFVLPPVTETGNFRLRIFT
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ORFNames=XC_1371;
Xanthomonas campestris pv.
Anthomonas roteobacteria;
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NCBI_TaxID=314565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 292;
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RC STRAIN-ATCC 3943/ NCPPB 528;
RC MEDLINE-ATCC 3943/ NCPPB 528;
RX MEDLINE-2022145; pubMed-12024217; DOI-10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Cimpina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,
RA Kateuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos of two Xanthomonas pathogens with differing
RT Trocomparison of the genomes of two Xanthomonas pathogens with differing
RT Trocomparison of the genomes of two Xanthomonas pathogens with differing
RT MSE, PSS-463(2002).
DR MSE, PSO:0009059; P:biosynthesis; IEA.
DR GO; GO:0009059; P:biosynthesis; IEA.
DR RANTHER, PTHR13774. PDC PAPF: 1.
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Best Local S
GHO EMENI
Q5AXHO EMENI
Q5AXHO;
10-MAY-2005
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10-MAY-2005
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Complete proteome; Hypothetical protein.
SEQUENCE 292 AA; 30927 MW; DB83DBBBE62636CA CRC64;
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OrderedLocusNames=XCC2742;
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01-OCT-2003
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                          -LAEDRLPGRQGR-----
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29.0%;
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30,

Created) Last sequence that annoted the contract of the contra

sequence update) annotation update)

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RESULT 12
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ID QSUZZ6;
AC QSUZZ6;
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DT 01-FEB-2005 (TrEMBLrel. 29, L
DT 01-FEB-2005 (TrEMBLrel. 29, L
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DT 01-FEB-2005 (TrEMBLrel. 29, L
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RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook P., Corwn B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Crown B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzderald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Ferreira P., Fitzderald M., Gage D., Galagan J.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Mihova T., Mabbitt R., McCarthy T., Nacdonald P., Najor J., Manming J.,
RA Mitchews C., Mauceli E., McCarthy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Nielsen C.B., Norbu C., Phunkhan P., Pierre N., Furcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Senauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Talanas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Lander E.,
RA Lander E.,
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Best Local S
Matches 78
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Wyman D.,
Lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
, AACD01000117; EAA61656.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: The sequence shown here is derived
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78; Conservative
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                                                                                                                                                                                                                                                                                                            AAADPADFPDDIA-------HYLWTWTDRSAGS--LRARWFAANLGVTEDE
                                                                                                                                                                                                                                    ATGAAAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSD
                                                                                                                                                                                                                                                                          GAVTTANGGEEASSSYLDAGWAEGMVTTYFYVKDVKDELLGRNVIRTRTI---
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                                                                                                                                                                                                ATGSAASGLTAYLS----LKEGR------
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Pred. No. 4.1e
34; Mismatches
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                     sequence update)
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                     update)
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RESULT 13
QALTD6 9BURK
QALTD6 9BURK PRELIMINARY; PRT; 286 AF
AC QALTD6;
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence up
13-SEP-2005 (TrEMBLrel. 31, Last sequence up
13-SEP-2005 (TrEMBLrel. 31, Last sequence up
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence up
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence up
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation
DB Phenazine blosynthesis PhzC/PhzF protein.
QC ORFNames=Bcen2424ARAFT 4678;
QS Burkholderia cenocepacia HI2424.
QC Burkholderia proteobacteria; Betaproteobacteria
QC Burkholderia proteobacteria; Burkholderia
QC Burkholderia proteobacteria; Burkholderia
QC NCBI_TaxID=331272;
RN UCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K.,
RA Copeland A., Lucas S., Lapidus A., Barry K.,
RA Hammon N., Israni S., Pitluck S., Richardsor
RT "Sequencing of the draft genome assembly of
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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 14:2221-2234(2004).

EMBL; AY59629; AAV47307.1; -; Genomic I GO; GO:0003824; F:catsyltic activity; II GO; GO:0009058; F:biosynthesis; IEA.

InterPro; IPR003719; PhzC PhzF.

InterPro; IPR001412; tRWA-synt I.

PANTHER; PTHR13774; PhzC PhzF; 1.

Pfam; PF02567; PhzC-PhzF; 1.

TIGRFAMs; TIGR00654; PhzF family; 1.

PROSITE; PS00178; AA TRNA LIGASE I; UNKO
                        US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia"
                                                                                                                                           Burkholderia cencepacia HI2424.
Bacteria; Proteobacteria; Beraproteobacteria; Burkhol
Burkholderiaceae; Burkholderia; Burkholderia cepacia
NCBI TaxID=331272;
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Date S.V., Marcotte E., Hood L
"Genome sequence of Haloarcula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15520287; DOI=10.1101/gr.2700304;
Ballga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman
Ballga N.S., Mannon P., Chiu Y., Weng R.S., Gan R.R., F
Dautech E.W., Shannon P., Hood L., Ng W.V.;
Date S.V., Marcotte E., Hood L., Ng W.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=phzC; OrderedLocusNames=rrnAC2502;
Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Pred. No. 1.3
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A Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

A Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

A Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,

A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,

A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,

A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

A Diaz J.S., Dodge S., Ferreira P., FitzGerald M., Gage D., Galagan J.,

A Gardyna S., Garre S., Graham L., Grand-Pierre N., Hafez N.,

A Gardyna S., Garre S., Graham L., Grand-Pierre N., Hafez N.,

A Gardyna S., Jones C., Kamal M., Kamat A., Karatas A.,

A Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

A Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

A Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

A Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

A Kells C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

A Mihova T., Mlenga V., Murphy T., Naylor J., Naylor J., Naylor J., Naylor J.,

A Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

A Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

A Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

A Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 87
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T5_GIBZE
Q412T5_GIBZE
                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. ORFNames=FG08473.1;
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                                                                                                                                                                                                                                                                                                                                  Hypocreomycetidae; Hypocreales;
NCBI_TaxID=229533;
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Eukaryota; Fungi; Ascomycota;
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13-SEP-2005 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
L; AAHL01000017; B
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Pred. No. 2e-08;
2; Mismatches
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XX MEDLINE=22022145, PubMed=12024217; DOI=10.1038/417459a;

XX MEDLINE=22022145, PubMed=12024217; DOI=10.1038/417459a;

XX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Almeida N.F., Jr., Alves L.M.C., do Amaral A.M., Curshin-Santos J.R.,

XX Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Curshin-Santos J.R.,

XX Ciapina L.P., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

XX El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C., Lemos M.V.F.,

XX All H. F., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

XX Martins B.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

XX Moreira H.M., Nowo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

XX Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

XX Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

XX Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Talamas J., Te
Vassiliev H.,
        Setubal J.C., Kitaj "Comparison of the host specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein XAC29
OrderedLocusNames=XAC2912;
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EMBL; AACW0100342; EAA71290.1; -;
Hypothetical protein,
SEQUENCE 309 AA; 33637 MW; BB70
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
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                                                                                        dos Santos M., Truf
J.C., Kitajima J.P.;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
protein XAC2912.
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D., Young G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas
            genomes
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Pred. No. 2.2e-08;
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L R., Vo A., Wang S., Wi
L, Zembek L., Zimmer A.,
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Search completed: April 14, 2006, 17:32:13 Job time : 88.1245 secs
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R MBL; ABG11933; AAM37757.1; -; Genomic_DNA.

R HSSP; P37757; ISDJ.

R GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

GO; GO:00030719; PhzC_PhzP.

R InterPro; IPR003719; PhzC_PhzP; 1.

R Pfam; PF02567; PhzC-PhzP; 1.

R Pfam; PF02567; PhzC-PhzP; 1.

R Pfam; PF02567; PhzC-PhzP; 1.

R TIGRPAMs; TIGR00654; PhzF_family; 1.

Complete proteome; Hypothetical protein.

G SEQUENCE 292 AA; 31038 MW; 2A9AADFE4816D976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.3%; Score 194; DB 2; Length 292; Best Local Similarity 29.1%; Pred. No. 3.1e-08; Matches 83; Conservative 21; Mismatches 107; Indels 74;
                                                             248 AQSRYVASQGREV----GRDGRVHVDVDAEGEVWIGGATLQVIDG 288
                                                                                          190 -----SRDLTITQGKGSLIHTTWSPEG--WVRVAGRVVSDG 223
                                                                                                                           188 RITQASAACGLAIYAPMHDHDADLVVRAFCPGDGIPEDPVTGSANACIAARLHGEDRLPG
                                                                                                                                                             150 LWTWTDRSAG-----SLRARMFAANLGVTEDEATGAAAIRITDYL-----
                                                                                                                                                                                           128 RARAIDTGDTYADALRAACAGLGASAQPAALWNNGPNWWLLBLADAQAVRQAAPDLAAIA 187
                                                                                                                                                                                                                           Gaps
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Result
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Perfect score:
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       92:
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US-09-940-3168-21
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Biocceleration
Sequence 65, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 2186, A Sequence 2934, A Sequence 27013, A Sequence 16787, A Sequence 6991, Ap Sequence 6991, Ap Sequence 20547, A Sequence 20547, A Sequence 6364, Ap Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	2
85	85	85	85.5	96	96	86	86	86.5	87	88	89	90.5	91	92	92	92	92
7.1	7.1	7.1	7.2	7.2	7.2	7.2	7.2	7.3	7.3	7.4	7.5	7.6	7.6	7.7	7.7	7.7	7.7
1253	1253	1253	545	1864	613	310	285	1232	197	279	3413	286	15281	6396	6396	1517	/ TCT
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US-09-688-842-3	US-08-466-277-3	US-07-920-281C-3	US-09-252-991A-21095	US-08-804-227C-3	US-09-248-796A-17277	US-09-724-623-122	US-09-328-352-4464	US-09-902-540-14264	US-09-605-703B-1974	US-09-328-352-5581	US-10-042-665A-8	US-09-134-000C-4899	US-08-471-119A-2	US-09-940-316B-72	US-09-410-551B-72	US-09-940-316B-19	05-04-6T0-52TB-TA
Sequence 3, A	Sequence 3, App.	Sequence 3, Appl	Sequence 21095	Sequence 3, App	Sequence 17277	Sequence 122,	Sequence 4464,	Sequence 14264,	Sequence 1974	Sequence 5581	Sequence 8, Appli	Sequence 4899	Sequence 2, Appl	Sequence 72, App.	Sequence 72, App.	Sequence 19,	sequence 19, App

# ALIGNMENTS

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APPLICANT: NIBBORN, NACASSE APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: PICORIO, WALLER
ITITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT PILING DATE: 1998-03-03
CURRENT FILING DATE: 1998-03-03
CURRENT FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: 0376/97
EARLIER FILING DATE: 1997-11-10
EARLIER FILING DATE: 1997-04-18
EARLIER PILING DATE: 1997-04-18
EARLIER PILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
FERRITER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-66
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Best Local Sim
Matches 228;
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Patent No. 6641814
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke
                                      181 AAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSDGVAQLD
                                                                                                                        61
                                                                                                                                             61 HATTIHTPRITETPRAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
                                                                                                                                                                                                                              1 MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA 60
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                                                                                                                                                                                                                                                                                                        Similarity
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6641814
                                                                                                                        HATTHTPRTEIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
                                                                                                                                                                                                     MAI EVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETI FVDLPSPGSTTA
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                 100.0%; Score 1192; DB 2; 100.0%; Pred. No. 1.1e-121; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         Length 228;
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RESULT 3
US-08-258-261B-20
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US-09-328-352-4558
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US-09-328-352-4558
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Patent No.
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4558
LENGTH: 292
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: Schupp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Uknes, Scott Joseph
TITLE OP INVENTION: Genes for the synthesis of
TITLE OP INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                             COUNTRY: U
                                                                                                                                                                           CITY:
                                                                                                                                                                                         ADDRESSEB: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 IAHYLWTWTDRSAGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 NALKQFSLDMKVTGSTIYGFYEESNEQKRIEVRSFAPAYGVNEDPVCGSGNGSVASFI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 INTLOVP--AGI----VQVSYHGDLTAISARSEWAPEPAIHDLDSLDALAAADPADPPDD 145
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08258261B
                                                                                                                                   USA
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Hill, Dwight Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schupp, Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- LRARMFAANLGVTEDEATGAAAIRITDYL 189
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           ADDRESSEE: Ciba-Geigy Co
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
 APPLICATION NUMBER:
                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20, 564377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 LRARMFAANLGVTEDBATGAAAIRITDYLSRDLTITQGK 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 LLGTDIALGAR-TUNHRLFLETOMGTIAFELERONGSVIAASMDQPIPTWTALGRDAELL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GNPVAVFFDADDLSAEQMQRIAREMNLSETTFV-LKPRNCGDALIRIFTPVNBLPFAGHP
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    278 amino acids
amino acid
    XGY: linear

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Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
                                                                                                                                                                                                                                                                                                          Lam, Stephen Ting
Hammer, Phillip B.
Uknes, Scott Joseph
VENTION: Genes for the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 145.5; DB ilarity 28.3%; Pred. No. 2e-07; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Gaffney, Thomas Deane
                                                                                                                                                                                                                               Ciba-Geigy Corporation
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US/08/456,837
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US-08-457-342-20
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, App. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/457,205
FILING DATE: 01-7UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-7UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
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PRIOR APPLICATION DATA:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                            COUNTRY: U
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                                                                                                                                                                                                                ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
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62; Conserv
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Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
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                            Version
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2e-07;
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US-08-457-646A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08457646A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
PILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
PILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/C
TELECOMMUNICATION INFORMATION:
TEST TRUNCES TO 10.5614
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 278 amino acid
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                     COUNTRY: USA
ZIF: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes for the s
TITLE OF INVENTION: antipathogenic
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          ADDRESSEB: Ciba-Geigy Corporation STREET: 7 Skyline Drive
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Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip B.
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      PatentIn Release #1.0, Version #1.25
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DB 1; 83;

Length 278; Indels

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US-08-458-076A-20
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TELEPAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino
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Best Local S
Matches 62
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Patent No. 5
COUNTRA.

ZIP: 10532

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

TWETTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Unnes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
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APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Biner, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
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                                                                                                                            CITY: Hawthorne
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01 CLASSIFICATION:
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Local Similarity 28.3%;
les 62; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 WRSKMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIBFGQ 232
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                                                                                                                                                                                          7 Skyline Drive
                                                                                                                                                                                                                   Ciba-Geigy Corporation
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; Pred. No. 2e-07;
33; Mismatches 83;
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RESULT 8
US-08-457-335A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-458-076A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08457335A Patent No. 5723759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.2%; Score 145.5; DB Best Local Similarity 28.3%; Pred. No. 2e-07; Matches 62; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
COUNTRY: USA
ZIF: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/458,076A
                                                                                                                                                                                                              TITLE OF INVENTION: Genes for the string of invention: antipathogenic
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                    ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 01-JUN
                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
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                                                                                                                                                                                                                                  Lam, Stephen Ting
Hammer, Phillip E.
Uknes, Scott Joseph
VENTION: Genes for the synthesis of
                                                                                                                                                                                                                                                                                                                Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                       Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                           Ligon,
                                                                                                                                                                                                                                                                                                                                                                                                             Schupp, Thomas
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                                                                                                                                                                                                                                                                                                                                                       , James Joseph
, Dwight Steven
                                                                                                                                                                                                                                                                                                                                                                                             James M
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                           APPLICANT: Hammer, Phillip
APPLICANT: van Pee, Karl-He
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes f
TITLE OF INVENTION: antipat
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CG
                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   ZIP: 10591
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5817502
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                                                                                                                                                                                                                                                                                                                        Hammer, Phillip B. van Pee, Karl-Heinz
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ilarity 28.3%;
Conservative 3
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                                                                                                                                                                                                                                                                                   Genes for the synthesis of
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Pred. No. 2e-07;
13; Mismatches 83;
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RESULT 10
US-09-028-934-20
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HOLECULE TYPE: protein
US-08-729-214-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Patent No. 6
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Best Local Similarity
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APPLICANT: Ligon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                            APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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LENGTH: 278 amino acids
TYPE: amino acid
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
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                                                                                                                                                                                                         ZIP:
                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                               CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                            Hammer, Philip E.
van Pee, Karl-Heinz
Kirner, Sabine
Young, Thomas R.
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                                                                                                                                                                                                                           USA
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Hill, Dwight S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lam, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435
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   US 08/729,214
                                                                           US/09/028,934
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Pred. No. 2e-07;
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                                                                                                                Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
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APPLICANT: Schroder, Harray
APPLICANT: Zelder, Oskar

APPLICANT: Zelder, Oskar

ITITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING P
ITITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
CURRENT FILING DATE: 2000-66-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
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US-09-602-777A-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6831165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 242, Application US/09602777A
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 19931636.8 FILING DATE: 1999-07-08
                                                                          APPLICATION NUMBER: DE 19932129.9 FILING DATE: 1999-07-19
                                                                                                                                                                                            APPLICATION NUMBER: DE 19932126.4 FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE 19932125.6
                                                                                                                APPLICATION NUMBER: DE 19932128.0 FILING DATE: 1999-07-09
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                  FILING DATE: APPLICATION |
                                                        APPLICATION NUMBER: DE 19932226.0
                                                                                                                                                      FILING DATE: 1999-07-09
                                                                                                                                                                          APPLICATION NUMBER: DE 19932127.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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DATE:
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                  NUMBER: DE 19932920.6
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US-09-602-777A-242
US-09-252-991A-21986
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SEQ ID NO 242
LENGTH: 211
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Best Local Similarity
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APPLICATION NUMBER: DE
FILING DATE: 1999-08-31
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APPLICATION NUMBER: DE 19933006.9
FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932973.7
FILING DATE: 1999-07-14
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FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932935.4
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                                                                          176 AYPEGAPHAFEVRAFAQGIG--EDPVTGSLNAFIAQWL
                                                                                                              160 -----SLRARMFAANLGVTEDBATGAAAIRITDYL 189
                                                                                                                                                    119 LDAACEALGISPDFIRAH---QWVDNGPGWAVVELPSAQHVLDLEPDFSAHPTLKLGVIG
                                                                                                                                                                                          133 ALAAADPADF-PDDI-AHYLWTWTDRSAG------
                                                                                                                                                                                                                              62 TLGTAHVFRELHGEQGTQL-VQECVAGLVAVRAIDGPASGLAFQA--PFTLKDGPLDASD
                                                                                                                                                                                                                                                                    78 TVGASWWLR----ERGTPINTLQVPAGIVQV-SYHGDLTAISARSEWAPEFAIHDLDSLD
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                                                                                                                                                                                                                                                                                                          2 GNPLAVIADADDLSAEQMARIARWINLSETTFLLKPTQEGADYRVRIFTPTGELPFAGHP
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26.6%; Pred. No. 2.1e-07;
:ive 26; Mismatches 79
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Gaps

159 118 132 61 77

GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

Sequence 21986, Application US/09252991A Patent No. 6551795

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US-09-252-991A-21986
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20934
LENGTH: 270
TYPE: TELLOW DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21986
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
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TYPE: PRT
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Local Similarity 27.6%;
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                                                                                                                                                                                                                        61 HATIHTPRTBIPFAGHPTVGASWWLRBR----GTPINTLQVPAGIVQVSYHGDLTAISARS 117
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                                                                                                                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                3 IEVSVLRVFTDSDGNF-GNPLGVINASK-VEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                      AVTARSQRFDFVSRWFGPNVGVNEDPVTGSAHTSLAPYWAQRLGKTRLSAEQGGARKGRL
                                                                                                              K-RPEPCATPDGLLEALGIAEAEVLKTD--DYLVVVDDEKTIAALAPDFARLKGLPCRGV 185
                                                                                                                                                  EWAPEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDR----------
                                                                                                                                                                                       RLRWFTPQVEVDLCGHATLATAWVLIHKLDDASPVLRFATRSGELSVRREGDSLAMDFPA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGSCQVWLNQGGGNAADEIVQECLAGLIRIRRKGALLSFA----APPLLRGGAVEDEV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVGA-SWWLRERG---TPINTLQVPAGIVQVSYHGDLTAISARSEWAPEF----AIHD-- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNAVAVVIGADRLSSROMLEFÄAWTQLSETTFLLRPTVABADYRVRIFTFLRELFFÄGHF 144
IHTTWSPEGWVRVAGRVVSDGVAQL 227
                                                                        --SAGSLR----ARMFAANLGVTEDEATGAAAIRITDYLSRDLTIT----
                                                                                                                                                                                                                                                           MELTIPOVDAFADSPPOGNPAAVCPLDAWLDDERLOAIABENNLSETAFV-VGRDGD--Y
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Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                        Score 125; DB 2;
Pred. No. 3.2e-05;
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; ORGANISM: Candida albicans US-09-248-796A-16787
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US-09-248-796A-16787
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US-09-252-991A-27013
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                                                                                            Sequence 16787, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION: WCLESC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: WCLESC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
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                                                                           SEQ ID NO 16787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc J.
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Best Local Similarity
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Patent No. 6551795
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TITLE OF INVENTION:
FILE REFERENCE: 107
                                        TYPE: PRI
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ORGANISM: Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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NVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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1:
              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MAIEVSVLRVPTDS
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(c) 1993 - 2006 Biocceleration Ltd
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US-10-166-087-30
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Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 13456, A Sequence 5118, Appl Sequence 210632, Sequence 6518, App Sequence 230986, Sequence 30, Appl Sequence 52819, A Sequence 52819, A Sequence 52819, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 52821, A Sequence 520127, Appl Sequence 730127, A Sequence 59017, A Sequence 59017, A Sequence 59017, A Sequence 59011, A Sequence 59012, A Sequence 7, Appl Sequence 23012, A Sequence 23012, A Sequence 23012, A Sequence 23012, A Sequence 23012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequence 30012, A Sequenc
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4 US-10-369-493-12173 3 US-09-940-316B-21 3 US-09-940-316B-17 3 US-09-940-316B-19 3 US-09-940-316B-19 3 US-09-940-316B-19 3 US-09-940-316B-19 4 US-10-741-600-1176 5 US-10-741-600-1177 4 US-10-741-600-1172 5 US-10-741-600-1173 5 US-10-741-600-1173 5 US-10-741-600-1173 5 US-10-741-600-1173 5 US-10-66693 4 US-10-042-665A-8 4 US-10-042-665A-8 4 US-10-042-665A-8 5 US-10-042-665A-8 5 US-10-042-665A-8 5 US-10-042-665A-8 5 US-10-042-665A-8 5 US-10-042-665A-8 5 US-10-042-665A-8	899	315	3413	3396	3396	3396	3396	3024	1642	1642	238	6396	1517	1509	1488	1482	327	CTC
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	US-10-203-295-30	US-10-425-114-66693	US-10-042-665A-8	US-10-631-467-773	US-10-741-600-1173	US-10-741-600-1172	US-10-788-792-170	US-10-408-765A-1977	US-10-741-600-1178	US-10-741-600-1176	US-10-425-115-248384	US-09-940-316B-72	US-09-940-316B-19	US-09-940-316B-23	US-09-940-316B-17	US-09-940-316B-21	US-10-369-493-12173	TO// %- NTT-C7%-0T-C0
	30, App	66693, 7	8, Appl:	773, App	1173, A	1172, A	170, Apj	1977, Ap	1178, A	1176, A	248384,	-	19, Appl	-		21, App	12173,	, TO! / B

# ALIGNMENTS

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Sequence 66, Application US/09791171

| Patent No. US20020094336A1
| GENERAL INFORMATION:
| APPLICANT: ANDERSEN, Peter |
| APPLICANT: MIELSEN, Rikke |
| APPLICANT: MIELSEN, Rikke |
| APPLICANT: MIELSEN, Rikke |
| APPLICANT: ROSENKRANDS, Ida |
| APPLICANT: ROSENKRANDS, Ida |
| APPLICANT: WELDINGH, Karin |
| APPLICANT: PLORIO, Walter |
| TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS |
| TITLE OF INVENTION: UNUMER: US/09/791,171 |
| CURRENT APPLICATION NUMBER: US/09/791,171 |
| CURRENT APPLICATION NUMBER: 09/050,739 |
| PRIOR APPLICATION NUMBER: 0376/97 |
| PRIOR APPLICATION NUMBER: 1277/97 |
| PRIOR APPLICATION NUMBER: 1277/97 |
| PRIOR APPLICATION NUMBER: 60/070,488 |
| PRIOR APPLICATION NUMBER: 60/070,488 |
| PRIOR APPLICATION NUMBER: 60/070,488 |
| PRIOR PILING DATE: 1998-01-05 |
| NUMBER OF SEQ ID NOS: 173 |
| SOFTWARE: Patentin Var 7 0 |
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US-09-791-171-66
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Best Local S
Matches 228
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SEQ ID NO 66
LENGTH: 228
TYPE: PRT
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                      121 PEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARWFAANI.GVTEDEATGA
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  PEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGA
                                                                                 HATIHTPRTEIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
                                                                                                         HATIHTPRTBIPPAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
                                                                                                                                                                   MAIRVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
                                                                                                                                                                                                                                                  100.0%; Score 1192; DB 3; llarity 100.0%; Pred. No. 1.8e-116; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            Length 228;
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228

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APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WICHEC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/50,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 0376/97
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
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Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 66
LENGTH: 228
LENGTH: 228
TYPE: PRT
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US-10-620-246-66
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US-09-804-980-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDERSEN, Peter APPLICANT: NIBLSEN, Rikke APPLICANT: OBTTINGER, Tho
FILING DATE: 1997-04-18
APPLICATION NUMBER: 60/070,488
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US-10-620-246-66
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PRIOR FILING DATE: 2002-05-02
PRIOR PELLING DATE: 2002-05-02
PRIOR PELLING DATE: 2001-02-20
PRIOR PELLING DATE: 2001-02-20
PRIOR PELLING DATE: 1999-10-08
PRIOR PELLING DATE: 1999-01-21
PRIOR PELLING DATE: 1999-01-21
PRIOR PELLING DATE: 1999-01-21
PRIOR PELLING DATE: 1998-10-08
PRIOR PELLING DATE: 1998-10-08
PRIOR PELLING DATE: 1998-10-08
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 228
Sequence 13456, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1192; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-116;
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                                                                                                                                         181 AAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSDGVAQLD 228
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GENERAL INFORMATION

APPLICANT: OMURA, SATOSHI

APPLICANT: ISEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REPERENCE: 249-262

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: UP 2001-272697

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                           SEQ ID NO 13456
LENGTH: 214
TYPB: PRT
                                                                                                                    Matches
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                                                                                                                                                Local
                                    4 EVSVLRVFTDSDGNFGNFLGVINASKV--EHRDRQQLAAQSGYSETIFVDLPSFGSTTAH 61
                                                                                                                 h 35.8%; Score 427; DB 4; Length 214; Similarity 43.9%; Pred. No. 3.6e-36; 98; Conservative 26; Mismatches 79; Indels
DYDVLRVPCGPGGGYGNELGVVREGSVLPECADRQALAAKLGFSETVFVDDPERGV----
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20,

Gaps

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Sequence 210632, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
US-09-738-626-6518

Sequence 6518, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI
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US-10-425-115-210632
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                                                                                                                          RESULT 6
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US-10-425-115-210632
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LENGTH: 306
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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NAME/KEY: unsure
LOCATION: (1)..(306)
OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAIEVSVLRVFTDSDGNF-GNPLGV--INAS--KVEHRDRQQLAAQSGYSETIFV-DLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                        TGAAAIRITDYLS----
                                                                                                                                                                                                                                                                 AVNVSSMEFKADNFLXPTGSKALSXFYHVITXLDHGRRRAGXQLRTRMMAHDL---EDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PG-STTAHATIHTPRTEIPFAGHPTVGASWWLRERG-----TPINTLQVPAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELPYVTLDVFTRT--RFAGNPLGVRTIPASGPKPTQAQKQSIAREFNFSETIFIHDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDIYTPTLRLPFAGHPCVGTAWLL-----DVPELVTPAGVVGTRLDGEFSWIBARPEWAP 113
                                                                                                                                                                                    TGSASCCLAAYMSIHGADKQTTQTRRYEFTQG 267
                                                                                                                                                                                                                                                                                                                                           IPHNVHLHATSLASYPGLEPAAHLQRNETIRQLELAAPVFSLVKGWTFVPIELPSLELLA 178
                                                                                                                                                                                                                                                                                                                                                                                                                         PATNITRTIDIFLITAEIPFÄGHPTIGGAVTLLSQGVTQIITKAGLIPVTPTGPDSVSIG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAAALLLTDRLGRALNIIQGRGSQILTAPQPAGWVEVGGRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATIHTPRTEIPPAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWAP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 179.5; DB 4
Pred. No. 5.8e-10;
                                                                                                                                                                                                                      RDLTITOG 198
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                                                                                                                    APPLICANT: GREENBERG, B. Peter
APPLICANT: SCHUSTER, MATTIN
APPLICANT: LOSTROH, CANDA
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 1999-09-03
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOPTWARE: PatentIn ver. 3.0
SEQ ID NO 6518
LENGTH: 280
    SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 621
LENGTH: 278
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                         Sequence 621, Application US/10389647 Publication No. US20040033549A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                        NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 TEIPFAGHPTVGASWWLR----ERGTPINTLQVPAGIVQV-SYHGDLTAISARSEWAPEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VFS-SEPFMGNPLAVIADADDLSAEQMARIARWINLSETTFLLKPTQEGADYRVRIFTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGTAIGRAGEIHISIBSHAIW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GELPFÄGHPTLGTAHVFRELHGEQGTQL-VQECVÄGLVAVRAIDGPASGLAFQA--PPTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTLKLGVIGAYPEGAPHAFEVŘAFÁQGIG--ÉDPVTGSLNASÍAQWLHRDGRAGEGYLAS
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKEDA, MASATO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 159.5; DB 3
Pred. No. 6.4e-08;
                                                                                     4.0
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US-10-156-761-14521
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-06-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-08-0
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14521
LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local S
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Local Similarity 28.1%; Pred. No. 4.4e-07;
                                                                                                                                                                                       120
                                                                                                                                         136
                                        188 YLSRDLTITQGKGSLIHTTWSP-EGWVR-----VAGRVVS--DG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 ALGLKGSTFPIEVYRNGÞRHVFVGLESVAÁLSÁLHÞDHRALCDFÞ-DLÁVNCFAGAGR--
                                                                                           180 RGIIATARAEDPAQGHDFV-------SRCFFPNVGIDEDPVTGSAHTALAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 -HWRSRMFSPAYGVVEDAATGSAAGPLAIHLARHRQIPYGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 GSLRARMFAANLGVTEDBATGAAAIRITDYLSRDLTITQGK 199
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                                                                                                                                                                                                                                                                                60 DWALRWFTPATEVAMCGHATLATAHVLHTSGTHEGPVRFATRSGVLIATPREDGSITLDF 119
                                                                                                                                                                                                                                                                                                                           61 HATIH--TPRTEIPFAGHPTVGASWWLRERGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LLGTAIALGABTDKDRLFLETRMGTVPFALERQDGKVVACSMQQPIPTWEHFSRPABLLA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 TVGASWWL-RERGTPINTLQVPAGIVQVSYH---GDLTAISARS---EW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                            1 MRIRIVDAFTDRP-FAGNPAGVILLDAFPDDAWLQDVAREVNHAETAFAHRLPRGEGGEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                       3 IEVSVLRVFTDSDGNFGNPLGVINASKV-EHRDRQQLAAQSGYSETIFVD-LPSPGSTTA
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                                                                                                                                                                                                                                  ---PINTLQVPAGIVQVSYHGDLTAISARS-----EWAPEFAIHDL-DSLDALA---- 135
FWSQRL----GRPDLTGLQASPRSGHVRTELRDDRTLLTGRAVTVIDG
                                                                                                                                       -----AADPADFPDDIAHYLWTWTDRSAGSLRARWFAANLGVTEDBATGAAAIRITD 187
                                                                                                                                                                                    PTAPLTPVETPEGVAEALGAEPLTACDTGPNVGDLLIELADEKTVRGLAPDLRALARYSE 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 128; DB 4; 23.6%; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches 100; Indels 88;
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APPLICANT: Ecopia Biosciences Inc.
APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-2US
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 274
TYPE: PATE
ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-30
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SEQ ID NO 230986
LENGTH: 120
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-10-166-087-30
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US-10-425-115-230986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_142252C.1.pep US-10-425-115-230986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 230986, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                Local Similarity
151 WTWTDRSAGSLRARMFAANLGVTED-----EATGAAAIRI-----TDYLSRDLTITQG
                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                  95 LQVPAGIVQVSYHGDLTAISARSEWAPEFAIHDLDSLDALAAADPADFPD----DIAHYL 150
                                                                                                                                                                                                             40 AQSGYSETIFVD-----LPSPGSTTAHATIHTPRTEIPFAGHPTVGASWWLRERGTPINT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 PINTLQVPAGIVQVSYH--GDLTA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 RQQLAAQSGYSETIFVDLPSPGS-TTAHATIHTPRTEIPFAGHPTVGASWW---LRERGT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KOEIAKEFNYSETIFVHPVDPQTPTQQRIDIFTTDRELPFAGHPTIGAASWALYLSPDKG 63
                                                                                                                                                                  AESG-SQWLWTDGHEVRVPFDGPVVHRGIPHDPALFGPYAGTPYAGGV-----GRAFNL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVTTLLTKÅGPIPISLRPSGDEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10166087
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                      9.4%; Score 112.5; DB 4; Length 274;
24.8%; Pred. No. 0.0054;
rative 22; Mismatches 71; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5%; Score 125; DB 4; Length 120
39.3%; Pred. No. 8.4e-05;
rative 11; Mismatches 34; Indels
                                                                          ----AEDPRTLPAPDPGRMRELGFTDLTVFR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Other Molecules Associated With
                                                                                                                                                                                                                                                             65;
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RESULT 11

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RESULT 12
US-10-450-763-52819
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn version 3.2
SEQ ID NO 87
LENGTH: 288
                                                                                                                                                                                                     Sequence 52819, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: EP 02028058.2
PRIOR PILING DATE: 2002-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHEN, JIE
APPLICANT: HU, LIPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 21525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             192
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                                                                                                                                                                                                                                                                                                                                                               244 HL----GKKEMHAFQCSHRGGELGISLRPDGRVDIRGGAAVVLEG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 TESVFRCTGSARGGSANVTITGRVWTGGTA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCGHATLASAAVLFHKIKNMNST-----LTFVTLSGEL-----RARRAEDGIVLDL---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNPAAVCLLENBLDEDMHQKIAREMNLSETAFIRKLHPTDNFAQSSCFGLRWFTPASEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNPLGY-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATI-----HTPRTEIP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSYWSQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DIAHYLWTWTDRSAGSLRA-----RMFAANLGVTEDEATGAAAIRITDYLSR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLYPAHPQDPHEVBDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSPLENLKVNTEN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGSLIHTTWSPEGW---VRVAGRVVSDGVA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W---DPDRGEVLARVFAPGFGIPEDAGCLPAAAALGVAALRLAADDRTSVTVRQVTV-RG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%; Score 110; DB 5; Length 288
21.4%; Pred. No. 0.011;
ative 38; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         --GSLIHTTWSPEGWVRVAG--RVVSDG 223
                                                                                                                                                              POLYPEPTIDES
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13432
LENGTH: 636
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; LENGTH: 375
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13432, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                Best
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Best Local :
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PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOPTWARE: CLETOM
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                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 9.2%;
Local Similarity 22.8%;
nes 53; Conservative 2
                                                                                                                                                                                                                                                                                                Local
    409
                                                                                          349 VTSVARYAĞHLDLFVVGTDSRVYSTWWDQSSGWAAWFRVGTLVARPGSTVNVVSRYSDHL 408
                                                                                                                                                                                296 PISVV-ARYPEHLDVFAVAADGRTMSDWWDAGSGWAGWPQVSGGLASPGGA-----GSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 TVAAHYVRAKVLGLGNCTIWQTSLAGKHRVTIEKHNDDYRISLEQGTPGFEPPLEGETRA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TAISKKIGCNGFFFFOIR------PGKNETDGRMFSPAIGIVEDFVTGNA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 DALAAADPAD--FPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 AIINALHLTEDDILPGLPIQVATTGHSKVMIPLKPEVDIDALSP------DLNAL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 GNSAGVVFPADNLSEAQMQLIARELGHSETAF--LLHSDDSDVRIRYFTPTVEVPICGHA 191
                                                                                                                                    68 RTEIP-FAGH-----PTVGASWWLRERGTP----INTLQVPAG-----IVQVSYHG 108
                                                                                                                                                                                                                          21 PLGVINASKVEHRDRQQLAAQ------SGYSETIFVD--LPSPGSTTAHATIHTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 -- INTLQ----- VPAGIVQVSYHG------
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                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                  Similarity
      DLFTTGSDGRTMSTWWDARTGWAADWFHVSGGVAANGATVTAVARHPFHLDVFTVGTDNR
                                                   DL-----
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SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                    8.4%; Score 100.5; Dilarity 24.5%; Pred. No. 0.31; Conservative 29; Mismatches
                                              TAISARSEWAPE-FAIHDLDSLDALAAADPADFP-----DDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 110; DB 5; Length 375; 
; Pred. No. 0.015; 
22; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                           97;
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                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                   Length 636;
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71;

Gaps

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RESULT 15
US-10-450-763-52821
Sequence 52821, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
FILE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
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; OTHER INFORMATION: Clone
US-10-424-599-178493
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US-10-424-599-178493
; Sequence 178493, Application US/10424599
; Publication No. US20040031072A1
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178493
LENGTH: 294
TYPE: PRT
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469
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                                                                                                                                                                                                                                                                                                                                                                                                                              187 DYLSRDLTITQGKGSLIHTTWSPEGWV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 ADPADFPDDIAHYL------WTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRIT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 DGEGASEDGLFIELDFFADTVTEFNSADISQISAALNDAPIIDIKRTTVGDHLLVELASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                     244 PYWAKKM----GKCDLSVYAASPRGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 ISLNRFRLRWFTPATEVBLCGHATLASAHVLFSSGLVKSDIIEFVTLSGVLTAKKVSGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ATIH-----TPRTEIPFAGHPTVGASWWLRERG-----TPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 IEVSVLRVFTDSDGNFGNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOVVBLQPDIGAIAKCPGGGILVSGTAPPESGFDYYCRTFFPKVGINEDPITGSAQCALA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKYFVVDAFTESAFK-GNPAAVCLLEBEKEDSWMQGVATEFNLSETCYL-TPIAESERSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYSAW-WDERSGWS---AWFALPGIVCRPDSTVTAVARHRDHL--DLFTTASDGRIMSTW 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDARSGWAPWFQVSGGAASAG 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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                                                                                                                                                                                  POLYPEPTIDES
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LENGTH: 217
TYPE: PRT
CORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(217)
OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-52821
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Matches
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NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 52821
LENGTH: 217
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                   Local
138 NALTAISKKIGCNGFFFFQIR-----PGKNETDGRMFSPAIGIVEDFVTGNA 184
                                 132 DALLAAADP-----ADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDBATGAA 181
                                                                     95 TV-AAHYVRAKVLGLGNCTIWQTSLAGKHRVTIBKHND--
                                                                                                         78 TVGASWWLRERGTPINTLQV----PAG--IVQVSYHGDLTAISARSEWAPEFAIHDLDSL
                                                                                                                                           38 GNSAGVVFPADNLSBAQMQLIARELGHSBTAFL-LHSDDSDV--RIRFTPTVBVPICGHA
                                                                                                                                                                               19 GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTBIPFAGHP
                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                               8.3%; Score 99; DB
27.4%; Pred. No. 0.1;
tive 20; Mismatches
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                                                                       -DYRI----SL
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Search completed: April 14, 2006, 18:40:30 Job time : 81.1108 Becs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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seq length: 2000000000
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   A_Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
3: geneseqp2001
4: geneseqp2001
5: geneseqp2002
6: geneseqp2003
7: geneseqp2003
8: geneseqp2003
8: geneseqp2003
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3552
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geneseqn1980s:*
geneseqn2000s:*
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geneseqn2003as:*
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geneseqn2003bs:*
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                                                                                                                                                                                                                                                                                                                                         Gapext 0.5
                                                                                                                                                                      summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	3 B	ID	Description
ב	3552	100.0	666	N	AAW72911	1
N	3552	100.0	666	N	AAY21928	
ω	3552	100.0	666	4.	AAB19846	
4.	3552	•	666	տ	ABU05989	
ហ	3552	100.0	666	თ	ABU37020	
σ,	1575	44.3	308	N	AAW72930	
7	1575	44.3	308	ผ	AAY21947	
80	1550	43.6		υ	ABU05359	
9	1550	43.6		o	ABU35716	
10	462.5	13.0		4	ABB70063	
11	420	11.8	697	œ	ADX72179	
12	416.5	11.7	800	8	ABO58564	
13	416	11.7	598	0	ABU37030	
14	410.5	11.6	386	9	ADZ47759	
15	410.5	11.6		ผ	AAW31852	
16	408.5			8	ADX97588	
17	408.5	11.5	1250	0	AA026231	
18	408.5	11.5	1250	œ	ADM87156	
19	402.5	11.3	708	v	ABB91504	
20	398	11.2	440	7	ABM90225	
21	397.5		406	4	ABG27250	
22	395	11.1	268	4	ABU52942	
23	391	11.0	572	N	AAW31855	
24	383.5	10.8	984	,	ALALA MARA	

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosi of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

diagnosis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 183-185; 163pp; English.

N-PSDB;

AAV63935.

WPI; 1998-542705/46.

Andersen P, Oettinger T,

Nielsen , Florio

Rosenkrands I,

Weldingh

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Rasmussen PB;

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SERUM INST. Z Z

444 544 544 544	30 30 40 40	2 C C C C C C C C C C C C C C C C C C C	25 26 28 29
363.5 363 360.5 359 358.5	364 364 364 364	369.5 369.5 367.5	381.5 380 375.5 375.5 373.5
10.2 10.2 10.1 10.1	10.2	10.4	10.7 10.7 10.6 10.6
270 639 1579 262 693	1151 330 408 408 408	261 639 574	256 277 261 694 258
40041	40044	40444	444046
ABU52939 ADN19622 ADS97981 ABU52944 ABP69529	ABB61598 AAW57645 AAW07539 AAB64007 AAB72737	ABU52940 ADN21309 ABG21919 AAG67370 AAM52322	ABU52945 ABU52936 ABU52943 ABB92421 ABU52941 ABU52941
Abu52939 Adn19622 Ads97981 Abu52944 Abp69529	Abu61598 Aaw57639 Aaw676307 Aab64007 Aab72737	Abu52940 Adn21309 Abg21919 Aag67370 Aam52322	Abu52945 Abu52936 Abu52943 Abu52943 Abu52941 Adm05164
Human mam Bacterial Protein f Human mam Human pol	Collagen- Collagen- Collagen CLP prote	Human mam Bacterial Novel hum Amino aci WASP homo	Human mam Human mam Human mam Herbicida Human mam Human pro

## ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                       01-APR-1998;
                                                                                                                                                                  08-OCT-1998.
                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                         Mycobacterium tuberculosis;
                                                                                                                                                                                                                     Mycobacterium tuberculosis antigen RD1-ORF9B.
                                                                                                                                                                                                                                                      AAW72911 standard; protein; 666 AA.
                                                                                                                                                                              WO9844119-A1
                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                                                    infection.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                         tuberculosis.
                                                                                                                          97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                       98WO-DK000132
                                                                                                                                                                                                         antigen; vaccine;
                                                                                                                                                                                                         immunological; immunogen;
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RESULT 2
AAY21928
ID AAY2
XX AAY2
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Best Local :
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  Mycobacterium tuberculosis
                               Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP7B; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                         AAY21928 standard;
                                                                                       Amino acid sequence of antigen RD1-ORF9B.
                                                                                                             06-SEP-1999
                                                                Immunogenic; Mycobacterium tuberculosis;
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                                                                                                                                                                                                                                                                                                                                                                                                      VVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADRVGRQSGATIADVLAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKVATGPSIQARLRABEASGAQLAPGTBPSPAPLGQPRSYLAPPTRPAPTBPPPSPSPQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKFNGQTPPPTSDDLSER
                                                                                                                                                                                                                                 ERAGRR 666
                                                                                                                                                                                                                                                           PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSDDF
                                                                                                                                                                                                                                                                      PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSDDF
                                                                                                                                                                                                                                                                                                                                                 ELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDADWHFIADPASRFYNLVLADCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPOHSRRARRGHRYRTDTERNV
                                                                                                             (first
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                                                                                                                                                         protein;
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                                                                                                             entry)
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Pred. No. 1.1e-213;
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NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK

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                                                                                                                                                                                                                                                                                                       The invention describes a substantially pure immunogenic polypeptide CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a CC protective immune response against infections by mycobacteria belonging CC to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (I) and at least CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second CC different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo CC degradation or post-translational processing; (3) a nucleic acid fragment CC that encodes the above polypeptides. The polypeptides and nucleic acid complex the above polypeptides. The polypeptides and nucleic acid complex the polypeptides of and as antigens for convis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the cuberculosis complex. The invention also describes the use of CFP7A or CFP3A or a T-cell epitope of for the induction of a strong immune CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin cest; use of CFP27, CFP10A, CFP16, CFP19, CFP23, CFP23A, CFP23B, CFP2B or a T-cell epitope of for the preparation of an immunological composition; and composition; and composition of a subunit vaccine
                                                                                                                                                                                                                          Query Match
Best Local Sim:
Matches 666;
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05-JAN-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                       Sequence 666 AA;
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                                                                                           IAGPEPAPEKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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98WO-DK000132.
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The present sequence is that of the Mycobacterium tuberculosis MTBN5 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB1982-49), encoded by 8 open reading frames (see AAB9035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic
                                                                                                                                                                          Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection.
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Mycobacterium tuberculosis. Mycobacterium leprae.

Mycobacterioses; survival; virulence; protective antigen; mycobacterial disease; tuberculosis; leprosy.

vaccine;

WO200274903-A2

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Matches 666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium tuberculosis and the marker protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2001; 2001US-0270123P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying and selecting genes for survival or virulence of mycobacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAADYDKLFRPHEGMEAFDDMAAQFFFDPSASFPPAPASANLFKPNGQTFPPTSDDLSER
               VVGLKGGAGKTTLTAALGSTLAQVRADRILAADADPGAGNLADRVGRQSGATIADVLAEK
                                                                                                                                                      NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK
                                                                                                                                                                                                                      GKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPSPQR
                                                              KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRRNPRGSYQIA
                                                                                 KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRRNPRGSYQIA
                                                                                                                                                                                                 GKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQR
                                                                                                                                                                                                                                                                 HQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNV
                                                                                                                                                                                                                                                                                              HQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNV
                                                                                                                                                                                                                                                                                                                                                              IAGPEPAPPKPFTPPMPIAGPAPTPTBSQLAPPRPFTPQTFTGAPQQPBSPAPHVPSHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                FVSAPPPPPPPPPPPPPPPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER
VVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADRVGRQSGATIADVLAEK
                                                                                                                               NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression co of the nucleic acid inhibits proliferation of a cell. Also included are: (Cl) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated colypeptide or its fragment whose expression is inhibited by the antisense concoding a polypeptide, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the proliferation or the activity of a gene in an operon required for containing the polypeptide; (6) inhibiting cellular contiferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for cellular proliferation or the biological pathway in which a proliferation—required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACA40890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; SEQ ID NO 64944; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     candidate molecules for rational drug
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Trawick JD,
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Forsyth
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                                                                                  PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSDDF
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Pred. No. 1.1e-213;
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18-APR-1997;
10-NOV-1997;
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products from the present invention, which describes protein frag-
and nucleic acid fragments derived from M.tuberculosis, can be use
the detection of and prevention of mycobacterial infections. In
particular, the proteins and nucleic acids can be used for the dia
of or vaccination against tuberculosis caused by M. tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                       africanum or M.
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 204-205; 163pp; English
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infection.
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                                                                                                                                                                                               1 MKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRRNPRGSYQ
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                 GEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSD
                                                              AGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDMLRNNGYQDLASRACVVINHIMP
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                                                                                                                                                              IAVVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADRVGRQSGATIADVLA
                                                  AGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGXQDLASRACVVINHIMP
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97US-0044624P.
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98US-0070488P.
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Pred. No. 1.8e
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                                                                                                                                                                                                         To the tuberculosis complex. The invention by my conditions of polypeptide comprising at least one polypeptide fragment (I) and at least cone fusion partner; (2) a fusion polypeptide fragment (I) and at least cone fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cone fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cone fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cone fusion partner from M. tuberculosis, or MPT59 and a second cone degradation or post-translational processing; (3) a nucleic acid fragment cone degradation or post-translational processing; (3) a nucleic acid fragment cone useful as pharmaceuticals, for diagnosis of and as antigens for concination against TB caused by Mycobacterium tuberculosis, africanum or concination against TB caused by Mycobacterium tuberculosis, africanum or concination against TB caused by Mycobacterium tuberculosis, africanum or concination against TB in a manual for diagnosis of TB use of CFP7A or concepts. The polypeptides are also useful for diagnosis on going or concepts of complex. The invention also describes the use of CFP7A or concepts of for the invention also describes the use of CFP7A or concepts of for the invention also describes the use of CFP7A or concepts of for the invention and strong immune concepts of for diagnosis of TB in a manual by performing a DTH type skin concepts use of CFP2A, CFP3A, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B, CFP3B
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05-JAN-1998;
01-APR-1998;
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                                                                                                                                                      Sequence 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic fragment of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX81047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective immune response against infections by mycobacteria belonging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
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                                           Local Similarity
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       Conservative
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99.7%;
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                                       Score 1575;
Pred. No. 1.
       Mismatches
                                           .8e-90;
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RESULT 8
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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and provent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis. Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis and M. leprae marker protein #10
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 172-174; 874pp; English.
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                              Mycobacterium leprae
                                                                                          Protein encoded by
                                                                                                                         19-JUN-2003
                                                                                                                                                                                   ABU35716 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPP--PAPS---RPSASPAEPPTRPAPQHSR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 AA;
                                                                                                                                                                                                                                                                                         YKRKVLBLAAALSDDFERAGR 665
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGRESEANIADLLADKOVKSYNDIRTHTSVNAVNLEVLEAAEYSTAQHALSGEDWNEAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRTRVRRPPRGSYQIGILGLKGGAGKTTVTVTLGSMFARVRNDRILVVDADTSCGNLADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARRGHHHRDETQQANPASATEPMIAPRARTAE---LRQAPHAAAEPAP------
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                                                                                                                                                                                                                                                             YRRRILBLAAALSDDFERAGR 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GAKKPSKVVAKRGWRHWVHTVTRINLGLSPDERYELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISEPPQWPPABAPEHQFAKABPPSVPIPINEPSP-----AKPATPMPMTPIDGSQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ 59
                                                            prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                        (first entry)
                                                                                          Prokaryotic essential gene #21243
                                                                                                                                                                                   protein; 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPEPSLAEFE-AQPPATPKPSLLPRPMSSPPEAPRPSANQHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
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Pred. No. 1.3e-88;
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문 δ

Matches

335;

Conservative

66;

Score 1550; DB 6; Pred. No. 1.3e-88; 6; Mismatches 168;

168;

Gaps

59

Length 586; Indels 112;

MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER 60 MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ

Query Match Best Local Similarity

43.6%;

몽

60 61

L----PPNPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP FVSAPPPPPPPPPPPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP

----KPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPB 169

121 IAGPEPAPP----

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cc encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated colypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (c) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or that inhibits cellular proliferation; (8) (c) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an companism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent convicts each of the strains is present in a culture or collection of convicts each of the strains is present in a culture or collection of convicts each of the strains is present in a culture or collection of corrections or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational corrections or screening homologous nucleic acids required corrections or screening homologous nucleic acids is acids.
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
Sequence 586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
Wall
                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Forsyth
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                           New isolated nucleic acid genes from Drosophila and
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N-PSDB; ABL14166.
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11-JUL-2000; 2000US-00614150
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   interactions
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                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 446 AA;
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DEAGSLGPDGYNYNKPAKP
                             RRRKRAAPDLDATQKSLRP 352
                                                                                        PRSYLAPPTRPAPT---EPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGG
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ADX72179 standard; protein; 697 ጀ

ADX72179;

21-APR-2005 (first entry)

Plant full length insert polypeptide seqid 41545

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;

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XX yield; plant growth; plant protein content.

Unidentified

US2004034888-A1

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Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide
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05-NOV-2001;
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SCREEN S B.
TABASKA J B.
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VSSPPQVEKTSPPPAPLSSPP--LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTP--
                                                                                                                                                                                            SPPPPPP-AKSTPPPEEYPTPPTSV--KSSPPPEKSLPPPTLIPSPPPQEKPTPPSTPSK
                                                                                                                                                                                                                             PPTPPMPIAGPEPAPEKPFTPPMPIAGPAPTPTESQLAPP------RPPTPQTPTG 163
                                                                                                                                                                                                                                                             SPPPPAPVASPPPPVKSPPPPTPVAS--PPPPAPVASSPPPMKSPPPPTPVSSP-PPPEK 162
                                                                                                                                                                                                                                                                                                                                                                PHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSAPPP---
                                                              SPPPAPLSSPPPAPQVK
                                                                                           ABPPT-----RPAPQHSRRARRGHRYRTDTBRNVGKVATGPSIQ-ARLRABBASGAQLAP 265
                                                                                                                                                             APQQPESPA-PHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAP-----
                                                                                                                                                                                                                                                                                              -PPPP-----PPPP---PPTPMPIAAGEPPSPEPAASKP-----PTPPMPIAGPEPAPPK 113
                                                                                                                            PPSSPEKPSPPKEPVSSPPQTPKSSPPP----APVSSPPPTPVSSPPALAPVSSPPSVKS
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for gene expression analysis, splicing events, for asse surveying tissues. assessing genomic

Claim 45; SEQ ID NO 32198; 80pp; English.

CC expression, comprising any of the 27,400 fully defined nucleotide concoding at least 8 amino acids of any of the 6888 amino acid sequences (cfully defined in the specification, or their complements or fragments, and cencoding at least 8 amino acids of any of the 6888 amino acid sequences (cfully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule (cxpressed in human cells or tissues. Also included are a spatially-cx addressable set of single exon nucleic acid probes for measuring human (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately (cand addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded paptide comprising at least 8 (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids of any of the above-mentioned amino acid (contiguous amino acids specifically to a peptide cited above, (contiguous amino acids specifically to a peptide cited above, (contiguous amino acids amino acid substitutions), an echodo of providing (contiguous amino acid of a customer desiring to measure gene expression, a method of providing (contiguous amino acids aci specific exon, The invention relates to a nucleic acid probe for measuring human expression, comprising any of the 27,400 fully defined nucleotide constructing genome-derived single exon microarrays gene that

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Matches 101
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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   New antisense nucleic acids, for homologous nucleic acids
                                                                                                                N-PSDB; ACA40900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design
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Pred. No. 1.3e
22; Mismatches
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   useful for identifying proteins or screening required for cellular proliferation to
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Xu HH;
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isolate candidate molecules for rational drug discovery programs

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense controlled the polypeptide; (6) inhibited by the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for required for proliferation or that has an activity against a biological pathway for equired for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that antibite partiferation of an organism activity; (11) a culture compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an organism; or (13) identifying an antibiotic; (10) profiling a compound that inhibite proliferation of an organism; or (13) identifying the target of compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of contiferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation is solate candidate molecules for rational Sequence 598 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to an isolated nucleic acid comprising any one ftp.wipo.int/pub/published\_pct\_sequences ₽,

밁 8 S S 밁 S 밁 밁 5 δ 밁 밁 밁 Matches 134; Query Match Local Similarity 319 AAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVKKVKPQKPKATK----PP 170 110 224 124 93 50 44 -KPNGQTPPPTSDDLSERFVSAPPPPP-----PPPPPPPPPPP--MPIAAGEPPSP--EP ø VAPWPPLPPLPNNHP-PAPPSAPVPGVPLAPLPISGRPVRAWVGSLIALRICCCRVCSGV AASKPPTPPMPIAGPEPAPPKPPTP----PMPIAG-----SRPNPPLPPVPPEPISKAAPPVPPVPPWPVVPMPPDPPVPPIPDRIPPAPPDPPSPPSAP FRPHEGMEAPDDMAAQPFFDPSASFPPAP------ASANLP-----RLSMPASPPAPPFPPTLIMLVPPLPPVPPAPNSPPEPPSPPAPPPKMPNPPGPPVPPAPN -----APPPPSGLDPPLPPAPPAAP RRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAP----GTEP--SPAPLGQP APPAPPVPPAPAKOP-----PPAPPAPPAPLSRPAFPAPPASKPSPPTPPAPPEP QQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEP--PPAPSRPSASPAEPPTRPAPQHS LAGALNPSRPSSCPPKPPAPAVPAGAPVPPLPPLPTLPTSTPLPPAPPLPPLPALPTSPG -----PEPAPPKP-----PTPPMPIAGPAPTPTSQLAPPRPPTPQTPTGAP FAPNPPAPPAPPLANSPPVPPAPAVPPAPIKFWERAAWPPVPAAPRNKPASPPRPPAPPV 109 Conservative 11.7%; 28.0%; 22; ----APPTRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQH Score 416; DB 6 Pred. No. 1e-17; Mismatches PSANSPPFPPAPPAPPVAPKAANPP 165, 6; Length 598; Indels 158; Gaps 484 3 277 223 288 165 169 123

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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide obtainable from a species of Mycobacterium and is immunoreactive with sera from a human, animal or avian species previously exposed to the Mycobacterium but is not immunoreactive with sera from a human, animal or avian species not previously exposed to Mycobacterium. The composition and methods are useful for diagnosing, preventing or treating tuberculosis or other diseases or conditions associated with M. tuberculosis or related organisms. This sequence represents the Mycobacterial antigen C17 matures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polypeptides derived from Mycobacterium tuberculosis related organisms, useful for diagnosing, preventing or treating tuberculosis or other diseases associated with M. tuberculosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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RRARRGHRYRTDTERNVGKVATGPSIQA----RLRAEBAS--GAQLAPGTEPSPAPLGQP
                                                                                                                                                                                                                                           PPKPPTPPMPIA-GPBPAPPKPPTPPM-----PIAGPAPTPTBSQLAPPRPPTPQTPTG
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Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                     This novel 74 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see AAT93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAW31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and anti-mycobacterial drugs. (Updated on 25-MAI 2003 to correct PR field.)
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Fig 13; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA and related proteins or RNA derived from M. tuberculosis - used for diagnosis of mycobacterial infections, monitoring vaccination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1996;
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6; Mismatches 10
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1 MAADYDKLFRPHEGMEAPDD......RKVLELAAALSDDFERAGRR
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#### SUMMARIES

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361 KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDSKYELDLHARVRRNPRGSYQIA

420 360 301 NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK 360

GKVATGPSIQARLRABEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPSPQR GKVATGPSIQARLRASEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQR

300

NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK

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181 HOPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPOHSRRARRGHRYRTDTERNV

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121 IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP 180

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## ALIGNMENTS

C;Accession: B70803

C;Accession: B70803

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 hypothetical protein Rv3876 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004 A;Gene: A; Cross-references: UNIPROT: 069740;
A; Experimental source: strain H37Rv A; Molecule type: DNA A; Residues: 1-666 < COL> A;Accession: B70803
A;Status: preliminary; nucleic acid sequence not shown; translation Query Match 100.0%; Score 3552; DB 2; Best Local Similarity 100.0%; Pred. No. 3.6e-153; Matches 666; Conservative 0; Mismatches 0; Rv3876 UNIPARC: UPI00000D105D; GB:AL022120; GB:AL123456; Length 666; not shown

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R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Whee: R;Cole, S.T., Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, eam, M.A.; Rutherford, K.M.
aam, M.A.; Rutherford, K.M.
nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Sqn
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9CDD8; UNIPARC:UPI00000C6C23; GB:AL450380; NID:g13092445; C;Genetics:
A;Gene: ML0048
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A;Molecule type: DNA
A;Residues: 1-586 <STO>
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                                                                                                                                                                                                            SPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPP--PAPS---RPSASPAEPPTRPAPQHSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADRVGRQSGATIADVLAEK
ATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELD
                                  ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
                                                                   TRPAPTEPPPSPSPGRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD
                                                                                                       HARRGHHRDETQQANPASATEPMIAPRARTAE---LRQAPHAAAEPAP-------
                                                                                                                                                                             TPV-----
                                                                                                                                                                                                                                                                             IAGPEPAPP-----KPTPPMPIAGPAPTPTESQLAPPRPTPQTPTGAPQQPB
                                                                                                                                                                                                                                                                                                                                                     FVSAPPPPPPPPPPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP
                                                                                                                                                                                                                                                                                                                                                                                       MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERAGRR 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQDLASRACVVINHIMPGE
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                                                                                                                                                                           -TSPEPSLAEFE-AQPPATPKPSILPRPMSSPPEAPRPSANOHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1550; DB 2;
Pred. No. 4.5e-63;
6; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 586;
                                                                                                                                                                                                                                                -AKPATPMPMTPIDGSQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 112;
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A.; Hamlin, N.;
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Holroyd,
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T10030
T10030
hypothetical protein MLCB628.11c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
Mol. Microbiol. 7, 197-206, 1993
A;Tile: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A;Reference number: Z16917; MUID:93188700; PMID:8446027
A;Accession: T10030
A;Steatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuses: 1-478 <BIG>
A;Cross-references: UNIPROT:033082; UNIPARC:UPI00000B6649; EMBL:Y14967; NID:92370268; P1
C;Genetics:
A;Note: MLCB628.11c
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                                                                                                                                                                                                                                                                                                                                                      59 ---PEPSLAEFEAOPPATPKPSL-----LPR-----PMSSPPEAP-RPSAN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 SKPPTPPMPIAGPEP--APPKPPTPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAP
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                                                                                                                                                            YKRKVLBLAAALSDDFBRAGR
                                                                     TVSKYYNVMLADCGVGLFDPVTRGVLSTASGVVIVTSTSVDAARQAAIALDWLRHNGYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLFAPEYSSAQRALSDADWHFIAD
   DADTSCGNLADRAGRESEANIADLLADKDVKSYNDIRTHTSVNAVNLEVLPAAEYSTAQH
                                DADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQR
                                                                                                                                          GVQTGRST----
                                                                                                                                                                                                                                                PLGQPRSYLAPPTRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTG
                                                                                                                                                                                                                                                                                                       EPPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPA
                                                                                                                                                                                                                                                                                                                                                                                                                          YRRRILELAAALSDDFERAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%; Score 1378.5; DB 2; llarity 51.1%; Pred. No. 1.9e-55; Conservative 53; Mismatches 126;
                                                                                                                                                                                                                                                                                   - OHSRHARRGHHHRDETQQANPASATEPMIAPRARTAE - - - LRQAPHAAABPA
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                                                                                                                                          -----GAKKPSKVVAKRGWRHWVHTVTRIN
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RESULT 4

R70545

R70545

R70546

R70546

R70546

R70547

C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: R70545

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-405 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70545
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   RINLGLSPDEKYELDLHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRI 449
                                                                                                                                                                                                                                                                                                                                                                                                                 GGRRRKRAAPDLDATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALT-- 389
HIAAGTBISLDLLDPIYKRKVLBLAAALSDDFBRAGRR 666
                                                                          QASVALDWLRUNGYQDLASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDR 628
                                                                                                                        ASSDAFSADDYTRTLDILERFYGLVLTDCGTGLLHSAMSAVLPRSDVLVVVSSGSIDGAR
                                                                                                                                                                SAGRALSDADWHFIADFASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQ 568
                                                                                                                                                                                                            VÄVDANPDRGTLSQKVPLETPATVRHLLRDADGIERYSDVRGYTSKGPSGLEVLASDSDP
                                                                                                                                                                                                                                                                                             LINAGEGPRAAHLNDLVAQVNRPLRGCYRIAVLSLKGGVGKTTITATLGATFADLRGDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQPRSYLAPPTRPAPTEPPP---SPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRTGVGAPDSGNGGTDH-------PTVQLPPVPSVGAPPAAAGGET
                                       SAAATLDWLQAHGHDDQVRNSIAVVNAVRPRAGKVDVGKVVEHFSRRCRAVRVV--PFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPS---RPSASPAEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSDADWHFIADPASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASV 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SPAERPPYRLEPVP------HTPYPEL---------
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Holroyd,
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R;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A. submitted to the EMBL Data Library, June 1994
A;Bescription: Pex genes: pollen-specific genes with extensin-like A;Reference number: S49915
A;Accession: S49915
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A;Molecule type: DNA
A;Residues: 1-1188 <RUB>
A;Cross-references: UNIPROT:Q41805; UNIPARC:UPI00000A1616; EMBL:Z34465; NID:g600117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extensin-like protein - maize
C;Species: Zea mays (maize)
C;Date: 05-Mar-1955 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49915
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910 PIVKSSPPPAMVSSPPMTPKSSPPPVVVS
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                                                                                                                                                                SSPPLAPVSSPPQVEKTSPPPAPLSSPP--LAPKSSPPHVVVSSPPPPVVKSSPPPAPVSS
                                                                                                                                                                                                                                                  SPPSVKSSPPPAPLSSPPPAPQVK-------SSPPPVQVSSPPPAPK 799
                                                                                                                                                                                                                                                                                                                                                                        TPQTPTGAPQQPESPA-PHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAP------
                                                                                                                                                                                                                                                                                                                                                                                                                   VSSPPPPEKSPPPPPPAKSTPP-PEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPPQEKPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSAPPP----PPPP--
                                                                                                                      PORNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGP 357
                                                                                                                                                                                                     SGAQLAP----
                                                                                                                                                                                                                                                                                         SRPSASPAEPPT----RPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQ-ARLRAEEA
                                    ---- PQKPKATKPPKVVS
                                                                               ---KPASPPAHVSSPPEVVKPSTPPAPTTVISPPSEPKSSPPPTPVSLPP
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                                                                                                                                                                                                       -GIEPSPAPLGQPRSYLAPPTRP-----APTEPPPSP--S
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PI

C;Accession: G86441

R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Rature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

RESULT G86441

unknown protein [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) (c;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001

#text\_change 09-Jul-2004

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A;Reference number: A86141; MUID:21016
A;Accession: G86441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1201 <STO>
A;Cross-references: UNIPROT:Q9C6S1; UN
C;Genetics:
extensin homolog T9E8.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 C;Accession: T06291 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I submitted to the Protein Sequence Database, April 1 A;Reference number: Z15588 A;Accession: T06291 A;Molecule type: DNA
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Pred. No. 1.2e-11;
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                                                       I.; Mewes, H.W.; Mayer, K.F.X.;
1999
                                                                                                       #text_change 09-Jul-2004
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R.ERTL, H.; Hallmann, A.; Wenzl, S.; Jumper, R.ERTL, H.; Hallmann, A.; Wenzl, S.; Jumper, R.ERTL, T.; Hallmann, A.; Wenzl, S.; Jumper, R.Title: A novel extensin that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular A.Title: A novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extension that may organize extracellular and the novel extracellular and the novel extracellular and the novel extracellular and the novel extracellular and the novel extracellular and
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A;Cross-references: UNIPROT:Q9TOX5; UNIPARC:UPI000009FB81; EMBL:AL049608
A;Experimental source: Cultivar Columbia; BAC clone T9E8
C;Genetics:
C;Genetics:
A;Map position: 4
A;Note: T9E8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extensin - Volvox carteri (fragment)
c;Species: Volvox carteri
c;Species: Volvox carteri
C;Date: 04-Dec-1992 #seguence revision 04-Dec-1992
C;Accession: $22697; $21006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-464 <HAL>
A;Cross-references: UNIPROT:Q41645; UNIPARC:UPI000009F7C8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S22697;
A; Accession: S22697
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                                                                                                                                                                                                                                                                                                                                                                                    30 SASFPPAPASANLPKPNGQTPPPTGDDLSERFVSAPPP----PPPPPPPPPPPTPMPIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 APDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPFTSDDLSERFVSAPPP---PPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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      PSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRABEASGAQL
                                                                                                                       TPTESQLAPPRPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKWPIGEPPA
                                                                                                                                                                                                                                                  EPPSPEPAASKPPTTPPMPIAG-PEPAPPKP-PTPPMPIAGPEPAPPKPPTPPMPIAGPAP
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34.5%; Pred. No. 5.5e-12;
tive 27; Mismatches 101
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Pred. No. 8.2e-12;
20; Mismatches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - PCEESPPPAPVVHHSPPPPMVHHSPPPPVIHQ
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C. Accession: Dispitation, M.K.; Cohnay, A.B.; Federspiel, N.A.; Kanl, S.; White, O.; Alonso, Chin, C.W.; Ghung, M.K.; Cohnay, A.B.; Cohnay, A.R.; Creasy, T.H.; Dewar, K.; Ramer, A.B.; Ghangha, B.; Millar, L.; Chinay, A.B.; Cohnay, A.R.; Creasy, T.H.; Dewar, K.; Ramer, A.B.; Ghangha, B.; Klan, K.; Liu, S.M.; Liu, S.X.; Martin, P.; Southwick, A.M.; Sun, H.; Tallon, kr. M.; Wh. D.; Yu, G.; Fraser, C.M.; Chin, P.; Southwick, A.M.; Sun, H.; Tallon, kr. M.; Wh. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M. A. Artitle: Sequence and analysis of chromosome of of the plant Arabidopsis. A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:11130712  A. Reference number: A66141; MUID:21016719; PMID:1130712  A. Reference number: A66141;	Db 398 PPPATAAANPS-PAPERSR. 423  Qy 264 APGTERSPAPLGQPRSYLAPPTRPAPTBPPPSPSPQRNSGRR 305  Qy 264 APGTERSPAPLGQPRSYLAPPTRPAPTBPPPSPSPQRNSGRR 305	
Oy 611 HE 613  OY 612 HE 613  DE 648 AFR 650  RESULT 10  G87008  COMBETCH MADOTHELICAL PROTEIN MAD798 [imported] - Mycobacterium leprae C;Becies: Mycobacterium R; Mycobacterium leprae C;Becies: Mycobacterium R; Mycob	446 490 502 542 557 592	

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C;Accession: E9636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chronosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Residues: 1-907 <STO>
A;Cross-references: UNIPROT:Q9C946; UNIPARC:UPI00000A9620; GB:AE005173; NID:g6751696;
C;Genetics:
hypothetical
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411
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                                                                                                                                   -KELSHYNDIRAH-----TSVNAVNLEV 501
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   Rv3888c
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27.0%; Pred. No. 1.3e-10;
 Mycobacterium tuberculosis (strain
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L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
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                                                                                                               ;Cross-references: UNIPROT:P96217; UNIPARC:UPI00000D0F42;
;Experimental source: strain H37Rv
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C;Accession: A70598

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Comnor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genomy A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-341 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:005456; UNIPARC:UPI00000D0F8A; GB:Z94121; GB:AL123456; A;Experimental source: strain H37Rv
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;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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334 PDAERAAQ 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 PRKIPPGTGWRKFVYSVSFHKINPGBSPRBRHYRNLQGRIRRHIRRQYVITVVSGKGGVG
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Pred. No. 6.3e-11;
5; Mismatches 126
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C.; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Ruther, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230 hypothetical protein Rv3860 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004 C; Accession: A70656

A; Accession: A70656

A; Molecule type: DNA A; Residues: 1-390 <COL> A; Status: preliminary; nucleic acid sequence not shown; translation not shown

GB: Z83864;

GB:AL123456;

NID:

genome

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Query Match Best Local Sin Matches 120; Similarity Conservative 10.8%; Score 383; DB 2 29.4%; Pred. No. 1e-10; Live 66; Mismatches 1 DB 2; 160; Length 390; Indels 62; Gaps 14

RESURY 14  RESIST  RESURY  RESIST  RESCRIPTION  RESCRIPTI	Qy  271 PAPLGQPRSYLAPPTRPAPTEPPSSSPORNSGRRAERRVHPDLAAQHAAQPDSITAAT 330
RESULT 15  PTSS18  PTSS18  hypothetical protein - Deinococcus radiodurans (strain R1)  c; Species : Deinococcus radiodurans  c; Species : Deinococcus radiodurans  c; Dec : Dec : 1999	Db 188 ASEIPPPPRHLPSPPASERP-STPPSDSEHPSPPPGHEKREQPPPPGSKR 238  Oy 226 ARRCHRYRTDTERNVGKVATGPSIQARLRAEBASGAQLAPGTEPSPAPLGQPRSYLAPPT 285  Db 239 PTPSPPSPSDSKRPVHPSPPSPP

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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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301 NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK 360	241 GKVATGESIQARLKABKASGAQLAPGTKESBAPLGQPKSYLAPETKEPETKEPESBSPQK 300	HOPRETAPAPMAKMP1GEPPAPSRPSASPAPPTERNV	121 IAGPEBAPEKPPTPEMPIAGPAPTPTESQLAPBRPPTPQTPTGAPQQPESPAPHVPSHGP 180 	61 FVSAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	1 MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLFKFNGQTPPFTSDDLSER 60	Query Match 100.0%; Score 3552; DB 2; Length 666; Best Local Similarity 100.0%; Pred. No. 4.5e-138; Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	NUCLEOTIDE SEQUENCE.  NUCLEOTIDE SEQUENCE.  STRAIN=AP2122/97;  MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;  MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;  MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;  MEDLINE=22709107; PubMed=12788972; Medina N., Mansoor H.,  Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,  Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,  Parkhill J., Barrell B.G., Cole S. T., Gordon S.V., Hewinson R.G.;  "The complete genome sequence of Mycobacterium bovis.";  Proc. Natl. Acad. Sci. U.S.A. 100:7977-7882 (2003).  EMBL; BX248347; CAD96092.1; -; Genomic DNA.  Complete proteome; Hypothetical protein.  SEQUENCE 666 AA; 70644 MW; -752E072FB8B10111 CRC64;	TIT 1  72 MYCBO RELIMINARY; PRT; 666 AA.  07TVG2; 01-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 00-OCT-2003 (TrEMBLrel. 25, Last annotation update) 00-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

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RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

RA Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III,

RA Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

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RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

RA Murphy L.D., Oliver S., Seeger K., Skelton S., Squares R.,

RA Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares R.,

RA Mulphy L.D., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

RA Suleton J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete 393:537-544(1998).

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RA Peterson J.E., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D.,

RA Aliberg S.L., Delther A., Utterback T.R., Weddman J.F., Khouri H.M.,

RY Nucleotide Company ison of Mycobacterium tuberculosis clinical and

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   "Whole-genome comparison of Mycob laboratory strains,";
J. Bacteriol. 184:5479-5490(2002)
EMBL; BX842594; CAA17968.1; -; Ge:
EMBL; AE000516; AAK48358.1; -; Ge:
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069740, MYCTU PRELIMINARY; PRT; 666 AA.
069740; Q7D4P3;
01-AUG-1998 (TYEMBLIPE). 07, Created)
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13-SEP-2005 (TYEMBLIPE). 31, Last annotation update)
CONSERVED HYPOTHETICAL PROLINE AND ALANINE RICH PRO
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OrderedLocusNames=MT3990,
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Bacteria; Actinobacteria; Actinobacteridae; Actinom
Corynebacterinae; Mycobacterium;
Mycobacterium tuberculosis complex.
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J.F., Khouri H.M.,
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Q9CDD8 MYCLE PRELIMINARY;
ID Q9CDD8;
AC Q9CDD8;
DT 01-UUN-2001 (TrEMBLrel. 17, C;
DT 01-UN-2001 (TrEMBLrel. 26, L;
DT 01-MAR-2004 (TrEMBLrel. 26, L;
DE Hypothetical protein ML0048.
GN OrderedLocusNames=ML0048;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; NCBI_TAXID=1769;
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TubercuList; Rv3876; -.
Complete proteome; Hypothetical
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                                   Mycobacteriaceae;
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                                  Actinobacteridae; Actino
teriaceae; Mycobacterium
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752E072FB8B10111
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4.5e-138;
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360 300 300 240 240 180 180 120 120 60

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RP NUCLEOTIDE SEQUENCE.

RC STRAIN=TN;

RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

RX Cole S.T., Rigimeier K., Parkhill J., James K.D., Thomson N.R.,

RX Mheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B.,

RX Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,

RX Mungall K.L., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RX Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RX Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RX Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RX Murphy L.D., Oliver K., Jagels K., Lacroix C., Maclean J., Moule S.,

RX Murphy L.D., Oliver K., Jagels K., Lacroix C., Maclean J., Moule S.,

RX Murphy L.D., Oliver K., Jagels K., Lacroix C., Maclean J., Moule S.,

RX Murphy L.D., Oliver K., Simon S., Simmonds M., Skelton J., Squares R.,

RX Murphy L.D., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RX Maplice Gene decay in the leprosy bacillus.";

RX Massive gene decay in the leprosy bacillus.";

RX Mature 409:1007-1011(2001).

RX Massive gene decay in the leprosy bacillus.";

RX Massive gene decay in the leprosy bacillus.";

RX Leproma, ML0048; -.

RX Complete proteome; Hypothetical protein.
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                          YKRKVLELAAALSDDFERAGR
                                                                                                    LASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPMDRHIAAGTEISLDLLDPI
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Pred. No. 4.4e-56;
6; Mismatches 168;
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2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27 2D 27
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OB2 MYCLE

OB3082 MYCLE 1

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MEDLINE=93188700; PubMed=8446027;

Eiglmeier K., Honore N., Woods S.A.,

"Use of an ordered cosmid library to

of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).
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Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Name=MLCB628.11c;
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GTEISLDLLDPIYKRKVLELAAALSDDFERAGR
                                                                                                        ALDWLRNNGYQDLASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAA
                                                                                                                                                                                           ALSDADWHFIADPASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASV
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Conservative 5
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(TrEMBLrel. 05, Last sequence up
(TrEMBLrel. 25, Last annotation
protein MLCB628.11c.
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Pred. No. 3.8e-49;
3; Mismatches 126
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OB6637;
O1-NOV-1998 (TrEMBLrel. 08)
O1-NOV-1998 (TrEMBLrel. 08)
O1-MAR-2004 (TrEMBLrel. 26)
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Nature 417:141-147(2002).
EMBL; AL939124; CAA20252.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 1083 AA; 112083 MW; AD42EDFE4C12126D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein SC05717.
OrderedLocusNames=SC05717; ORFNames=SC3C3
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Bacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                               PQAPQPAPAGWDAPPAPQPGYGFPQPGAQAPQPQPHSPAQPPGGYGF----
                                                                                                                                                                                                                                                                                                                                            PRPPTPQTPTGAPQQPESPAPHVPS----HGPHQPR-----RTAPAPP-----WAKMPIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPEPESEPVVLAAVAESESESAERVGDEPEDSVPTADVPVDAVPDDAAPPADSVPQDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PKPPTPPMPIAGPAPTPTES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPDEPFVSTGFTDADTDAETDVDTESDFESVSDQAPDAESGGGHGDVADPRLGGSAPDAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPEPEPEVRTPEPEPKAVAEPAPAADLASPAALPSFPAGGFQLQAPVPPPPAEEPGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGMEAPDDMAAQPFFDPSASFPPAPASANLPKP--NGQTPPPTSDDLSERFVSAP----
GPSPQQQPYPGVPQQQAPQAQGGQAPPAQPGQPAQPGQPMQPGQPGQSGQPGQAPSAPQ
                                                                                                                                                                                                                            ---PPPAPSRPSASPAEPP-
                                                                                                                                                                                                                                                                                                  PQDATPPAPEGMPPLPPSYPPVAPAAHQWPAQPQPPTQPQTAPAPPEQPGVAAQQPPFQ
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el. 08, Last sequence update)
el. 26, Last annotation updat
SCO5717.
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01-JUN-2003
01-MAR-2004
                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572948; DOT=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermittilis: deducing the ability of producing secondary
                                                                                                        metabolites.";
proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
EMBL; BA000030; BAC70255.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 810 AA; 86244 MW; F8D19CDA203FDC26 CR
                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative analysis microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nb5820;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames-SAV2544;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pred. No. 8.8e
72; Mismatches
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F8D19CDA203FDC26 CRC64;
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142 NOCFA
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25-OCT-2004
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                      InterPro;
PROSITE; F
                                                                          NUCLEOTIDE SEQUENCE.
STRAINHIFM 1015;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino
Shiba T., Hattori M.;
                                                                                                                                                                                       OrderedLocusNames=nfa3070;
                                                                                                                                           NCBI_TaxID=37329;
                                                                                                                                                         Corynebacterineae; Nocardiaceae;
                                                                                                                                                                    Bacteria; Actinobacteria;
                                                                                                                                                                               Nocardia farcinica.
Complete genomic sequence of Nocardia farcinica
Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

APPO06618, BAD55149.1; -j. Genomic DNA.

PEPPO; IPRO00194; ATPASE a/bcentre.

PERO00194; ATPASE ALPHA BETA; UNKNOWN 1.

PERO00152; ATPASE ALPHA BETA; UNKNOWN 1.

PEROCE 525 AA; 55760 MW; P404FE46B85AA09D CRC64
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RESULT 8
QSZLL5_NOCFA
ID QSZLL5_
AC QSZLL5_
DT 25-OCT-2004 (7)
DT 25-OCT-2004 (7)
DT 25-OCT-2004 (7)
DT 25-OCT-2004 (7)
DB Hypochetical particular
GN OrderedLocusNe
OS Nocardia farci
OC Bacteria pacteria
OC Corynabacteria
OX NCBI_TaxID=373
RN [1]
RP NUCLEOTIDE SEC
RC STRAIN=IFM 101
RX PubMed=1546671
RA Shiba T., Hatt
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Best Local Similarity
Matches 194; Conserv
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25-OCT-2004 (TREMBLIRE)
25-OCT-2004 (TREMBLIRE)
Hypothetical protein.
   NUCLEOTIDE SEQUENCE.
STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino Shiba T., Hattori M.;
                                                                                                                                                                                                                                                                                                OrderedLocusNames=nfa8310;
Nocardia farcinica.
                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria;
                                                                                                                                                                                           NCBI_TaxID=37329;
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EMBL; AY223810; AAP73957.1; -; Genomic_DNA.
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Pred. No. 1.
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RESULT 10
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Best Local Similarity
Matches 191; Conser
                                                                                                                                          Hypothetical protein.
OrderedLocusNames=MAP4026;
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Pred. No. 1e-18
77; Mismatches
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Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinaes; Mycobacteriacaae; Mycobacterium;
Mycobacterium avium complex (MAC).

Zhang to the

Q., Amonsin A., Alt D., Kap EMBL/GenBank/DDBJ databases

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RESULT
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11 MYCPA
073VH1 MYCPA PRELIMINARY;
                                                                                                                                                                                                                                                     Li L., Bannantine J., Zhang
Submitted (SEP-2003) to the
EMBL; AE017238; AAS05591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinon Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                             SEQUENCE 388 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1770;
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                                                               Local Similarity
les 153; Conser
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ete proteome; Hypothetical protein.
NCE 434 AA; 46331 MW; 73A47808AD6D13B1 CRC64;
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      GHRYRTDTERNVGKVATGPS I QARLRABEASGAQLAPGTEPS PAPLGQPRSYLAPPTRPA
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                                                                                                                                                                                                                                                     Q., Amonsin A., Alt D., Kapu
EMBL/GenBank/DDBJ databases
-; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
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                                                               Score 532.5; DB 2;
Pred. No. 1.5e-14;
4; Mismatches 162;
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Pred. No. 6.3e-16;
B; Mismatches 185
                                                                                                                                                                                             60868ADE9317FD09
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                                                                  Indels
                                                                                                                                                                                                                                                                                                                       Kapur
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RA HICKEY B
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Best Local S
Matches 155
                                                                                                                                                                                                                                                                                      Hypothetical SEQUENCE 4
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J. Bacteriol. 184:547
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QBVKJ9_MYCTU PRELIMINARY; PRT; 405 AA.
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QBVKJ9;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mypothetical protein.
QrderedLocusNames=MT0552;
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Mycobacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                    J. Bacteriol. 184:5479-5490(2002).
EMBL; AB000516; AAK44775.1; -; Genomic_DNA.
TIGR; MT0552; -.
                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.

STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed-12218036;

MEDLINE-22206494; PubMed-12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,

Pleterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey B.K., Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D.,

Salzberg S.L., Delcher A., Utterback T.R., Weldman J.F., Khouri H.M.,

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome comparison of Mycobacterium tuberculosis clinical
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                                            PQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPS----RPSASPAEP
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                                                                                                 14.9%; Score 530; DB 2;
29.9%; Pred. No. 1.9e-14;
tive 62; Mismatches 167
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BEBL; BX842573; CAB08981.1; -; Genomic DNA.
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01-JUL-1997 (TrEMBLrel. 04,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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TubercuList; Rv0530; -.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein MD0543.
OrderedLocusNames=MD0543;
Mycobacterium bovis.
                                                                                                                                                                                      MEDIJINE-2279107; PubMed=12788972; DOI=10.1073/pnas.1130426100; MEDIJINE-22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoox H., Pryox M., Duthoy S., Grondin S., Lacton, Monsempe C., Simon S. Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.F. Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:787-7882(2003).
EMBL; BX248335; CAD93405.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
Complete proteome; Hypothetical protein.
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                                                                                         Score 530; DB 2;
Pred. No. 1.9e-14;
62; Mismatches 167
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74 PPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMPIAGPEPAPPKPPT 133	17 APDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPFTSDDLSERFVSAPPPPPPPPP 73	Query Match 13.9%; Score 495; DB 2; Length 3889; Best Local Similarity 33.3%; Pred. No. 4.4e-12; Matches 125; Conservative 35; Mismatches 143; Indels 72; Gaps 15;	IPR006315; IPR003882; R01222; ATRC R01218; PSTL TIGR01414; 3889 AA;	Fight Cell 17:597-515(2005).  EMBL; AY450929; AAS07042.1; -; Genomic DNA.  GO; GO:0005199; F:structural constituent of cell wall; IEA.  InterPro; IPR002951; Atrophin.	fenschmidt S., Umen J.G., Goodenough U.W.; Sexual Agglutinins from Ch	ROTIDE SEQUENCE. IN=CC-621; ed=15659633; DOI=10.1105/tpc.104.028035;	Chlamydomonas reinhardtii. Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas. NCBI_TaxID=3055; [1]	05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Minus agglutinin. Name=SAD1;		629 HIAAGTEISLDLLDPIYKRKVLELAAALSDDFERAGRR 666  -	569 QASVALDMLRNNGYQDLASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDR 628 	509 SAQRALSDADWHFIADPASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQ 568 ::	450 LALDADPGAGNIADRYGRQSGATIADVLAEKE-LSHYNDIRAHTSVNAVNLEVLPAPEYS 508	390 RINIGLSPDEKYELDLHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRI 449 	332 GGRRKKAAAPDLDATQKSLRPAAKGPKVKKYKPQKPKATKPPKVVSQRGWRHWVHALT 389	275 GOPRSYLAPPTRPAPTEPPSPSPORNSGRRAERRVHEDLAAQHAAAQPDSITAATT 331	

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## RESULT 1 US-09-050-739-70 ; Sequence 70, Application US/09050739 ; Patent No. 6641814 ; GENERAL INFORMATION: APPLICANT: NIELSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Peter Birk APPLICANT: NIELSEN, Rikke APPLICANT: ROSENKRANDS, Ida APPLICANT: ROSENKRANDS, Ida APPLICANT: ROSENKRANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: NUENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS TITLE OF INVENTION: DRIVENTED FROM M. TUBERCULOSIS FILE REFERENCE: 670001-2002.1 CURRENT APPLICATION NUMBER: US/09/050,739 CURRENT FILING DATE: 1998-03-30 CEARLIER APPLICATION NUMBER: 1277/97 EARLIER APPLICATION NUMBER: 60/044,624 EARLIER APPLICATION NUMBER: 60/044,624 EARLIER APPLICATION NUMBER: 60/044,624 EARLIER APPLICATION NUMBER: 60/044,624 EARLIER FILING DATE: 1998-01-05 INMBER OF SEQ ID NOS: 173 SOFTWARE PATENTING DATE: 1998-01-05 INMBER OF SEQ ID NOS: 173 SOFTWARE PATENTING DATE: 1998-01-05 ILENGTH: 666 TYPE: BRT ORGANISM: Mycobacterium tuberculosis US-09-050-739-70

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MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER

Query Match Best Local Similarity

100.0%; Score 3552; DB 2; 100.0%; Pred. No. 2.8e-241;

Length Indels

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GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: PLORIOR, Thomas
APPLICANT: ROSENKRANDS, Ida
APPLICANT: RELDINGH, Karin
APPLICANT: RELDINGH, Karin
APPLICANT: FLORIO, Waller
TITLE OF INVENTION: NUCLER
CURRENT FLORION: NUCLER
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT FLING DATE: 1998-03-30
CURRENT FLING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-02
CARLIER APPLICATION NUMBER: U3/09/05
EARLIER FILING DATE: 1997-11-10
EARLIER APPLICATION NUMBER: 00/044,624
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1998-01-05
NUMBER OP SEQ ID NOS: 173
SOPTWARE: PatentIn Ver. 2.0
LENGTH: 308
LENGTH: 308
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US-09-050-739-94
; Sequence 94, Application US/09050739
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TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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US-09-461-774-10
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                 RSYLAPPTRPAPTEPPPSPSPQRNSGR 304
LPYSSPPAPPACPVPGAPLAPLPISGR
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Sequence 10, Application US/09461774

Patent No. 6887481

GENERAL INFORMATION:

APPLICANT: CHUNG, Maxey Ching Ming

APPLICANT: CHUNG, Maxey Ching Ming

APPLICANT: LIN, Renee Lay Hong

TITLE OF INVENTION: Bacterial-derived molecules and therapeutic and

TITLE OF INVENTION: diagnostic uses therefor

FILE REFERENCS: 1781-0180P

CURRENT APPLICATION NUMBER: US/09/461,774

CURRENT FILING DATE: 1999-12-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 386

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 11.6%; Score 410.5; DB 2; Local Similarity 33.3%; Pred. No. 4.2e-21; hes 109; Conservative 20; Mismatches 119;
                                                                                                                                                                                                                                          111 PPKPPTPPMPIA-GPBPAPPKPPTPPM-----PIAGPAPTPTESQLAPPRPPTPQTPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 MEAPD-----DMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSA 64
                                                                                                                                                                                                                                                                                                                                                                                                   APQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHS
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                                                 RRARRGHRYRTDTERNVGKVATGPSIQA----RLRAEEAS--GAQLAPGTEPSPAPLGQP
                                                                                                PPAPPMPPAPNSPAAPP----SPPSPPVPVFPTPPGPPAPPEPNSSPPAPPAAP--
                                                                                                                                                                                                   PPAPPAPPLENSPPPPPPPPPPPPLTLNPPVPPAPPAANTSNSPLRPPAPPAPPLKPG
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RESULT 5
US-07-609-716-65
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Best Local Similarity
Matches 101; Conserv
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APPLICANT: CAPPELLO,
APPLICANT: FERRARI, I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application US/08642255 Patent No. 5773249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 910 277299 FHT UR
TELEX: 910 277299 FHT UR
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
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High Molecular Weight Collagen-Like
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Pred. No. 6.4e-18;
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RESULT 6
US-08-475-411A-65
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GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                      Sequence 65, Application US/08475411A Patent No. 6140072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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GENERAL INFORMATION:
APPLICANT: Perrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
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ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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                                                                                                                                                                                                                                 258 PGP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                    138 IAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTA----PAPPWA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 10.2%; al Similarity 33.8%; 101; Conservative
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                                                                                                                                                                                                                                                                     TGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQRNSG 303
                                                                                                                                                                                                                                                                                                                AGPVGSPGAPGPPGPPGPPGPPGPPGPPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSASFPPAPA----SANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPM-PIA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGPPGPPGPAGPVGSPGAPGPPGPPGPPGPP-----GAPGPPGPPGPPGPPGPAGPV- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSPGAPGPPG--PPGPPGPPGAPGPPGPPGPPGPPGP-AGPVGSPGAPGPPGPPGPPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bertram
                                                                                                                                                                                                                                 -AGPVGSPGAPGPPGPPGPP----GPPGAPGPPGPPGPPGPPGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 364; DB 1; Length 408; Pred. No. 8.2e-18; B; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-55186-3/BIR
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Suite 3400
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RESULT 7
US-08-478-029A-65
; Sequence 65, Application US/08478029A
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STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING FALENTIN Release #1.0, Ve-
SOPTWARE: PatentIn Release #1.0, Ve-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
PILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: TRECENTIN, RICHARD F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-398-3249
INPORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                            258
                                                                                                                                                                        245 TGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQRNSG 303
                                                                                                                                                                                                                           194 KMPIGEP-----PPAPSRPSASPAE--PPTRPAPQHSRRARRGHRYRTDTERNVGKVA 244
                                                                                                                                                                                                                                                                                                                         165 PGAPGP---PGPPGPPGPPGPAGPVGSPGAPGPPGPPGPPGAPGPPGPPGPPGPPGP 221
                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                       138 IAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTA----PAPPWA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 AGEPPSPERAASKPPTPPMPIAGP-EPAPPKPPTPPMPIAGP----EPAPPKPPTPPMP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 PSASFPPAPA----SANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPPPPM-PIA 83
                                                                                                                            PGP-
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                                                                                                                                                                                                                                                                                                                                                                                                                            -GSPGAPGPPG--PPGPPGPPGAPGPPGPPGPPGPPGP-AGPVGSPGAPGPPGPPGPPGP 164
                                                                                                                               AGPVGSPGAPGPPGPPGPP----GPPGAPGPPGPPGPPGPPGPAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 364; DB 2;
Pred. No. 8.2e-18;
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TITLE OF INVENT  INTER OF INVENT  NUMBER OF SEQUI  CORRESPONDENCE  ADDRESSEE:  ADDRESSEE:  ADDRESSEE:  ADTREST FOUL  CORTON FOUL  CORTON FOUL  F	
TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF COURTES STREET CITY: STATE: COUNTE: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP: ZIP	
NVENTION: Synthetic Protein Polymer SEQUENCES: 119 ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE TORM: YEB: Flehr, Hohbach, Test, Albritton Four Embarcadero Center, Suite 3400 CA US US US US III ENDEC Compatible SYSTEM: PC-DOS/MS-DOS PATENTION DATA: ION NUMBER: US/08/478,029A ATTS: 07-JUN-1995 ICATION DATA: ION NUMBER: US 07/609,716 ATE: 06-NOV-1996 ICATION DATA: ION NUMBER: US 07/269,429 ATE: 09-NOV-1986 ICATION DATA: ION NUMBER: US 07/269,429 ATE: 09-NOV-1986 ICATION DATA: ION NUMBER: US 06/927,258 ATE: 04-NOV-1986 ICATION DATA: ION NUMBER: US 06/927,258 ATE: 04-NOV-1986 ATE: 04-NOV-1986 ATE: 04-NOV-1986 ATE: 04-NOV-1986 ATE: 05-OCT-1987 ICATION NUMBER: US 06/927,258 ATE: 05-OCT-1987 ICATION NUMBER: US 06/927,258 ATE: 04-NOV-1986 ATE: 04-NOV-1986 ATE: 04-NOV-1986 ATE: 05-OCT-1987 ICATION NUMBER: US 06/927,258 ATE: 05-OCT-1987 ICATION NUMBER: US 06/927,258 ATE: 05-OCT-1989 ATE-398-3249 FOR SEQ ID NO: 65: HARACTESTICS: 408 amino acids mino acids mino acids mino acids mino acids mino acids MNSS: Bingle I 10.2%; Score 364, DB 2; MILETATION DATA: INFORMATION: ENTRY SECOND SERE SASPPAPASANLPKPNGGTPPPTSDDLSERE SASPPAPASANLPKPNGGTPPTSDDLSERE SASPPAPA	ORMATION: ORMATION: Cappello, Joseph INVENTION: Functional

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US-07-757-022B-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gesner
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
PILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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ZIP: 0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: 19910910
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 941 amino acida
TYPE: AMINO ACID
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                     369
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                                                                                                                                             81
                                                                                                                                                                                                                             28 DPSASFP--PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPP-----PPPPPPPTPM 80
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                                                                                                                                                                                  EPAPTTPKEPTPTTPKEPAPTTKEPAPTTP--KEPAPTAPKKPAPTTPKEPAPTTPKEPA 308
                                                                                                                                          PIAAGEP----PRPEPAASKPPTP--PMPIAGPEPAP--PKP 114
                     PAPTTPKKPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT 428
                                                        PTP-----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                      PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)876-5851
                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                          9.8%;
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                                                                                                                                                                                                                                                                      58; Mismatches 259;
                                                                                                                                                                                                                                                                                          Score 347; DB 2; Length 941; Pred. No. 3.4e-16;
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                                                                                                                                                                                                                                                                      Indels 112;
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                      368
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US-07-757-022B-84
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Patent No. 64
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 07/643,502
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                 PILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryc
REGISTRATION NUMBER: 31,82:
REFERENCE/DOCKET NUMBER: G:
TELECOMMUNICATION INFORMATION
                                                                            APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                      APPLICATION NUMBER:
PILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 EPTSTTSDKPÅPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA- 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4, Application US/07757022B 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SORGWRHWVHALTRINIGLSPDEKYBLDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT 431
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87 CambridgePark Drive
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                                                                                                                                                              UMBER: US 07/457,196
29-DEC-1989
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RESULT 10
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US-07-757-022B-84
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INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                         Sequence 74, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 146;
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                   TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140
                                                     CITY: Cambridge
                                                                      STREET:
                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------EPGVPTT
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Pred. No. 3.8e-16;
                                                                                            Inc
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Best Local Similarity
Matches 146; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino aci
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 29-DEC-
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 199109 CLASSIFICATION: 530
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                                                                                                               665 --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
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   TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR
                                                                        SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                                                                                                               AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV
                                                                                                                                                                                        EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
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                                        1038 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 347; DB 2; I
illarity 25.4%; Pred. No. 3.9e-16;
Conservative 58; Mismatches 259;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-757-022B-58
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US-07-757-022B-58
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PARIOR SAPILICATION: 530

PRIOR DATE: 1910910

CLASSIFICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION: 530
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                                                                                                                                                       Matches
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Best Local Similarity
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APPLICANT: Gesner
                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino aci
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: CBETT, LUBIN
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-JUN-
PRIOR APPLICATION DATA:
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ADDRESSEE: Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                               DPSASEP---PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPP-----PPPPPPPPTPM 80
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                                     PIAAGEP----
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PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 476
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87 CambridgePark Drive
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                                                                                                                                                   9.8%; Score 347; DB 2; Length 1049;
25.4%; Pred. No. 3.9e-16;
tive 58; Mismatches 259; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 07/546,114
                                                                                                                                                                                                                                                                                                                                                 58:
                                   -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
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                                                                                                                                                     Indels 112;
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US-07-757-022B-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                             APPLICATION NUMBER: US/07/
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 29-UN-1990
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cambridge
STATE: Massachusetts
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 DATE:
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SYSTEM: PC-DOS/MS-DOS
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   08-AUG-1989
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Best Local S
Matches 146
                                                                                                                             Sequence 44, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
               TITLE OF INVENTION: ME NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                             APPLICANT: Geener, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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es 146; Conserv
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                      KTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
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Genetics Institute,
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                               Megakaryocyte Stimulating : 143
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US-07-757-022B-44
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: CBETT, LUARIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI :
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PRIFIT OF THE TOTAL OF A TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: li
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FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
US 07/643,502
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Massachusetts
                                                                                        AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
--PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
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NO: 44:
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25.4%; Pred. No. 4.9e-16;
vative 58; Mismatches 259; Indels 11
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RESULT 14
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; MOLECULE TYPE:
US-07-757-022B-42
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                                                                                    Query Match
Best Local :
                                                                                                                                                                                               TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acida
TYPE: AMINO ACID
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                                                               Matches
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GITELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                            al Similarity
146; Conserv
28 DPSASEP--PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPP-----PPPPPPPTPM 80
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7: U.S.A.
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ilarity 25.4%;
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08-AUG-1989
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                                                          ; Score 347; DB 2; Length 1311; ; Pred. No. 5.1e-16; 58; Mismatches 259; Indels 112; Gaps
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US-07-757-022B-142
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                                   COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PAttentin Release #1.0, Version #1.25
SOPTWARE: PAttentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/757,022B
PILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakary
                                                                                                                                                                                                                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                 STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
                         FILING DATE:
                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
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87 CambridgePark Drive
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                         29-JUN-1990
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143
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Search completed: April 14, 2006, 17:37:56 Job time: 63.5832 secs
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FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBetr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
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INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                          871
                                                                                                                                                                                                          490 AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                             811 KTPÄÄTKPEMTTTAKOKTTEROLRTTPETTTAÄPKMTKETATTTEKTTESKITATTTQVT
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                                                                                                                                                                                                                                                                                                                                                 TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                    SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------EPGVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT 763
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## ALIGNMENTS

US-09-791-171-70

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Sequence 70, Application US/09791171

| Sequence 70, Application US/09791171
| GENERAL INFORMATION:
| APPLICANT: ANDERSEN, Peter |
| APPLICANT: ANDERSEN, FRIKE |
| APPLICANT: RADERSEN, PETER |
| APPLICANT: RADERSEN, PETER |
| APPLICANT: RASMUSSEN, PETER |
| APPLICANT: RASMUSSEN, PETER |
| APPLICANT: RESUNTANDS, Ida |
| APPLICANT: RESUNTANDS, Ida |
| APPLICANT: WELDINGH, KARIN |
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; SEQ ID NO 70
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; ORGANISM: Mycobacterium tuberculosis
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Sequence 70, Application US/09804980
Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITILE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 70
LENGTH: 666
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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RESULT 3
US-10-080-170-640
US-10-080-170-640
Sequence 640, Application US/10080170
Publication No. US20030129601A1

REMERAL INFORMATION:
GENERAL INFORMATION: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PATEMENT OF MYCOBACTERIOSES
TYPE: PRI
ORGANISM: MYCOBACTERIUM tuberculosis
ORGANISM: MYCOBACTERIUM tuberculosis
                                                                                                                                                                                        Local Similarity
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GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Wang, Liangsu

APPLICANT: Malome, Cheryl

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APPLICANT: Malome, Kari

APPLICANT: Content Content

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APPLICANT: Trawick, John

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APPLICANT: Yamamoto, Robert

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APPLICANTON NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/20,335

PRIOR APPLICATION NUMBER: 60/230,335

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US-10-282-122A-64944

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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64944
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64944
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Pred. No. 2.5e-180;
; Mismatches 0;
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RESULT 5 US-10-20-246-70 ; Sequence 70, Application US/10620246 ; Publication No. US20040115211A1

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PRIOR PILLING DATE: 1998-03-30
PRIOR PILLING DATE: 1997-04-02
PRIOR PILLING DATE: 1997-04-02
PRIOR PILLING DATE: 1997-04-02
PRIOR PILLING DATE: 1997-11-10
PRIOR PILLING DATE: 1997-11-10
PRIOR PILLING DATE: 1997-04-18
PRIOR PILLING DATE: 1997-04-18
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/791,171
PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR PILLING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR PILLING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 1281/98
PRIOR PILLING DATE: 1999-01-08
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Matches 666; Conserv
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APPLICANT:
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NUMBER OF SEQ ID NOS: 173
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FLORIO, Walter
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RASMUSSEN, Peter Birk
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100.0%; Pred. No. 2.5e-180;
ative 0; Mismatches 0;
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Sequence 640, Application US/10080170

Publication No. US20040121322A9

GENERAL INFORMATION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOI

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROI

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

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APPLICANT: COLE, STEWART
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 10/080,170
PRIOR APPLICATION NUMBER: 10/080,170
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR PILING DATE: 2001-02-22
SOFTWARE: PRIOR ALENTIN VERS: 655
SOFTWARE: PASTENTIN VERS: 655
SOFTWARE: 666
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Publication No. US20040197896A1
GENERAL INFORMATION:
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Pred. No. 2.5e-180;
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APPLICANT: Brosch, Roland
APPLICANT: Majlessi, Laleh
APPLICANT: Demangel, Caroline
APPLICANT: Demangel, Caroline
APPLICANT: Leclerc, Claude
ITILE OF INVENTION: Identification of virulence associated regions RD1 and
ITILE OF INVENTION: mbc leading to improve vaccine of M. bovis BCG and M.
ITILE OF INVENTION: microti
FILE REFERENCE: D20217
CURRENT APPLICATION NUMBER: US/10/510,021
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: BT 02/290864
PRIOR FILING DATE: 2003-04-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 66
LENGTH: 666
TYPE: PRIOR
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US-10-510-021-66
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APPLICANT: Pym, Al
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                                                                                                                                                                                                                                                                                  Local Similarity
121 IAGPEPAPEKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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100.0%; Pred. No. 2.5e-180;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR PILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
NUMBER: OF SEQ ID NOS: 173
SOPTWARE: PALENTIN VEY: 2.0
SEQ ID NO 94
LENGTH: 308
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; LENGTH: 308
TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-94
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APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEEC ACIDS FRAGMENTS AND FOLYPEPTIDE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
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Sequence 94, Application US/09804980

Publication No. US20030147897A1

GENERAL INFORMATION:

APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter

TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 67001-2002.4

CURRENT APPLICATION NUMBER: US/09/804,980

CURRENT FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 257

SOFTWARE: Patentin version 3.0

SEQ ID NO 94

LENGTH: 308

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-804-980-94
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Pred. No. 6.9e-76;
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APPLICANT: ROSENKANDS, IGA
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: UUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
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US-10-620-246-94
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Best Local Similarity
Matches 307; Conserv
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LENGTH: 308
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PRIOR APPLICATION NUMBER: 09/791,171
PRIOR FILING DATE: 2001-02-20
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PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
PRIOR PRIOR PRICING DATE: 1998-01-05
PRIOR PRIOR PRIOR SAFET 1998-01-05
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   GEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSD
                               GEPNVAVKOLVRHFEQQVQPGRVVVMPWDRHIAAGTBISLDLLDPIYKRKVLELAAALSD
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RASMUSSEN, Peter Birk
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CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 586
TYPE: PRT
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US-10-080-170-10
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APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
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Publication No.
585 LASRACVVINHIMPGEPNVAVKDLVRHFBQQVQPGRVVVMPWDRHIAAGTBISLDLLDPI
                                                           445 TVSKYYNVMLADCGVGLFDPVTRGVLSTASGVVIVTSTSVDAARQAAIALDWLRHNGYQD
                                                                                                                      525 PASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQD
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49.2%; Pred. No. 2.9e-74;
tive 66; Mismatches 168
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RESULT 13
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NUMBER OF SEQ ID NOS: 78614
SOPTWARE: PatentIn version 3.1
SEQ ID NO 63640
LENGTH: 586
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931
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Trawick, John
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Zyskind, Judith
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Malone, Cheryl
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Pred. No. 2.9e-74;
66; Mismatches 168;
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PRIOR PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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US-10-080-170-10
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                                                                                                                                                                              Best
                                                                                                                                                                Matches
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
                                                                                                                                                                                                                                                                TYPE: PRT
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                                 60 L----PROPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP
                                                            61 FVSAPPPPPPPPPPPPPPPPPPPAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP
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                                                                                                                                                              h 43.6%; Score 1550; DB 4;
Similarity 49.2%; Pred. No. 2.9e-74;
35; Conservative 66; Mismatches 168
                                                                                            MAADYDKIFRIDDGAYASPDQAAEQIFDDAPLYPPPIIFTCTTTPNGEVASP-MPDWSEQ
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                                                                                                ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
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                                                                                                         TRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD
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Search completed: April 14, 2006, 18:40:36 Job time : 238.816 secs

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Maximum
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Perfect score:
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1: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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1 MAADYDKLFRPHEG
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US-11-169-232-14
US-11-169-232-94
US-11-169-232-14
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US-11-036-256-5
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   Sequence 95, Appli Sequence 96, Appli Sequence 28799, A Sequence 28799, A Sequence 2501, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 104, Appli Sequence 44, Appli Sequence 44, Appli Sequence 44, Appli Sequence 47, Appli Sequence 48, Appli Sequence 50, Appli Sequence 50, Appli Sequence 50, Appli Sequence 50, Appli Sequence 51, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli
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	US-10-995-561-988	15	US-11-036-256-158	US-11-036-256-31	US-11-108-172-1068	US-10-330-773-661	US-11-059-982-1	US-11-096-568A-12552	US-11-096-568A-30285	-11	-11	US-11-188-298-18316	US-11-087-099-7887	US-10-330-773-663	US-11-096-568A-27755	US-11-096-568A-27756	-11-096	US-11-096-568A-29626	-11-096-568A-2895	-11-096-568A-
	988, App	159, App	•	31, Appl	1068, Ap	661, App	1, Appli	12552, A	30285, A	30286, A	30287, A	18316, A	7887, Ap	663, App	27755, A	27756, A	27757, A	29626, A	28958, A	28959, A

## ALIGNMENTS

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US-11-036-256-95
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SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 95, Application US/11036256 Publication No. US20060026719A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/602,562
PRIOR FILING DATE: 2004-08-18
PRIOR PPLICATION NUMBER: 60/582,027
PRIOR FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR FILING DATE: 2004-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANEMIO
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REPERENCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
CURRENT FILING DATE: 2005-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1000
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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214 PPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAP 273
                                                                                 154 RPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAE
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                                                                                                                                                                                                                                                 34 PPAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPPMPIAAGEPPSPEPA 93
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RESULT 3
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US-11-036-256-5
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NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/11036256 Publication No. US20060026719A1 GENERAL INFORMATION:
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Best Local S
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APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REPERENCE: 27211/04130
CURRENT PAPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR PILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR PILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: 60/536,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KBY: MOD_RES
LOCATION: (2)...(1001)
OTHER INFORMATION: This region may encompass 2 to 1,000 residues of
OTHER INFORMATION: Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid motif
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                      94 ASKPPTPPMPIAGPEPAPPKPPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPP 153
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Similarity 35.5%;
                                                                                                       LGQPRSYLAPPTRPAPTEPPPSPSP 298
                                                                                                                                                                           PPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRABBASGAQLAPGTEPSPAP 273
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Sequence 28799, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA F
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILLING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 28799
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APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REFERENCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR PILING DATE: 2004-08-18
PRIOR PILING DATE: 2004-08-20
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-14
PRIOR PILING DATE: 2004-01-14
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                                                                                                                                                                                                                                                                                                                        RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.5%; Score 444; DB 7; Length 1001; Best Local Similarity 35.5%; Pred. No. 4.4e-18; Matches 94; Conservative 0; Mismatches 115; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: This sequence may encompass 2-1,000 OTHER INFORMATION: between positions 1 and 1,000
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LOCATION: (1001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: amino acid motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1001
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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LENGTH: 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                             274 LGQPRSYLAPPTRPAPTEPPPSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 PPPPPPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 PPTRPAPOHSRRARRGHRYRTDTERNVGKVATGPSIOARLRAEEASGAOLAPGTEPSPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 RPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPTGEPPPAPSRPSASPAE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 ASKPPTPPMPIAGPEPAPPKPPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 PPAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPPPMPIAAGEPPSPEPA 93
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                                                                                                                                                                      Corresponding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
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Indels Length

263;

53 97

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; TYPE; PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(717)
; OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-28799
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US-11-096-568A-29818
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Sequence 29818, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 165; Conserv
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                                                                                                                                                                                                                                                                                             ASSGKLTEKSDVF-----SPGVVLLE-----
                                                                                                                                                                                                                                                                                                                                                           KFEAKVADFGLAKIA-------SDTNTHVSTRVMGTFGYLAPEY
                                                                                                                                                                                                                                                                                                                                                                                         ---ALDADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLPAPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLKEGSSQGEREFQAEVGIISRVHHRHLVALVGYCIADAQRLLVYEFVPNNTLEFHLHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPKVVSQRGWR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLPPPSPGLALGIGIYQGTFNYEELSRATNGFSEANLLGQGGFGYVFKGMLRNGKEVAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAITPSPPLTPSPLPPSPTTPSPPPPSPSIPSPPLTPSPPPSSPLRPSSPPPPSPATPST 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT----PQTPTGAPQQPESPAPHVPSHG-PHQPRRTAPAPPWAKMPIGEPPPAPSRPSA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- PTPPMPIAGPEPAPPKPPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSAPPPGGTPSPPPQP----LPIPPPPQPLPVTPPPPPTALPPAL--PPPPPPTALPP
                                                                                                                                                              MDQVARVLEGNISPSDL----NQGITPG
                                                                                                                                                                                                                                                             QQASVALDWLR-----
                                                                                                                                                                                                                                                                                                                           SSAQRALSDADWHFIADPASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGA
                                                                                                                                                                                                                                                                                                                                                                                                                           GRPTMEWSSRLKI------AVGSAKGLSYLHENCNPKIIHRDIKASNILIDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SPQRNSGRRAER---RVHPDLAAQHAAAQPDSITAATTGGRRRKKAAPDLDAT---QK 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAEPPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASG-AQLAPGTE
                                                                                                                                                                                                                              ----LVDWARPLLNQVSELGNFEVVVDKKLNNBYDKBEMARMVACAAACVRSTAPRRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGSSPPAQSSKELSKGAMVGIAIGGGFVLLVALALIFFLCKKKRRRDNEAPPAPIDGVPY
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                                                                                                                                                                                            ----NVAVKDLVRHFEQQVQPG 619
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               and Corresponding Polypeptides
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CURRENT APPLICATION NUMBER: US/11/
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29818
LENGTH: 694
TYPE: PRT
 RESULT 6
US-11-036-256-89
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Matches
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OTHER INFORMATION: Ceres Seq...
5-11-096-568A-29818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 ALPPPPPPTTVP-PIPPSTPSPPPPLT-PSPLPPSPTTPSPPLT-PSPTTPSPPLTPSPP 110
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                                                                   ----NQGITPG
                                                                                                 VRHPEQQVQPG
                                                                                                                                SELGNPEVVVDKKLINNEYDKEEMARMVACAAACVRSTAPRRPRMDQVARVLEGNISPSDL
                                                                                                                                                                                                                                                                                                                                                                                                                      TEPP-----PSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSKGAMVGIAIGGGFVLLVALALIFFLCKKKRRRDNEAPPAPI-----VPPPKSPSSAP
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                                                                                                                                                                                              ----SFGVVLLE-----
                                                                                                                                                                                                                              PASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLR-----
                                                                                                                                                                                                                                                                                             VGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDADWHFIAD
                                                                                                                                                                                                                                                                                                                                                           GGAGKTTLTAALGSTLA-------QVRADRIL-----ALDADPGAGNLADR
                                                                                                                                                                                                                                                                                                                                                                                           GIISRVHHRHLVALVGYCIADAQRLLVYEFVPNNTLEFHLHGKGRPTMEWSSRLKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGGRRRKRAAPDLDATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRPPHFMSSGSSGDYDSNYSDQSVLPPPSPGLALG------LGIYQGTFNYBBLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATNGPSEANLLG-----QGGFGYVPKG----MLRNGKEVÄVKQLKEGSSQGEREFQAEV
                                                                                                                                                              -----NGYQD-----LASRACVVINHIMPGEP-----NVAVKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 2.4e-14;
8; Mismatches 242;
                                                                                                                                                                                                                                                                -SDTNTHVSTRVMGTFGYLAPEYASSGKLTEKSDVF----
                                                                                                                                                                                                  LITGRRPIDVNNVHADNS----LVDWARPLLNQV
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FILE REPERENCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR FILING DATE: 2004-05-22
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR PILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
SOPTWARE: PALENTIN Ver. 3.3
SEQ ID NO 89
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                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 2501
                                                                                                                                                                                                                                                                                                          Sequence 2501, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 112; Conserv
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                                                                                                                 CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANEBNG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
                                                                                                                                                                                         FILE REFERENCE: 2750-1592PUS2
                   LENGTH: 681
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: amino acid construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 PTPPM-----PIAGPEPAPPKPPTP--PMPIAGPAPTPTESQLAPPRP-----PTPQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 PTPPPGPHSPPPPLSPSPTPTPPLGPHSPPPTLSPSPTPTPPPGVPGPHSPPPPLSPSPT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 PHSPPPTLSPSPTPTPPPGPHSPPPPLSPSPTPTPPLGPHSPPPTLSPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQLAPGT-EPSPAPLGQPRSYL-APPTRPAPTEPPP-----SPSP
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No. US20060026719A1
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                                                                                                                                                                   US/11/096,568A
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                                                                                                                                                                                                                                        Polypeptides
                                                           Sequence 33, Application US/11036256

Publication No. US20060026719A1

GENERAL INFORMATION:

APPLICANT: KIELIZZEWSKI, MARCIA
APPLICANT: XU, JIANFENG

ITILE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN I

CURRENT FILING PEPTIDES/PROTEINS PRODUCED THEREBY

ILE REFERENCE: 27211/04130

CURRENT APPLICATION NUMBER: US/11/036,256

CURRENT APPLICATION NUMBER: 60/602,562

PRIOR APPLICATION NUMBER: 60/582,027

PRIOR APPLICATION NUMBER: 60/582,027

PRIOR APPLICATION NUMBER: 60/582,027

PRIOR APPLICATION NUMBER: 60/582,027

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PRIOR APPLICATION NUMBER: 60/582,027

PRIOR APPLICATION NUMBER: 60/582,027

PRIOR PILING DATE: 2004-06-22

PRIOR PILING DATE: 2004-01-14

NUMBER OF SEQ ID NOS: 173

SOFTMARE PATENTIN Ver. 3.3
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US-11-036-256-33
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; LCCATION: (1)..(681)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-2501
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                        SEQ ID NO 33
LENGTH: 346
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 ELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDAD 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 FVGYTMPPSAYSSPQGSDVVLFNSRSSAPPKMRSHSGSDYMYASSDS---GMVSNQRSRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 PPAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPPMPIAAGEPP----
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Pred. No. 1.9e-13;
0; Mismatches 207;
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RESULT 9
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Publication No. US20060025570A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 101; Conserv
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                                APPLICATION NUMBER: US/10/124,557

PILING DATE: 16-Apr-2002

APPLICATION NUMBER: US 07/643,502

PILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

PILING DATE: 29-UN-1990

APPLICATION NUMBER: US 07/457,196

PILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

PILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901

PILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATB: 28-JUN-2005
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megakaryocyte Stimulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTAPAPPWAKMPIGEPPPAPSR--PSASPAEPPTRPAPQHSRRARRGHRYRTDTERNVGK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMPIAGPAPTPTESQLAPPRP-----PTPQTPTG--APQQPESPAP-HVPSHGPHQPR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGEPP---SPEPAASKPP---TPPMPIA-GPEPAPPKPPTPPMPIAGPEPAPPKPPTP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
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  NAME: Cserr,
REGISTRATION
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Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hewick, Rodney M. Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description of Artificial Sequence: amino acid construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics Institute,
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33.9%; Pred. No. 9.40
117;
14 (ve 22; Mismatches 117;
  NUMBER: 31,822
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                                                                                                                                                                                            RESULT 10
US-11-169-232-84
; Sequence 84, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
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Jacobs, Kenneth
Hewick, Rodney M.
Geener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Sti
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, I
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                        APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION
TELEPHONE: (6
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                                                                                                                                                                                                                                                                                                                                  STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTP-----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 941 amino acids
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(617)876-1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 1.4e-12;
58; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 347; DB 7;
Pred. No. 1.4e-12;
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                                                                              Stimulating
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US-11-169-232-84
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CBETT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                               681
                                                                                           321 AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                             622
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    377
                                                                                                                                                                                                                                                                                        214 P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
                                                                                                                                                                                                                                                                                                                                                                                  160 TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 DPSASFP--PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPP----PPPPPPPTPM
                                                                                                                                                                                       EPS----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT 509
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SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT 431
                                                 --PKELAPTITKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
                                                                                                                                                                                                                                                                                                                                       TPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTP-----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                           EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
                                                                                                                                                                                                                                         PAPTTPKEPAPTTPK-----ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%;
ilarity 25.4%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 347; DB 7; 1
Pred. No. 1.6e-12;
8; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                            621
                                                                                                                                                                                                                                                                                        267
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, MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-11-169-232-74
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US-11-169-232-74
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                                                              Query Match 9.8%; Score 347; DB 7; Length 1038; Best Local Similarity 25.4%; Pred. No. 1.6e-12; Matches 146; Conservative 58; Mismatches 259; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/11169232 Publication No. US20060025570A1
                                                                                                                                                                                                                                                                                    TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

RILING DATE: 16-Apr-2002

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-UN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MENTUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 784 KTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     737 SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK----
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                      LENGTH: 1038 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turner, Katherine
Clark, Stephen C.
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Gesner, Thomas G.
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RESULT 12
US-11-169-232-58
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                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver
SOPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/169,232
PILING DATE: 28-Jun-2005
CLASSIPICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SAVERLESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
ADDRESSEE: GrambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377
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  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT-- 267
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTB 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQRGWRHWVHALTRINLGLSPDEKYBLDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPBKLAPTTPBKPAPTTPBBLAPTTPBBPTPTTPBBPAPTTPKAAAPNTPKBPAPTTPKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTP----PMPIAGPEPAP--PKPPTP----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIAAGEP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPLGOPRSYLAPPTRPAPTEP-PPSPSPORNSGRRAERRVHPDLAAQHAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inc.
                                                                                                                                                                                                                                  Version #1.25
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                                                                                                                  RESULT 13
US-11-169-232-104
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                                             Sequence 104, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS: LENGTH: 1049 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBett, LUADID
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
APPLICANT: Turner, Katheri
Clark, Stephen
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TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                               764
                                                                                                                                                                                                                                                                                                                                                                                                                                            377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                            STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE
                                                                                                                                                                                                                                                     AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                  TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AOPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 476
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                          Katherine
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Pred. No. 1.6e-12;
B; Mismatches 259
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US-11-169-232-104
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                       895
  268
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                                                                                                                                                                                                                                                                                                                                                       PIAAGEP----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
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FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
                                             PAPTTPKEPAPTTPK-----STAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
                                                                                    P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
                                                                                                                                                                           TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE
                                                                                                                                                                                                                       PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT
                                                                                                                                                                                                                                                                PTP----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1140 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Hewick, Rodney
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617)876-5851
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; Pred. No. 1.7e-12;
58; Mismatches 259;
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US-11-169-232-44
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Publication No. US2006
GENERAL INFORMATION:
                                                                                                                                    INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetic
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Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
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                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SORGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                TOPOLOGY: linear
                                                                                                                                                       TELEFAX:
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                                                                                         LENGTH: 1270 amino
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(617)876-5851
      SEQ ID NO:
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US-11-169-232-42
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 42, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                         Hewick, Rodney M.

Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetice Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Turner, Katherine
Clark, Stephen C.
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                                                                                                                         CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTP----PMPIAGPEPAP--PKPTP----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
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APPLICATION NUMBER: US/11/169,232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQRGWRHWVHALTRINLGLSPDEKYBLDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
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                                                                                                                                                                                                                                                                                                                   Jacobs, Kenneth
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25.4<del>1</del>;
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Pred. No. 2e-12;
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                                 Version
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Matches
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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             STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTB
                                                  AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                    AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                  P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
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                                                                                       KTPÄÄTKPEMTTTAKÖKTTERÖLRTTPETTTAÄPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                         TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKBLSHYNDIR 489
                                                                                                                                                                                             SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                                                                                                                                                                                                                                                                                                         EPS-----PAPLGOPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
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                                                                                                                                                             SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------EPGVPTT
                                                                                                                                                                                                                                    --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-Jun-2005
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25.4%; Pred. No. 2e-12;
Live 58; Mismatches 2
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Search completed: April 14, 2006, 18:42:14 Job time : 31.5386 secs

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Perfect score:
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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

africanum

or M

bovis

New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis.

against used

for

N-PSDB;

WPI; 1998-542705/46. N-PSDB; AAV63937.

Oettinger T,

Andersen P,

Nielsen Florio

Σ, N

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

(STAT-)

STATENS SERUM INST.

Claim 1; Page 196; 163pp; English.

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# ALIGNMENTS

### RESULT 1 AAW72927 02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 01-APR-1998; 08-OCT-1998 Mycobacterium Mycobacterium tuberculosis; antigen; vaccine; infection. Mycobacterium tuberculosis antigen RD1-ORF3 AAW72927; AAW72927 standard; protein; WO9844119-A1 21-JAN-1999 (first entry) tuberculosis. 97DK-00000376. 97US-0044624P. 97DK-00001277. 98US-0070488P 98WO-DK000132 86 8 immunological; immunogen;

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                  The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CPP7A or CPP3OA or a T-cell epitope of for the induction of a strong immune.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunogenic fragment of Mycobacterium tuberculosis
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                                                  The present sequence is that of the Mycobacterium tuberculosis MTBN2 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB1982-49), encoded by 8 open reading frames (see AAB9035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium boyis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for disgnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and disgnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gennaro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide encoded by open reading frames present in Mycobacterium culosis genome and not by the BCG strain of M. bovis, useful as
                                                                                                                                                                                                                                                                                                                                                                                                    11; Fig 1; 35pp;
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Pred. No. 3.3e-46;
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                                                                                                                    The invention relates to a novel diagnostic reagent comprising a peptide epitope from a protein encoded by the RD1 or RD2 regions of the Mycobacterium tuberculosis, M. bovis or M. africanum genome. The diagnostic reagents comprised within the kit are selected so that they are able to differentiate between M. bovis, M. tuberculosis or M. africanum-infected mammals and mammals vaccinated against M. bovis, M. tuberculosis or M. africanum. The polypeptide or its variant or fragment is useful as a medicament provided that the polypeptide is not a MPT-64 polypeptide or a polypeptide encoded by the Rv1984c region of the M. bovis, M. tuberculosis or M. africanum genomes. The nucleic acid which encodes the polypeptide or the diagnostic reagents can be used as a vaccine, especially against Mycobacterium infections. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; antitubercular; tuberculostatic; vaccine;
diagnostic reagent; epitope; RD1 region; RD2 region;
Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium africanum.
                                                                                                                                                                                                                                                                                                                                                                    New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1985, Rv3878, Rv1983, Rv3873 or Rv3879 derived from and RD2 regions of Mycobacterium, useful as vaccines against Mycobacterium infections.
                                                                                                                                                                                                                                                                                                                                    Claim 19; SEQ ID NO 2; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-903652/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cockle PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2002;
27-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG15730
                                                                                                          corresponds to a protein used to derive the peptide epitopes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG15730 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UKEN-) UK SEC FOR ENVIRONMENT FOOD & RURAL AFF
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Local Similarity 100.0%;
hes 98; Conservative (
                Local Similarity
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                                                                                         the invention.
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2002GB-00009724.
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             100.0%;
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             Score 479; DB 7;
Pred. No. 3.4e-46;
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Pred. No. 3.4e-46;
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                              tuberculosis and in preparing a vaccine against tuberculosis caused by convirulent mycobacteria. The vaccine or immunogenic/pharmaceutical composition can be used prophylactically in a subject not infected with a convirulent mycobacterium, or therapeutically in a subject already infected with a virulent mycobacterium. The protein is useful for preventing, converting and detecting infections caused by species of tuberculosis complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may be used for effecting in vivo expression of the antigen, and in configuration assays for detecting the presence of pathogenic organisms in a sample. The vaccine is an improvement of the living BCG vaccine presently cavailable, where one or more copies of the DNA sequence encoding one or more polypeptide has been incorporated into the genome of the microorganism to allow the microorganism to express and secrete the collapseptide. Incorporation of more than one copy of a nucleotide sequence enhances the immune response. The present sequence represents an M.
                                                                                                                                                                                                                                                                                                                                               The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv0455c, Rv0569, Rv1195, Rv1386, Rv3477, Rv3878, Rv3879c or Mr3106.1 (also disclosed are ORF13A and Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% sequence identity to the polypeptide and is immunogenic. The protein is useful in preparing a pharmaceutical composition for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infections caused by species of tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 73-74; 111pp; English.
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21-FEB-2001;
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2001DK-00000283
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Query Match Best Local Similarity

21.4%;

Score 102.5; DB Pred. No. 0.0015;

DB 5;

Length

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RESULT 6
AEB26458
cc pharmaceutical composition comprising a fusion polypeptide having contrigens from Bacillus Calmette Guerrin (BCG) administered to a person congrising a fusion polypeptide having conjugation with BCG or to a person who has previously been vaccinated with CC BCG. Also described are: (1) an immunogenic composition, vaccine or CC pharmaceutical composition comprising a fusion polypeptide which CC comprises two or more immunogenic polypeptide, or its analogue, selected from Ag85A, Ag85B TB10.4, ORP2C, Rv0285, Rv0287 and Rv1036G, or CC comprises amino acid sequences encoding the fusion polypeptides selected CC from Ag85A, TB10.4, Ag85B-TB10.4-Ag85A, Ag85B-TB10.4-Ag85A, Ag85B-TB10.4-Ag85A, Ag85B-TB10.4-Ag85A, Ag85B-TB10.4-Ag85A, TB10.4-Rv1036, Ag85B-TB10.4-Ag85A, TB10.4-Rv1036-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag85A, TB10.4-Ag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an immunogenic composition, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenicity; vaccine; pharmaceutical; fusion protein; Rv0285;
mycobacterium tuberculosis infection; infection; immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB26458 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g a fusion polypeptide with antigens administered together with BCG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical compositions from Bacillus Calmette Guerrin
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07-JUL-2005

WO2005061534-A2 Synthetic.

Mycobacterium tuberculosis. tuberculostatic; mutein.

22-DEC-2004;

2004WO-DK000907

23-DEC-2003; 2003DK-00001942

Jes D,

Andersen P,

2005-479440/48.

(STAT-)

STATENS

SERUM INST.

M. tuberculosis

fusion polypeptide,

TB10.4-Rv0285-Ag85A

fusion protein; lon; infection; i

Rv0285; TB10.4;

immunogenicity; vaccine; pharmaceutical; fusi
Ag85A; mycobacterium tuberculosis infection;

pharmaceutical composition comprising a fusion polypeptide having antigens from Bacillus Calmette Guerrin (BCG) administered to a person together with BCG or to a person who has previously been vaccinated wit BCG. Also described are: (1) an immunogenic composition, vaccine or pharmaceutical composition comprising a fusion polypeptide which comprises two or more immunogenic polypeptide, or its analogue, selecte from Ag85A, Ag85B, TB10.4, ORF2C, RV0285, RV0287 and RV1036C, or comprises amino acid sequences encoding the fusion polypeptides selecte from Ag85B-TB10.4, Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-RV1036, Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-RV1036-Ag85A, TB10.4-RV1036-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-Ag85B-TB10.4-RV1036-Ag85B-TB10.4-Ag8

selected selected

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with

New immunogenic compositions, vaccines or pharmaceutical compositions having a fusion polypeptide with antigens from Bacillus Calmette Guerrin (BCG) administered together with BCG.

The invention relates to an immunogenic composition, vaccine

85pp; English.

Disclosure; SEQ ID NO 16;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for the preparation of an immunogenic composition, vaccine or pharmaceutical composition for a prophylactic or therapeutical vaccination against an infection caused by a virulent mycobacterium, where the immunogenic composition is to be administered to a person has previously been vaccinated with BCG. This sequence represents Mycobacterium tuberculosis Rv0285 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                              AEB26444 standard; protein; 487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 102
                                                                                                                                                                                                                                                                                                                                                                                              AEB26444;
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Best Local
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                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                 Claim 25; SEQ ID NO 64609;
                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                              N-PSDB;
                                                                                                                                               WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #22212.
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Trawick JD,
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Forsyth
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The invention relates to an isolated nucleic acid comprising any one

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; gastrointestinal-gen.; urinary tract infection; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                           06-FBB-2004; 2004IN-DB000173.
20-JUL-2004; 2004US-0589227P.
                                                                                                                                                                                         07-FEB-2005; 2005WO-IN000037
                                                                                                                                                                                                                                                                     18-AUG-2005
                                                                                                                                                                                                                                                                                                                                                WO2005076010-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbial pathogen adhesin protein sequence, SEQ ID NO:165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-0CT-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHEQFVQLMSAGAAQYASAEAANSSPLQIVGQTALDAINSPVQTLTGRPLIGNGANGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IQLLASNASA-----QDQLHRAGEAVQDVARTYSQ-----IDDGAAGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 92.5; DB ilarity 27.1%; Pred. No. 0.23; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC identifying adhesin and adhesin-like proteins, by computing the sequence computed stributes of protein sequences using five attribute modules of a coneural network software, training an artificial neural network (ANN) for cach of the computed five attributes, and identifying the adhesin and conditions of the computed five attributes, and identifying the adhesin and conditions of a condition adhesin lake proteins having probability of being an adhesin (Pad) as conditing adhesin and adhesin-like proteins, having 274 fully defined 162-conditing adhesin and adhesin-like proteins, having 274 fully defined 162-conditions and adhesin-like proteins, having 105 fully conditions as conditions and adhesin-like proteins, having 105 fully conditions and adhesin-like proteins, having 105 fully defined 306-1876 base pair (SEQ ID NO: 12-79); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-291 base pair (SEQ ID NO: 12-79); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying adhesin and adhesin-like proteins, of therapeutic potential, and identifying and short-listing consists. (M1) is useful for identifying and short-listing consists to eliminate diseases caused by various pathogenic organisms. (M1) is consisted to identifying putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, consisting the proteins, and from bacteria belonging to a wide consistency adhesin shate are adhesine from consisting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sachdeva
                  21-MAR-2002; 2002WO-US009107
                                                      03-OCT-2002.
                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #22472.
                                                                                                                                                                                                                                                       19-JUN-2003
                                                                                                                                                                                                                                                                                              ABU36945
                                                                                                                                                                                                                                                                                                                              ABU36945 standard; protein; 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a computational method (M1)
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les 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHEQFVQLMSAGAAQYASAEAANSSPLQIVGQTALDAINSPVQTLTGRPLIGNGANGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IQLLASWASA-----QDQLHRAGEAVQDVARTYSQ-----IDDGAAGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATIGSAIS-----RANAEALVPITALLPAGADDVSAAIAALFATHGQAYQELSAHAVA
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                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%;
27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 92.5; DB; Pred. No. 0.23; 15; Mismatches
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                                                                                                                                                                          grug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сарв
                                                                                                                                                                          design.
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ADM40790;

ADM40790

ADM40790 standard; protein;

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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                   Sequence 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 64869; 1766pp; English
                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                             ANIGSALS
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Trawick JD,
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                   AA;
                                                                               ----AANAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA
                                                                                                                                                                            18.8%;
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Carr G
----FVQALTGAGGSYA
                                                                                                                                                      ; Score 90; DB; pred. No. 0.3:
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Forsyth
                                                                                                                                                          24;
                                                                                                                                                                                            Length 588;
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Xu HH;
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ABU36540
ID ABU3
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AC ABU3
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AC ABU3
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DB Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for the early detection of mycobacterial disease or infection in a subject. The method comprises assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies specific for one or more early Mycobacterium tuberculosis antigens. The invention further relates to: a kit for early detection of M. tuberculosis disease, and an antigenic composition for early detection of the M. tuberculosis disease or infection. The compositions of the invention have antibacterial activity. The method is useful for early detection of mycobacterial disease or infection in a subject and for preparing a vaccine against M. tuberculosis infection. This sequence represents the protein derived from the gene Rv3367 relating to the mycobacterial disease or infection method of the invention.
   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barly detection of mycobacterial infection in a subject by assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies for early Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2001; 2001WO-US020545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2001; 2001WO-US020545
                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                              Protein encoded by Prokaryotic essential gene #22067.
                                                                                                                                                               ABU36540 standard; protein; 606
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               588
                                                                                                                                                                                                                                                                              -QDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
                                                                                                                                                                                                                                                                                                                                            ADIGTOVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGI--QLLASNASA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4; 105pp; English.
                                                                                                                                                                                                                                               LHDQ-----FVQALTGAGGSYA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zolla-Pazner
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease
                                                                                                                                                                                                                                                                                                                                                                                              18.8%;
                                                                                                                                                                                                                                                                                                              ----ANAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection method related Rv3367 protein
                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                             Score 90; DB 7;
Pred. No. 0.39;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 588;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                               71
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S 밁 8

69 19 H

QDQLHRAGEAVQDVARTYSQID

72

FHE--RFIQALSTAAGAYGSAE

91

Query Match Best Local :

Similarity

18.3%;

; Score 87.5; DB 6; ; Pred. No. 0.79; 15; Mismatches 29;

29;

11;

Gaps

Length 606; Indels

Conservative

ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68

---AANAAALAPTTGVLAAGADEVSAAVASLFSGHAQAYQTLGTQAAA

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression to the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid complete acid; (2) a host cell containing the vector; (3) an isolated complete acid; (2) a host cell containing the vector; (3) an isolated complete acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the complete acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the complete activity of a gene in an operon required for complete activity of a gene in an operon required for complete activity of a gene in an operon required for complete activity of the gene product or that that inhibite cellular proliferation; (8) identifying a compound that inhibits proliferation; (8) compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits are useful for proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, C. and discovery programs, or for screening homologous nucleic acids are useful for cequired for proliferation in cells other than S. aureus, S. typhimurium, C. and compound that inhibits is cellular proliferation of a compound that inhibits are nucleic acids are u
21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
Sequence 606
                                                           the target prokaryotic essential genes. Note: The sequester the form part of the printed specification, in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BLIT-)
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Trawick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Carr G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 2
                                                                                  but was obtained
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Xu HH;
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RESULT 13
AEB91453
cc identifying adhesin and adhesin-like proteins, by computing the sequence computed network software, training an artificial neural network (ANN) for ceach of the computed five attributes, and identifying the adhesin and cc each of the computed five attributes, and identifying the adhesin and cc each of the computed five attributes, and identifying the adhesin and cc equal or greater than 0.51. Also claimed is a set of 274 annotated genes cc encoding adhesin and adhesin-like proteins, having 274 fully defined 162-cc 11151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical cc genes encoding adhesin and adhesin-like proteins, having 274 fully defined 51-1876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated cc adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base cair (SEQ ID NO: 1-279); a set of 279 annotated cc pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-3291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-3291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-3291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like cc proteins, having 105 fully defined 106-3291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like cc proteins, of therapeutic potential, and identifying and short-like in the string of the string putative adhesins that are important in drug custor of the string putative adhesins that are important in drug discovery and preventing therapeutics for whooping cough, pneumonia, constructs a suide from a state of string the string habeter is a ball of the string the string the string habeter is a suide from a string the string habeter is a suide from a string the string habeter is a suide from a string the string habeter is a suide string the string habeter is a suide from the string habeter is a
                                                                         distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antilnflammatory; respiratory-gen; gastric ulcer; antiluleer; gastrointestinal-gen; urinary tract infection; antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-2004; 2004IN-DE000173.
20-JUL-2004; 2004US-0589227P.
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                                                 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a computational method (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sachdeva G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal-gen.; urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbial pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brahmachari SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; antimicrobial; uropathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
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ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68

Query Match Best Local S

l Similarity 27; Conserv

Conservative

15;

Score 87.5; DB 9; Pred. No. 0.79; .5; Mismatches 29;

29;

Indels 11;

Gaps

Sequence

102

Length 606;

18.3%;

Sequence

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The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv0365, Rv0569, CC Rv1195, Rv1386, Rv3477, Rv3878, Rv3879c or MT3106.1 (also disclosed are CRV1195, Rv1386, Rv0387c), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% cs sequence identity to the polypeptide and is immunogenic. The protein is cuseful in preparing a pharmaceutical composition for diagnosing ct uberculosis and in preparing a vaccine against tuberculosis caused by virulent mycobacterium, are transpeutically in a subject not infected with a virulent mycobacterium, or therapeutically in a subject not infected with a virulent mycobacterium. The protein is useful for preventing, composition and detecting infections caused by species of tuberculosis compositic assays for detecting caused by species of tuberculosis may be used for effecting in vivo expression of the antigen, and in a sample. The vaccine is an improvement of the living BCG vaccine presently caused into the genome or more polypeptide has been incorporated into the genome of the composition of more than one copy of a nucleotide sequence enhances the immune response. The present sequence represents an M. CC cuberculosis protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infecaused by species of tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; Tuberculostatic; antibacterial; vaccine; Rv0284; Rv0285; Rv0455c; Rv0569; Rv1195; Rv1386; Rv3477; Rv3878; Rv3879; MT3106.1; ORF13A; Rv0284ct; Mycobacterium bovis; Mycobacterium africanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis Rv1386 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 77; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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CC identifying adhesin and adhesin-like proteins, by computing the sequence-
CC based attributes of protein sequences using fire attribute modules of a
CC neural network software, training an artificial neural network (ANN) for
CC each of the computed five attributes, and identifying the adhesin and
CC edual or greater than 0.51. Also claimed is a set of 274 annotated genes
CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes
CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-
CC 1151 base pair (SEQ ID NO: 385-558) sequences; a set of 105 hypothetical
CC genes encoding adhesin and adhesin-like proteins, having 105 fully
CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated
CC adhesin and adhesin-like proteins, having 205 fully defined 53-3716 base
CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like
CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)
CC based on (M1). (M1) is useful for identifying adhesin and adhesin-like
CC proteins, of therappeutic potential, and identifying and short-listing
CC proteins for further testing in development of new vaccine formulations
CC useful for identifying putative adhesins that are important in drug
CC discovery and preventing therapeutics for whooping cough, pneumonia,
CC gastric ulcer and urinary tract infections. (M1) identifies adhesins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antihilarmatory; respiratory-gen.; gastric ulcer; antihileer; gastrointestinal-gen.; urinary tract infection; antimicrobial; uropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-2004; 2004IN-DE000173.
20-JUL-2004; 2004US-0589227P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a computational method (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; SEQ ID NO 157; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-597835/61.
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26.6%; Pred. No.
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AVHAQFVBALSAGAGAYASABAAGAAVLA
                                                                 IGTQVSDNALHGVTAG---STALTSVTGLVPAGADBVSAQAATAFTSEGIQLLASNASAQ
                                            LGSAATDLÄALGSVLGAADAAÄAATTTGIVAÄAQDEVSÄAIÄALFSAHGRAYQVASÄQÄA
                    DOLHRAGEAVODVARTYSQIDDGAAGVFA
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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probable PE protei PE-family protein hypotherical glyci		transducer protein conserved hypothet hypothetical prote	hypothetical glyci hypothetical glyci probable PE protei	halobacterial tran Htr7 transducer [i probable PE protei hypothetical glyci

## ALIGNMENTS

RESULT 2
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C70799
probable PB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004 probable PE protein - Mycobacterium tuberculosis (strain H37RV)

(;Species: Mycobacterium tuberculosis

(;Species: Mycobacterium tuberculosis

(;Cspecies: Mycobacterium tuberculosis

(;Accession: F70802

C;Accession: F70802

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Commor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Commor, R.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: F70802

A;Active States C;Accession: C70799
R;Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T., Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S; Comnor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70799 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-111 <COL> 문 S 문 ঠ A; Molecule type: DNA
A; Residues: 1-99 <COL>
A; Cross-references: UNIPARC: UPI00000C1571; GB:AL022120;
A; Experimental source: strain H37Rv A;Status: preliminary; nucleic acid sequence not shown; translation not shown Genetics: Query Match Best Local ( Matches 61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98 2 Н 1 MEKMSHDPIAADIGTQVSDNALHGVTAGSTALISVTGLVPAGADEVSAQAATAFTSEGIQ 60 98; Similarity MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQ 60 Conservative 100.0%; Score 479; DB 2; 100.0%; Pred. No. 3e-37; 0; Mismatches 0 98 Length Indels GB:AL123456; NID:g3261558; 99; 0 Gaps 0 PIDN

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probable PE protein - Mycob
C;Species: Mycobacterium tu
C;Date: 17-Jul-1998 #sequen
C;Accession: C70836
R;Cole, S.T.; Brosch, R.; P
; Connor, R.; Davies, R.; D
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C;Accession: D70931
R;Cole, S.T.; Brosch, R.;
; Connor, R.; Davies, R.;
A;Cross-references: UNIPARC:UPI00000D3B03;
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70931
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A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70836
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PE
                                                                                                                                                                                                                                                                               hypothetical glycine-rich protein Rv1803c - Mycobacterium tuberculosis (strain c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003 C;Accession: D70931
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                                                                                             Status: preliminary; nucleic
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;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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Best Local :
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                                                                                                                                                                                                                    Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D
Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
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52.1%;
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Pred. No. 1.9e-14;
5; Mismatches 30
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Pred. No. 0.011;
7; Mismatches
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                                       GB:AL022021;
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A;Experimental source: strain C;Genetics: A;Gene: Rv0872c
                                                                                                A;Accession: H70816
A;Status: preliminary; nucleic
A;Molecule type: DNA
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                                                                A;Cross-references: UNIPARC:UPI00000D3AFD;
                                                                                 A;Residues: 1-606 <COL>
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hypothetical glycine-rich protein Rv0872c - Mycobacterium tuberculosis (strain C,Species: Mycobacterium tuberculosis C,Species: Mycobacterium tuberculosis C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003 C,Accession: H70816
R,Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamin, N.; Ho; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from
A;Reference number: A70500; MUID:98295987; PMID:9634230
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A; Residues: 1-588 < COL>
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003
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Pred. No. 0.74;
15; Mismatches
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Holroyd,
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S

acid

sequence not shown; translation

not

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GB:AL022004;

GB:AL123456; NID:g3261550;

PIDN

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squax Nature 393, 537-544, 1998
A;Authors: Sqares, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70824
                                                                                                                                                                                                                                                                                                                                           hypothetical glycine-rich protein Rv0746 - Mycobacterium tuberculosis (stra C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: E70824
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A;Authors: Squares, S.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70898
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                                                                              A; Cross-references: UNIPROT: 053809; A; Experimental source: strain H37Rv
                                                                                                                 A;Status: preliminary; nucleic A;Molecule type: DNA A;Residues: 1-783 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
;Accession: H70898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P71656; Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAAQGVEELGRSGVGVAESGASYAARDALAAASY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNASAGDQLHRAGEAVQDVARTYSQIDDGAAGVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHB--RFIQALSTAAGAYGSAE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDQLHRAGEAVQDVARTYSQID 90
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                  elastin
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                  related uncharacterized
                                                                                                                                                                                                                                                                              Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                                                              acid
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Pred. No. 2;
15; Mismatches
                                                                                                 UNIPARC: UPI00000D4FCA;
                                                                                                                                                              sequence
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                glycine-rich
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                                                                                                 GB:AL021958;
                  protein,
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                  В
                                                                                                                                                                                                                       complete
                  motif
                                                                                                   GB:AL123456;
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Query Match
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Square Nature 393, 537-544, 1998
A;Authors: Sqares, F.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the c A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70806
                                                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Bar A;Title: Deciphering the biology of Mycobacterium tuberculosis from A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: D70807
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                                                  A; Molecule type: DNA
A; Residues: 1-1901 <COL>
                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, Connor, R.; Davies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI00000D3AEB;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1489 < COL>
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A; Experimental
                         A;Cross-references:
                                                                                           A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 LHRAGEAVQDVARTYSQIDDGAA
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  UNIPROT:053553;
ce: strain H37Rv
                                                                                                                                                                                                                                          R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hoers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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28.9%; Pred. No. 7;
tive 18; Mismatches
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                         UNIPARC: UPI000013C2A6;
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                         GB:AL022022;
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Holroyd,
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C;Date: 17-Ju1-1996 #BEQUEST. C;Date: 17-Ju1-1996 #BEQUEST. C;Accession: F70824
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; ; Connor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, Sadares, S
                                                                                                                                  Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: P70824

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-9801 <COL>
A;Cross-references: UNITROT:053810; UNIPARC:UPI0000139C61; GB:AL021958; GB:AL12
A;Cross-references: UNITROT:053810; UNIPARC:GPI0000139C61; GB:AL021958; GS:AL12
C;Gene: Kr0747
C;Gene: Kr0747
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70726
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8; Mismatches
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: A70900
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the completa; Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70983
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-487 <COL-
A;Residues: 1-487 <COL-
A;Residues: 1-487 <COL-
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                                                                                                                                                                           A;Gene: KV1.3700
C;Superfamily: uncharacterized glycine-rich
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Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sul
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G;Species: Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis (strain C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Species: Mycobacterium tuberculosis
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A;Experimental source: strain H37Rv
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                                                                                                                      Similarity
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Pred. No. 2.7;
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Search completed: April 14, 2006, 17:34:26 Job time : 7.7465 secs	Oy 10 AADIGTQVSDNALHGVTAGSTALTSVTGLVEAGADEVSAQAATAFTSEGIQLLAS 64	Query Match 17.1%; Score 82; DB 2; Length 562; Best Local Similarity 31.6%; Pred. No. 5.9; Matches 37; Conservative 13; Mismatches 29; Indels 38; Gaps 6;	A;Molecule type: DNA A;Residues: 1-562 <col/> A;Cross-references: UNIPROT:050458; UNIPARC:UPI0000165283; GB:AL021006; GB:AL123456; NID A;Experimental source: strain H37Rv C;GenetLcs: A;Genet Rv1243C	lston, J.E.; Taylor, K.; Whitehead, S.; Barrel biology of Mycobacterium tuberculosis from the O; MUID:98295987; PMID:9634230	C;Accession: B70953 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	RESULT 15  B70953  hypothetical glycine-rich protein Rv1243c - Mycobacterium tuberculosis (strain H37RV) C/Species: Mycobacterium tuberculosis C/Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004	Qy 69 QDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
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OF9F93, OCTUP PRELIMINARY; PRT; 99 AA. O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F93; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94; O79F94;
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34 MYCBO
77VVG4_MYCBO PRELIMINARY; PRT; 98 AA.
07TVVG4;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PE FAMILY-LIKE PROTEIN.
Name=PE35; OrderedLocusNames=Mb3902;
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STRAIN=AF2122/97;
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III,
RA Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RN Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RN Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
TDeciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RN RULL BX842584, CAE55646.1; -; Genomic_DNA.
DR SMBL, BX842584, CAE55646.1; -; Genomic_DNA.
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STRAIN=CDC 1.551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.I

Salzberg S.L., Delcher A., Utterback T.R., Weldman J.F., Khouri H

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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Corynebacterinese; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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J. Bacteriol. 184:54
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AE000516; AAK48354.1; -; Gen
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MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Cole S.T., Brosch R., Palpheier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin J. Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.
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Name=PE34; OrderedLocusNames=Rv3746c;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat PROBABLE PE FAMILY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriacaae; Mycobacterium;
Mycobacterium tuberculosis complex.
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MEDLINE-2206494; PubMed-12218036;

DOI=10.1128/JB.1844.19.5479-5499.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M. Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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OrderedLocusNames=MT3854;
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Nature 393:537-544(1998).
EMBL; BX842584; CAE55636.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome comparison of Mycobacterium tuberculosis clinical laboratory strains.";
[Bacteriol. 184:5479-5490(2002).
WBL; AB000516; AAK48218:1; -; Genomic_DNA.
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Local Similarity 52.1%;
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SEQUENCE
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SEQUENCE 102 AA;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ
EMBL, AE017240; AASO6331.1; -; Genomic_DNA.
InterPro; IPR000084; PB_region_N.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium;
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Hypothetical protein.
OrderedLocusNames=MAP3781;
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A Harris D.E., Gordon S.V., Eiglameier K., Gas S., Barry C.B. III,

A Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

A Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,

A Rogers J., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"complete genome sequence.";

Nature 393:537-544(1998).

REMBL, BX842573; CAE55265.1; -; Genomic DNA.

REMBL, BX842573; CAE55265.1; -; Genomic DNA.
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Q7DA36; Q6MX53;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
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13-SEP-2005 (TrEMBLrel. 31, Last annot
PE family protein.
Name=PE5; OrderedLocusNames=MT0298, Rv
Q79FJ9;
05-JUL-2004
05-JUL-2004
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TubercuList; Rv0285; -
InterPro; IPR000084; PI
Pfam; PF00934; PB; 1.
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MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
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J. Bacteriol. 184:5479-5490(2002).
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NUCLEOTIDE SEQUENCE:

STRAIN=CDC 1551 / Oshkosh;

STRAIN=CDC 1551 / Oshkosh;

MEDLIXMS=22206494; PubMed=12218036;

MEDLIXMS=22206494; PubMed=12218036;

Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
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SEQUENCE
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Name=PE PGRS32; OrderedLocusNames=Rv1803c; Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae Corynebacterineas; Mycobacteriaecae; Mycobacteriaecae; Mycobacterium tuberculosis complex.
                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
PE PGRS family protein.
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ProDom; PD001223; PE region N; 1.
PROSITE; PS00583; PFKB KINASES_1; UNKNOWN_1.
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                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
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InterPro; IPR000084; PE region_N.
InterPro; IPR002173; PfkB.
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                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MNYC/BZ/62/M379;
Adhiambo C., Formey J.D., Asai D.J., LeBowitz J.H.;
"Cytoplasmic dynein 2 isoform is required for flagella a
Leishmania mexicana.";
Submitted (UN-2004) to the EMBL/GenBank/DDBJ databases.
SMBL; AY671898; AAU93603.1; -; Genomic DNA.
SEQUENCE 4470 AA; 500686 MW; 81CF1DAF0226A8D2 CRC64;
                                                       01-OCT-2003 (TremBLrel.
01-OCT-2003 (TremBLrel.
01-MAR-2004 (TremBLrel.
PE-PGRS FAMILY PROTEIN.
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13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
Cytoplasmic dynein heavy chain
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J. Bacteriol. 184:5479-5490(200
EMBL; AB000516; AAK46124.1; -;
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                              Mycobacterium bovis.
                                          Name=PB_PGRS32a;
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; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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                                           OrderedLocusNames=Mb1832c;
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Harris D.B., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin I
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S.,
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PE-PGRS FAMILY PROTEIN.

Name=PE PGRS51; OrderedLocusNames=Rv3367;

Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium;

Mycobacterium tuberculosis complex.
                                                                                                                                                                                          EMBL; BX842582; CAE55590.1; -;
Tuberculist; Rv3367; -
InterPro; IPR002952; Eggshell.
InterPro; IPR000084; PB region
InterPro; IPR002173; PfkB
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                                                                                                     PRINTS; PRO1228; EGGSHELL.
PROSITE; PS00583; PPKB_KINASES_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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ProDom; PD001223; PE_region_N; 1.
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Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX249340; CAD94535.1; -; Genomic_DNA.
InterPro; IPR000084; PE_region_N.
                                                                                                                                                                        Pfam; PF00934; PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
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588 AA;
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Best Local S
Matches 30
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A Garnier T., Eiglmeter K., Camus J.-C., Medina N., Mansoor H.,
A Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
A Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
A Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
T "The complete genome sequence of Mycobacterium bovis.";
E. Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
B. EMBL; BX248345; CAD95560.1; -, Genomic DNA.
GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0015671; P:oxygen transporter activity; IEA.
R [InterPro; IPR002932; Eggshell.
R InterPro; IPR002932; Eggshell.
R InterPro; IPR002173; pfkB.
R [Pfam; PF00934; PE; ].
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QTTWM2;
QTTWM2;
QTCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence
01-MAR-2004 (TrEMBLrel. 26, Last annotati
PE-PGRS FAMILY PROTEIN.
Name=PE_PGRS51; OrderedLocusNames=Mb3402;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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STRAIN=AF2122/97;
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PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                   18.8*; Score 90; DB 2; Length 626; 33.0*; Pred. No. 8.8; tive 13; Mismatches 24; Indels
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Maximum I
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Listing first 45 s
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Perfect score:
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re greater than or equal to the score of the result being put
is derived by analysis of the total score distribution.

    69
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   US-10-620-246-88
479
1 MEKNSHDPIAADIGTQVSDN......VQDVARTYSQIDDGAAGVFA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   April 14, 2006, 17:32:59; Search time 9.0618 Seconds (without alignments) 894.107 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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2 US-09-073-009-32

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2 US-09-125-619-32

2 US-10-222-566-32

2 US-10-143-024A-32

2 US-10-125-619-39

3 US-10-222-566-39

3 US-10-222-162-39

2 US-10-222-162-39

3 US-10-222-162-39

3 US-10-222-162-39

3 US-10-222-162-39

4 US-09-603-703B-293

5 US-09-603-703B-2330

8 US-09-902-540-12224

8 US-09-540-236-3595

8 US-08-548-159-5

8 US-08-435-991A-20127

8 US-08-435-991A-20127

8 US-09-252-991A-32442

8 US-09-356-447A-5

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8 US-09-356-447A-5
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Sequence 88, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 292, Appl
Sequence 292, Appl
Sequence 292, Appl
Sequence 2, Appl
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Sequence 3955, Ap
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# ALIGNMENTS

US-09-050-739-88

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GENERAL INFORMATION:

APPLICANT: ADDRESH, Peter

APPLICANT: NIELSEN, Rikke

APPLICANT: OBTINGER, Thomas

APPLICANT: RASMUSSEN, Peter Birk

APPLICANT: RASMUSSEN, Peter Birk

APPLICANT: ROSENKRANDS, Ida

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WICTERIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

TITLE OF INVENTION: NUTURER: US/09/050,739

CURRENT APPLICATION NUMBER: US/09/050,739

CURRENT APPLICATION NUMBER: 0376/97

EARLIER APPLICATION NUMBER: 1997-04-02

EARLIER FILING DATE: 1997-04-02

EARLIER APPLICATION NUMBER: 60/044,624

EARLIER APPLICATION NUMBER: 60/044,624

EARLIER APPLICATION NUMBER: 60/044,624

EARLIER APPLICATION NUMBER: 60/070,488

EARLIER FILING DATE: 1997-04-18

EARLIER FILING DATE: 1998-01-05

NUMBER OF SEQ ID NOS: 173

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 88

LENGTH: 98

TYPE: PRT
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                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-050-739-88
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Best Local S
Matches 98
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GENERAL INFORMATION:
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                      61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
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LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA
                                                                                                                                                                                       100.0%; Score 479; DB 2; ilarity 100.0%; Pred. No. 5.6e-50; Conservative 0; Mismatches 0;
98
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RESULT 2
US-09-073-009-32
; Sequence 32, Application
; Patent No. 6555653

US/09073009

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ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-073-009-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.6%;
Best Local Similarity 39.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Alderson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 206-622-49
TELEPAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/09/073,009

FILING DATE: 05-MAY-1998

CLASSIFICATION:

ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / ATTORNEY / AT
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKST NUMBER: 210121.441C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
LENGTH: 99 amino acid
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STATE: Washing
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TYPE: amino acid
STRANDEDNESS: single
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 STREET:
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Pred. No. 0.21;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Alderson, Mark
                                                                                    TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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MOLECULE TYPE:
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 05-MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 98104
                 STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                     TELEPHONE:
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                                                                  LENGTH:
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                                                  H: 99 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto, Antonio
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Skeiky, Yasir A.W.
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Pred. No. 0.21;
8; Mismatches 18;
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ORIGINAL SOURCE:

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RESULT 6
US-09-125-619-32
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US-09-073-010-33
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US-09-073-010-32
                                                                                                                                                                                                                                                       US-09-073-010-33
Sequence 32, Application US/09125619
PAtent NO. 6437116
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                Matches
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APPLICANT: Alderso
APPLICANT: Dillon
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linn
                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.440C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 500
STREET: 500
TTY: Seattle
Washing
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                                                                                                                                                                                                            Similarity
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                                                                                                                                    IGTTM--NAQNAAAAPT----TGVVPAAADEVSALTAAQPAAHAQMYQTVSAQAAA 71
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05-MAY-1998
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Pred. No. 0.21;
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Pred. No. 0.21;
B; Mismatches 18;
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                                                                                                                                                                                           18;
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 Sequence 32, Application US/10143024A
Patent No. 6740744
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
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; ORGANISM: Borrelia burgdorferi
US-10-222-566-32
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US-10-222-566-32
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                                                                                                                                                   Query Match 15.6%; Score 74.5; DB Best Local Similarity 26.7%; Pred. No. 0.62; Matches 20; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                          SEQ ID NO 32
LENGTH: 212
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LENGTH: 212
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD3
CURRENT APPLICATION NUMBER: US/10/222,566
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR PILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: JING-RI
APPLICANT: HARDHAI
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TITLE OF INVENTION: WP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 199-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                            TYPE: PRT
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Local Similarity 26.7%;
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70. 671998
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                                    81 DVARTYSQIDDGAAG 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
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GAGKLPGKVDDAHAG 111
                                                                           GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10222566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                          DB 2;
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                                                                                                                                                     Gaps
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILIN K.
APPLICANT: HOWELL, JERRILIN K.
APPLICANT: HOWELL, JERRILIN K.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VWP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD4
CURRENT APPLICATION NUMBER: US/10/222,162
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HOWELL, JERRILYN K.

APPLICANT: HARBOUR, ALAN G.

APPLICANT: WEINSTOCK, GEORGE M.

FILE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA

FILE REFERENCE: UTSH:234USD1

CURRENT APPLICATION NUMBER: US/10/143,024A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: PCT/US97/02952

PRIOR APPLICATION NUMBER: 60/012,028

PRIOR APPLICATION NUMBER: 60/012,028

PRIOR FILING DATE: 1996-02-21
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// ORGANISM: Borrelia burgdorferi
US-10-143-024A-32
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US-10-222-162-32
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Best Local S
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SEQ ID NO 32
LENGTH: 212
TYPE: PRT
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Best Local Similarity
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SEQ ID NO 32
LENGTH: 212
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                                                                                                                                                                   y Match 15.6%; Score 74.5; DB 2;
Local Similarity 26.7%; Pred. No. 0.62;
hes 20; Conservative 21; Mismatches 29;
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GAGKLFGKVDDAHAG 111
                                      DVARTYSQIDDGAAG 95
                                                                                GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
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; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-125-619-39
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US-09-125-619-39
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PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
LENGTH: 213
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Patent No. 6437116
GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 39
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APPLICANT: WEINSTOCK
TITLE OF INVENTION:
FILE REFERENCE: UTSH
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Patent No. b, ....
Patent INFORMATION:
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APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILLYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NORRIS,
APPLICANT: JING-RI
APPLICANT: HARDHAN
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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CURRENT FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Borrelia burgdorferi
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                                                                   39 GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
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                                  81 DVARTYSQIDDGAAG 95
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
 GAGKLFGKVDDAHAG 111
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VENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
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                                                                                                                                               Conservative
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                                                                                                                                               15.6%; Score 74.5; DB 26.7%; Pred. No. 0.63; tive 21; Mismatches
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APPLICANT: JUGG-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WINSTOCK, GEORGE M.
TITLB OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILER REFERENCE: UTSH:2344USD4
CURRENT APPLICATION NUMBER: US/10/222,162
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: WEINSTOCK, GEORGE M.

FITTLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA

FILE REFERENCE: UTSH:234USD1

CURRENT APPLICATION NUMBER: US/10/143,024A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR APPLICATION NUMBER: 05/012,028

PRIOR APPLICATION NUMBER: 05/012,028

PRIOR APPLICATION NUMBER: 05/012,028

PRIOR APPLICATION NUMBER: 05/012,028

PRIOR APPLICATION NUMBER: 1997-02-21

PRIOR APPLICATION NUMBER: 05/012,028
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; ORGANISM: Borrelia burgdorferi
US-10-143-024A-39
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US-10-222-162-39
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                                                                                                                                                    SEQ ID NO 39
LENGTH: 213
TYPE: PRT
Query Match
Rest Local Similarity 20...
20; Conservative
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LENGTH: 213
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Best Local Similarity 26.7%;
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APPLICANT: JING-R
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APPLICANT: JING-RI
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SOFTWARE: PatentIn Ver. 2.1
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
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                                         15.6%; Score 74.5; DB 26.7%; Pred. No. 0.63;
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                         21;
                         Mismatches
                                                           DB 2; Length 213;
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PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/14
PRIOR APPLICATION NUMBER: 60/15
PRIOR APPLICATION NUMBER: 60/15
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19
PRIOR APPLICATION NUMBER: DE 19
PRIOR APPLICATION NUMBER: DE 19
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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SEQ ID NO 292
                                                                                                                                                          Matches
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APPLICANT: Kim, Hyung-Joon
TITLE OP INVENTION: CENYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OP INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: DE PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                           LENGTH: 505
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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DE 19941382.7
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( APPLICATION NUMBER: DE 1
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                                   57 EGIQLLASNASAODO-LHRAGEAVODVARTYSOIDDGAA 94
                                                                           41 EFGVRIVDNMLVGFSTLGDGMNQAAEGATTLSDGVGSANDGAVQLADGAVTLRDGIASAN 100
                                                                                                                12 DIGTQVSDNALHGVTA------GSTALTSVTGLVPAGADEVSAQAAT-----AFTS 56
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                                                                                                                                                                               Similarity
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EGAQSLADGASQLDTGLGSAATGSQTLADGLSSLSAGTA 139
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Schroder, har-
Schroder, Oskar
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RESULT 15 US-09-605-703B-2330 ; Sequence 2330, Application US/09605703B

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PATERIAL INFORMATION:
APPLICANT: NEFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
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APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Haberhauer, Gregor
ITILE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
ITILE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
ITILE OF INVENTION: CORNEBR: 60/142,764
PRIOR FILING DATE: 1990-07-08
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-09-03
INVENTIOR APPLICATION NUMBER: 60/142,764
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INVENTIOR APPLICATION INVERSE: 60/142,764
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•	`.	æ	Sequence 33, App	-	Sequence 33, App	Sequence 32, App	Sequence 204201,	64362	Sequence 64397, A	327,	327,	327,	64405,	Sequence 64786, A	62341,	Sequence 7902, A	Sequence 56, App

ALIGNMENTS

#### GENERAL INFORMATION: APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: OETTINGER, Thomas APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter APPLICANT: RESENERANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, KARIN APPLICANT: WELDINGH, KARIN APPLICANT: WELDINGH, KARIN APPLICANT: WELDINGH, KARIN APPLICANTON: NETURE FRAGMENTS AND POLYPEPTIDE FRAGMENTS ITILE OF INVENTION: NETURE FROM M. TUBERCULOSIS FILE REFERENCE: 670001-2002.1 CURRENT APPLICATION NUMBER: US/09/791,171 CURRENT APPLICATION NUMBER: 0376/97 PRIOR APPLICATION NUMBER: 0376/97 PRIOR APPLICATION NUMBER: 1277/97 PRIOR PILING DATE: 1997-04-02 PRIOR APPLICATION NUMBER: 60/044,624 PRIOR APPLICATION NUMBER: 60/044,624 PRIOR PILING DATE: 1997-04-18 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR PILING DATE: 1998-01-05 NUMBER OF ESQ ID NOS: 173 SOPTWARE: Patentin Ver. 2.0 SEQ ID NO 88 LENGTH: 98 TYPE: PRT ORGANISM: Mycobacterium tuberculosis 밁 S 밁 S ; ORGANISM: Mycobacterium tuberculosis US-09-791-171-88 RESULT 1 US-09-791-171-88 Sequence 88, Application US/09791171 Patent No. US20020094336A1 Best Local Query Match Best Local Similarity INFORMATION 61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA -1 MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAPTSEGIQ 98; MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAPTSEGIQ 100.0%; Score 479; DB 3; llarity 100.0%; Pred. No. 1.4e-42; Conservative 0; Mismatches 0; 98 98 Length 98; Indels 0 Gaps 60

RESULT 2 US-09-804-980-88

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GENERAL INFORMATION:

APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
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                                                               ; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-138-473-88
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CURRENT APPLICATION NUMBER: US/10/138,473
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US 10/660,428
PRIOR PILING DATE: 2002-01-29
PRIOR PPLICATION NUMBER: US 09/415,884
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-01-21
PRIOR PILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: UK 1998 01281
PRIOR APPLICATION NUMBER: US 60/070,488
PRIOR PILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: UK 1997 01277
PRIOR PILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: UK 1997 01277
PRIOR PILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: UK 1997 01277
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LENGTH: 98
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Query Match
Best Local Similarity
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PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 174
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PRIOR FILING DATE: 1997-04-18
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TITLE OF INVENTION: TB Diagnostic Based On Antigens From M. tuberculosis
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Local Similarity 100.0%;
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APPLICATION NUMBER: US 60/044,624
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SKJORT, Rikke Louise Vinther
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RASMUSSEN, Peter Birk
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100.0%;
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Pred. No. 1.4e-42;
Score 479; DB 4;
Pred. No. 1.4e-42;
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APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: PILORIO, Walter
TITILE OF INVENTION: NUCLERIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITILE OF INVENTION: DERRIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT FILING DATE: 2003-07-15
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1997-04-18
PRIOR PILING DATE: 1997-04-18
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PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 00/70,488
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
RESULT 5
US-10-510-021-62
; Sequence 62, Application US/10510021
; Publication No. US20050220811A1
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PRIOR FILING DATE: 2001-02-20
PRIOR PELICATION NUMBER: 09/415,884
PRIOR PELICATION NUMBER: 09/416,673
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR PILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 1281/98
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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SEQ ID NO 88
LENGTH: 98
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APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Tho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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RASMUSSEN, Peter I
ROSENKRANDS, Ida
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100.0%; Pred. No. 1.4e-42;
tive 0; Mismatches 0;
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                                                                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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SEQ ID NO 62
LENGTH: 99
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/510,021
CURRENT FLIING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: PCT/IB03/01789
PRIOR FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: EP 02/290864
PRIOR FILING DATE: 2002-04-05
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APPLICANT: Demangel, Caroline
APPLICANT: Leclerc, Claude
TITLE OF INVENTION: Identification
TITLE OF INVENTION: RD5 leading to
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NUMBER OF SEQ ID NOS: 75
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APPLICANT: Pym,
APPLICANT: Brose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Rv3872-PE35 - PE family-related protein
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                              APPLICATION NUMBER: 60/230,347
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Malone, Cheryl
Haselbeck, Robert
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                    Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari
Zyskind, Judith
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100.0%; Pred. No. 1.4e-42;
60/242,578
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RESULT 7
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
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OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR PILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR PILING DATE: 2000-10-25
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR PILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-05
OR APPLICATION NUMBER: 60/269,308
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Zyskind, Judith
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Prior Application data removed -

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Best Local S
Matches 30
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SOFTWARE: Patentin version 3.1
SEQ ID NO 64869
LENGTH: 588
                                                                                                                                                                                                                                                  Sequence 64464, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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SEQ ID NO 4
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TITLE OF INVENTION: WYCOBACTERIAL PROTEINS AS
FILE REFERENCE: 32004-173355
CURRENT APPLICATION NUMBER: US/10/481,563A
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/212,048
PRIOR PILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                 ITLE
REFERENCE: ELITRA.034A
              OF INVENTION: Identification of Essential Genes
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                                                                                                                  Wall, Daniel
                                                                                                                              Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                   Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                             Forsyth, R.
                                                               Yamamoto,
                                                                              Trawick, John
Carr, Grant
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                                                                  Robert
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33.0%; Pred. No. 1;
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                LENGTH: 60
TYPE: PRT
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                               Local
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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72
                                   69 QDQLHRAGEAVQDVARTYSQID 90
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FHE--RFIQALSTAAGAYGSAE
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ilarity 32.9%; Pred. No. 2;
Conservative 15; Mismatches
91
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR APPLICATION NUMBER: 60/230,335
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APPLICANT: Zamudi
APPLICANT: Malonu
APPLICANT: Haselil
APPLICANT: Ohlses
APPLICANT: Zyskii
APPLICANT: Zyskii
APPLICANT: Trawic
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Malone, Cheryl
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Forsyth, R.
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US-10-282-122A-64547
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                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-06
PRIOR FILLING DATE: 2000-09-06
PRIOR FILLING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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TYPE: PRT
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                                 APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                     APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
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APPLICATION NUMBER: 60/267,636
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Yamamoto, Robert
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Trawick, John
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Zyskind, Judith
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Malone, Cheryl
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; Pred. No. 2.8;
14; Mismatches
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RESULT 12
US-10-282-122A-64514
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US-10-282-122A-64514
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 64547
LENGTH: 576
                                                                                  SEQ ID NO 64514
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Publication No. US20040029129A1
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TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
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PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-03-21
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          TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                          ENGTH: 562
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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PILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
PILING DATE: 2000-12-22
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Carr, Grant
Carr, Grant
Carr, Grant
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Wall, Daniel
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Malone, Cheryl
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US-10-282-122A-64589
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
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Publication No. US20040029129A1
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Best Local Similarity
Matches 37; Conserv
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Best Local
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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  59 IQLLASNASA 68
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                                                                                                                                    Similarity
                                                                        MSHDPIAADIGTQVSDNALHGV-----TAGSTALTSVTGLVPAGADEVSAQAATAFTSEG 58
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                                        MSFLLVEPDLVTAAAAN-LAGIRSALSEAAAAASTPTTALASAGADEVSAAVSRLFGAYG 59
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Forsyth, R.
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Zyskind, Jud
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31.6%; Pred. No. 6.8;
tive 13; Mismatches 29; Indels
                                                                                                                Score 81; DB Pred. No. 18; 7; Mismatches
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; LENGTH: 319
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62423
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CURRENT APPLICATION NUMBER: U9/10/282,122A
CURRENT FILING DATE: 2003-02-0
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
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Publication No. US20040029129A1
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                                                69 -QDQ-LHRAGEAVQDVARTY--SQIDDGAA 94
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Zyskind, Judith
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Xu, H.
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Malone, Cheryl
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; Sequence 64606, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

RESULT 15

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	7521, Ap	17, Appl	307, App	10, Appl	6068, Ap	4, Appli	20, Appl	17929, A	22522, A	17876, A	18562, A	368, App	20, Appl	3320, Ap	2864, Ap	19377, A	21, Appl	7300, Ap	6, Appli

#### ALIGNMENTS

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RESULT 2
US-11-052-554A-163
; Sequence 163, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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; Sequence 165, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID:
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PO'
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILLING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                               21 ATTGSAIS-----RANAEALVPITALLPAGADDVSAATAALFATHGQAYQELSAHAVA 73
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                                                                                                                                                                                                                                                                      RESULT 4
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US-11-052-554A-157
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                                                                                                                                                                         Sequence 135, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: PatentIn version 3.3 SEQ ID NO 157 LENGTH: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local !
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Best Local :
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APPLICANT: Sachdava, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND J
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

PRIOR FILING DATE: 2004-02-06
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR FILING DATE: 2004-07-20
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PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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30.3%;
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RESULT 6
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US-11-052-554A-162
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                                                                                                                                                                       Sequence 166, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 162, Application US/11052554A Publication No. US20050288866A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REPERENCE: 3083/4039A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL FILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILLING DATE: 2005-02-07 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR FILING DATE: 2004-07-20
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                                                                                                                                                     APPLICANT: Sachdeva, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sachdeva, et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASAQD 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Th 17.8%; Score 85.5; DE Similarity 30.7%; Pred. No. 0.37; 27; Conservative 10; Mismatches
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28.9%; Pred. No. 1.6;
tive 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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GENERAL INFORMATION:

GENERAL INFORMATION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: UN 173/DEL/2004

PRIOR APPLICATION NUMBER: UN 173/DEL/2004

PRIOR PILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: UN 173/DEL/2004

PRIOR PILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOPTWARE: Patentin version 3.3

SEQ ID NO 149

LENGTH: 853
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; Sequence 149, Application US/11052554A
; Publication No. US20050288866A1
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; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-164
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GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

RUMBER OF SEQ ID NOS: 763

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NUMBER OF SEQ ID NOS: 763
SOPTWARE: PatentIn version 3.3
SEQ ID NO 166
LENGTH: E01
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGIGSAIS-----SANAAAAVNTTGLLTAGADEVSTAIAALFGAQGQAYQAASAQA 69
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; Pred. No. 0.74;
14; Mismatches 2
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID.
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PO
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
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                                                                              ; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-02-06
  Matches
                                                                                                                                      SEQ ID NO 137
LENGTH: 1660
                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20050288866A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.3 SEQ ID NO 160
                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 160, A Publication No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEG--IQLLASNASA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AGIGSALAB-----ANAAALAPTTALLAAGADEVSAAIAALFGAHGQAYQTVSAQASA 71
  34; Conservative
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADLGSTIAG-----ANAAAAANTTSLLAAGADEISAAIAALFGAHGRAYQAASAEA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/11052554A o. US20050288866A1
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                  16.8%;
  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 80.5; DB; Pred. No. 2.5; 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80.5; DB 7; Pred. No. 2.3;
                  Score 80.5;
Pred. No. 5.
red. No. 5.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
                                                                                                                                                                                                                                                                                                                                                             IDENTIFYING ADHESIN AND ADHESIN-LIKE POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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  26;
                                       Length 1660;
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  Indels
  17;
  Gaps
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11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68

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Sequence 147, Application US/1105254A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR PRILING DATE: 2004-07-20
PRIOR PRILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOPTWARE: Patentin version 3.3
SOPTWARE: Patentin version 3.3
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis H37Rv
USATION OF 147
LENGTH: 923
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 3083/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR RILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR APPLICATION NUMBER: 10 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PATENTIAN VERSION 3.3

SEQ ID NO 154

LENGTH: 767
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US-11-052-554A-154
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US-11-052-554A-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 154, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
ETIT PREPENCE: 1005507
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -IDDGAAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYQAVSAQMSAFHAQFMQALTGAGGAYAAAEAVNVSAAQSVEQDLLAAINARFERIFGRP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EAVQ-DVARTYSQ-----
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16.7%;
30.9%;
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Score 80;
Pred. No.
DB 7;
                                                                                                                                                                                                                                                                                                                       IDENTIFYING ADHESIN AND ADHESIN-LIKE POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
                   Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
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Best Local :
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 Matches
                                   Query Match
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US-11-052-554A-139
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US-11-052-554A-139
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CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
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US-11-052-554A-152
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APPLICANT: Sachdeva, et al.
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 139
SEQ ID NO 139
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                          Best Local Similarity
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
                                                                                                                                         LENGTH: 1306
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                      ORGANISM: Mycobacterium tuberculosis H37Rv
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o. US20050288866A1
  Conservative
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  15.8%; Score 75.5; 1
34.1%; Pred. No. 13;
tive 11; Mismatches
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31.3%; Pred. No. 4.9;
11;
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                                                DB 7;
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  20;
                                             Length 1306;
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    Indels
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    25;
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RESULT 15
US-11-052-554A-159
IS-quence 159, Application US/11052554A
Publication No. US20050288866A1
Publication No. US20050288866A1

Publication No. US20050288866A1

GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
PILE REFERENCE: 30853/40359A
CURRENT PAPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SEQ ID NO 159
LENGTH: 837
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis H37RV
US-11-052-554A-159
Search completed: April 14, 2006, 18:42:11 Job time : 5.1937 secs
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                                                                                                                                                                                                                                            10 AADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASAQ 69 | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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#### ALIGNMENTS

# AAW72928 standard; protein; 139 \$

AAW72928;

Mycobacterium tuberculosis antigen RD1-ORF4.

(first entry)

21-JAN-1999

Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen; infection.

Mycobacterium tuberculosis.

WO9844119-A1

08-OCT-1998.

01-APR-1998; 98WO-DK000132

02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 97DK-00000376. 97US-0044624P. 97DK-00001277.

(STAT-) STATENS SERUM INST.

98US-0070488P

Andersen P, Oettinger T, Nielsen R, Florio W; Rosenkrands I, Weldingh K, Rasmussen PB;

WPI; 1998-542705/46. N-PSDB; AAV63938.

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. ę

Claim 1; Page 198; 163pp; English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

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                   The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; rusion polypeptide; pharmaceutical; vaccination; M. af CFP7B; CFP29; CFP27; CFP30A; RD1-OCFP25A; CFP30B; CFP7B.
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98US-0070488P.
98WO-DK000132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ntide; T-cell epitope; ESAT-6; MPT59; T
M. africanum; M. bovis; CFP7A; CFP30;
RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
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Pred. No. 6.8e-63;
     useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response; infection; epitope; ESAT-6; MPT59; TB;
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The invention relates to a novel DNA derived from a human adult brain, tonsil, hippocampus and human fetal brain and its encoded polypeptide, given in the specification. The novel DNA is useful as a diagnostic agent. The encoded polypeptide is useful as a reagent for screening pharmaceutical compounds which inhibit the biological activity of the polypeptide. A gene containing the novel DNA is useful as a probe for diagnosing the increased expression of damage, mutation or expression reduction in the human DNA. This sequence represents the protein derive from a novel human DNA sequence used in the screening and disgnostic method of the invention. Note: This sequence is an embedded protein tal from the coding DNA shown in the sequence listing of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP30A or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MFT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, RD1-ORF3, RD759-ESAT6, ESAT6-MPT59, CFP30A, CFP16, CFP19, CFP23A, CFP30B, CFP70B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                 hippocampus and human fetal whole brain and encoding as gene diagnostic agent.
                                                                                                                                                                                                                                                                                                       WPI; 2003-793311/75
N-PSDB; AEB86042.
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                                                                                                                                                                                                    Claim 4; SEQ ID NO 20; 87pp; Japanese
                                                                                                                                                                                                                                                                       Novel DNA derived from human adult brain,
                                                                                                                                                                                                                                                                                                                                                        (KAZU-)
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Pred. No. 6.8e-63;
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reticulendotheliosis viral oncogene-B Rel homology domain (RelB RHD).
The invention also relates to a method of identifying at least one test compound that alters binding of RelB RHD to the RelB-kappa-B sequence involving contacting the nucleotide sequence with the polypeptide sequence in the presence and absence of the test compound and detecting sequence of the test compound and detecting altered specific binding of the nucleotide with the polypeptide in the presence of the test compound and detecting altered specific binding of the nucleotide with the polypeptide in the presence of the test compound compared to that in the absence of the test compound that alters binding of RelB Rel homology domain (RelB RHD) with RelB-C that alters binding of RelB Rel homology domain (RelB RHD) with RelB-C nuclear factor kappa-B kinase alpha (IKK-alpha) subunit related pathologies. The isolated nucleotide segments are effectively and selectively recognized by RelB:p52 in comparison to ReaL:p50 and RelB:p50 domains. The isolated mucleotide sequence does not bind to RelB, ReaL, p50, RelB:p50, ReaL:p50 and ReaL:p50 and RelB; ReaL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences mediating functions of inhibitor of nuclear factor kappa-B kinase alpha subunit useful for identifying therapeutic compounds that alter the subunit related pathologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reticuloendotheliosis viral oncogene-B Rel homology domain; RelB nuclear factor kappa-B; NFk-B; gene expression.
                                                                                                                                                                                                                                                           The invention
                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 130; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-273503/28.
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Pred. No. 0.21
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                          Modulating a steroid receptor or steroid receptor process for treating onset of labor and cancer, comprises administering a polypyridimine tribinding protein-associated splicing factor polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the nucleotide sequence with a polypeptide having a RelB RHD inc: transcription of a required nucleic acid sequence thant is operably to the nucleotide sequence and links induction of chemokines to activation of the IKK-alpha-dependent NF-kappa B signaling pathway. sequence represents an NFk-B protein of the invention.
                                                                                                                                                                                      GENBANK;
                                                                                                                                                                                                                              Lye S,
                                                                                                                                                                                                                                                                                                                                     WO2005068501-A1
                                                                                                                                                                                                                                                                                                                                                                             parturition;
                                                                                                                                                                                                                                                                                                                                                                                                           Human PSF proline/glutamine rich polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB31351 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                      15-JAN-2004; 2004US-0536598P
                                                                                                                                                                                                                                                                                           14-JAN-2005;
                                                                                                                                                                                                                                                                                                                 28-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                        Protein-associated splicing factor; PSF; PSF-A; labor; premature labor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB31351;
                                                                                                                                                                                                                                                   (MOUN)
                                                                                                                                                                                              2005-522812/53
DB; AEB31356, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                   MOUNT SINAI HOSPITAL
                                                                                                                                                                                                                              Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                       AAH51192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPPGAPPPTPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPPPQDSSKPVVAQGPGPAPGVGSTPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                            2005WO-CA000042
                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gynecological; tocolytic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                               AEB31357.
                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SSGVPTTPPQAGGPPPPPAAVPGPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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The invention relates to a method of modulating a steroid receptor or a process mediated by a steroid receptor in a cell comprising administering a polypyridimine tract binding protein-associated splicing factor (PSF) polypeptide, a polypucleotide encoding a PSF polypeptide (PSF) polymucleotide), an isolated complex of a PSF polypeptide and a steroid receptor (PSF complex) and/or their agonist or antagonist. The invention also relates to a method of inhibiting transactivation domains of a steroid receptor in a cell by administering to the cell a PSF polypeptide, polymucleotide, complex, and/or their agonist, a method of stimulating transactivation domains of a steroid receptor in a cell by

a PSF polypeptide,

polynucleotide and/or a PSF

Claim

22;

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91pp;

English.

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cc mediated by a steroid receptor or characterized by an abnormality in a condition interaction between a PSF polypeptide and a steroid receptor by cc disrupting or promoting the interaction in cells or inhibiting or promoting the activity of a PSF complex, and a method of preventing or treating a condition mediated by a steroid receptor by administering or cc promoting the activity of a PSF complex and a method of preventing or treating a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor or process mediated by a steroid receptor or characterized by an abnormality in a steroid receptor signal transduction pathway and/or an abnormality in a steroid receptor or characterized by an condition mediated by a steroid receptor or characterized by an abnormality in a steroid receptor or characterized and a steroid receptor. The methods are useful for preventing or treating a condition mediated by a steroid receptor in a subject and for evaluating a condition pathway and/or an abnormal level of interaction between a PSF polypeptide and a steroid receptor and a test substance, where the PSF polypeptide and a progesterone receptor and a test substance, where the PSF polypeptide and receptor bind to form a complex and comparing to a control in the absence of the substance to determine if the substance constrollates the onset of labor. The methods are also useful for preventing or treating a condition mediated by a subject. For preventing or treating a condition mediated by a substance to determine if the substance constrollated to the receptor and thus regulates the onset of labor. For inducing labor in a subject in a constrollate of the substance to determine if the substance constrollated by a substance to determine if the substance constrollated by a substance constrollated by a condition mediated by a substance construction in an animals, such as domestic construction in animals, such as domestic construction in animals, such as domestic construction in animals, such as
RESULT 6
ABO14750
ID ABO1
XX
ABO2
XX
ABO2
XX
DT 25-A
XX
UNOVE
XX
HUMB
ETA
KW HUMB
KW BChi
KW BChi
KW BChi
KW BChi
KW 1nfl
KW COlo
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KW HOMO
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Best Local :
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                                                                                                                                                            Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; parkinson's disease; epilepsy; multiple sclerosis; schizophrenis; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia;
   WO2003023002-A2
                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protein #123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO14750 standard; protein; 1526
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                                                                                                                                       infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPPGAPPPTPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPPPQDSSKPVVAQGPGPAPGVGSTPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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Pred. No. 0.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                                                                               CC polypeptide, nucleic acid and antibody are useful as therapeutics, as particularly in the manufacture of a medicament for treating a syndrome CC associated with a human disease, which includes a pathology associated CC with MOVX polypeptide. The DNA encoding the protein is useful in gene CC with MOVX polypeptide. The DNA encoding the protein is useful in gene CC therapy for treating the disease or condition. In particular, the NOVX CC polypeptide or polynucleotide is useful for treating endocrine/
CC metabolism-related diseases (e.g. obseity or diabetes), central nervous CC system disorders (e.g. Alzheimer's disease, Parkinson's disease, CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune CC estematory disearers (e.g. sporiasis, allergy, lupus erythematosus, CC asthma, inflammatory bowel disease, rheumatoid arthritis or CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver CC cirrhosis), lung diseases (e.g. colon, lung, liver, breast, ovarian, CC diseases), lung diseases (e.g. viral, bacterial or parasitio). CC These are also useful in developing powerful assay system for functional CC analysis of various human disorders, as well as in diagnostic capplications, and for monitoring the effects of drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein
                                                                                                                  Matches
                                                                                                                                    Query Matc
Best Local
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17-SEP-2001;
17-SEP-2001;
17-SEP-2001;
17-SEP-2001;
19-SEP-2001;
20-SEP-2001;
20-SEP-2001;
25-SEP-2001;
25-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieger
Lepley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a new isolated polypeptide (NOVX). polypeptide, nucleic acid and antibody are useful as there
                                                                                                                                                                                        Sequence 1526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001;
07-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-313242/30.
DB; ACD19443.
                                              893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Page 349; 586pp;
           57
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                                                                                o
                                                                                                                  33;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURAGEN CORP.
                                            PPLPGAGIPPPPPLPGVGIPPPPPLPG---AGIPPPPPL----PGAGIPPPPPLPGAGIP
                                                                               PPAPGSDSARSRPAPALG--PDPPASGWFDSGLVPSRPICAASSSAGLPPP-----VP
         PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWV-----AAGGNWPTGVELPGEGIP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan M,
Vernet CAM,
1, Leach MD,
Taupier RJ,
Edinger SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0318120P.
2001US-0318430P.
2001US-032836P.
2001US-0322781P.
2001US-0322816P.
2001US-0322817P.
2001US-0323636P.
2001US-0323636P.
2001US-0323636P.
2001US-0323639P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
2001US-032363P.
                                                                                                                   Conservative
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                                                                                                                                  13.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4, Gorman L, Li L,
Blerman K, Berghs
Catterton B, Kekuda
Shenoy SG, Liu X,
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                   œ
*
                                                                                                                                    Score 104.5;
Pred. No. 1.6;
                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li L, Anderson ..., G
Berghs C, Rothenberg MB, G
Kekuda R, Ji W, Miller CE;
Liu X, Padigaru M, Alsobrook
                                                                                                                                                     DB
                                                                                                                  31,
                                                                                                                                                     6;
                                                                                                                   Indels
                                                                                                                                                     Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                   43;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo X;
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RESULT 7
AAM40927
                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM38642-AAM42213) with mootropic, communosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC system, such as peripheral nervous injuries, peripheral neuropathy and CC alzheimer's, Parkinson's disease, Huntington's diseases, such as CC alzheimer's, Parkinson's disease, Huntington's diseases, such as CC alzheimer's, Parkinson's disease, Huntington's diseases, andotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders. Note: The sequence data for this patent did not form CC part of the printed specification
Query Match
Best Local Similarity
Matches 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999;
21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                      as central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442253/47
N-PSDB; AAI60083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
Wang Z,
Goodrich
                                                                                                                                                                                                                                                                                                                                        2; SEQ ID NO 5858; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00471275.
; 2000US-00488725.
; 2000US-00552317.
; 2000US-00598042.
; 2000US-00620312.
; 2000US-006213450.
; 2000US-00662191.
; 2000US-00693036.
; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
                13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac
                                                                                                                                                                                                                                                                                                                                                                      injuries.
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Xu C,
IC RT;
Score 103.5; DB 4;
Pred. No. 0.42;
6; Mismatches 41;
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The invention relates to a method of modulating a steroid receptor or a CC process mediated by a steroid receptor in a cell comprising administering CC a polypyridimine tract binding protein-associated splicing factor (PSP) CC polypyridimine tract binding protein-associated splicing factor (PSP) CC polypyridimine tract binding protein-associated splicing factor (PSP) CC polypyridimine tract binding a PSP polypeptide (PSP) CC polypucleotide), an isolated complex of a PSP polypeptide and a steroid receptor (PSP complex) and/or their agonist or antagonist. The invention CC also relates to a method of inhibiting transactivation domains of a steroid receptor in a cell by administering to the cell a PSP complex, and/or their agonist, a method of CC polypeptide, polynucleotide, complex, and/or their agonist, a method of complex antagonist, a method of treating a subject with a condition CC mediated by a steroid receptor or characterized by an abnormality in a steroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSP polypeptide and a steroid receptor by CC disrupting or promoting the interaction in cells or inhibiting or CC promoting the activity of a PSP complex, and a method of preventing or treating a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor or inhibiting. The methods are useful for modulating a steroid receptor or characterized by an accondition mediated by a steroid receptor or characterized by an accondition mediated by a steroid receptor or characterized by an accondition pathway and/or an abnormal level of interaction between a PSP polypeptide and a steroid accondition pathway and/or an abnormal level of interaction between a PSP polypeptide and a steroid condition pathway and/or an abnormal level of interaction between a PSP polypeptide and a steroid condition pathway and/or an abnormal level of interaction between a PSP polypeptide and a steroid condition pathway and/or an abnormal level of interaction betwee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22;
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Matches 35
                                                                       Modulating a steroid receptor or steroid receptor process for treating onset of labor and cancer, comprises administering a polypyridimine trabinding protein-associated splicing factor polypeptide.
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                                  Claim 22; SEQ ID NO 4; 91pp; English
                                                                                                                                                              GENBANK; AAH04534.
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28.0%;
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Pred. No. 0.63;
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The invention relates to a method of modulating a steroid receptor or a

Protein-associated splicing factor; PSF; PSF-F; labor; parturition; cytostatic; gynecological; tocolytic.

premature labor;

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RESULT 10
AEB31352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc stroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSF polypeptide and a steroid receptor by complex and promoting the interaction in cells or inhibiting or promoting the activity of a PSF complex, and a method of preventing or treating a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor or process mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor signal transduction pathway and/or an ceptor. The methods are useful for preventing or treating a condition mediated by a steroid receptor in a subject or individual having a condition.

Cc abnormal level of interaction between a PSF polypeptide and a steroid receptor. The methods are useful for preventing or treating a condition mediated by a steroid receptor in a subject and for evaluating a control in the absence of the substance to flabor by reacting to a control in the absence of the substance to determine if the substance of preventing and/or treating pre-term labor, for inducing labor in a subject, for preventing or treating a condition mediated by a progesterone receptor, for modulating the onset of labor. For preventing condition for reducing the order to the receptor of the substance of premature labor, for stopping labor preparatory to Cesarean delivery or for controlling the timing of parturition in animals, such as domestic on timals. This sequence represents a human SFPQ protein used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8×4×4×4×4×4×4×4×8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                        Human PSF short form, PSF-F.
                                                                                                                                                                           06-OCT-2005
                                                                                                                                                                                                                         AEB31352;
                                                                                                                                                                                                                                                                       ABB31352 standard; protein; 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                106 -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 SAPPGAPPPTPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105
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28.0%;
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Pred. No. 0.77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SSGVPTTPPQAGGPPPPPAAVPGPGP 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 634;
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CC abnormality in a steroid receptor signal transduction pathway and/or an CC abnormality in a steroid receptor signal transduction pathway and/or an CC abnormality in a steroid receptor in a subject and for reacting a condition CC mediated by a steroid receptor in a subject and for evaluating a CC substance for its ability to regulate the onset of labor by reacting a CC PSF polypeptide and a progesterone receptor and a test substance, where CC the PSF polypeptide and receptor bind to form a complex and comparing to CC a control in the absence of the substance to determine if the substance CC stimulates or inhibits the binding of the PSF polypeptide to the receptor and thus regulates the onset of labor. The methods are also useful for CC greventing and/or treating pre-term labor, for inducing labor in a CC subject, for preventing or treating a condition mediated by a CC greterm or premature labor, for reducing the onset of labor, for preventing CC pre-term or premature labor, for reducing the risk of pre-term or premature labor, for preparatory to Cesarean delivery or CC premature labor, for stopping labor preparatory to Cesarean delivery or CC premature labor, for preventing in the onset of labor, such as domestic controlling the thing of parturition in animals, such as domestic controlling the thing of parturition in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC process mediated by a steroid receptor in a cell comprising administering conjugation and a steroid receptor in a cell comprising administering conjugation apolynucleotide encoding a PSF polypeptide (PSF) coplypeptide, a polynucleotide encoding a PSF polypeptide (PSF) coplypeptide (PSF) complex) and/or their agonist or antagonist. The invention collower of the polynucleotide in the invention collower of the polynucleotide in the invention collower of the polynucleotide in a cell by administering to the cell a PSF complex, and/or their agonist. The invention collower of the polynucleotide in a cell by administering to the cell a PSF collower of their agonist, a method of complex in a cell by administering to the cell a PSF collower of their agonist, a method of complex antagonist, a method of treating a subject with a condition complex antagonist, a method of treating a subject with a condition complex antagonist, a method of treating a subject with a condition complex antagonist in a steroid receptor by an abnormality in a steroid receptor signal transduction pathway and/or an abnormal level of complex in a cell by a steroid receptor by administering or complex in the activity of a PSF collower of their agonist or inhibiting or complex and/or their agonist or antagonist. The methods care useful for modulating a steroid receptor by administering a condition mediated by a steroid receptor or process mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or characterized by an analyce and or an anomality in a steroid receptor or characterized by an analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce and or analyce analyce and or analyce and or analyce and or analyce analyce and or analyce an
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 669 AA;
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                                                                                                                                                      PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                            PPAPGSDSAR-----SRPAPALGPDPPASG----
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                                           immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitys such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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N-PSDB; AAI58297.
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2286; 10078pp; English
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21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          central nervous system injuries.
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7 2000US-00598042.

7 2000US-00620312.

7 2000US-00653450.

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      The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying an agent CC expressed in an animal subjected to pain, a method for identifying a compound which regulates CC compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound control of the polynucleotide, a method for more of the polynucleotide, a method for more of the polynucleotide sequence the composition and control of the polynucleotide sequence the composition and control of the polynucleotide sequence the composition and control of the polynucleotide sequence the composition and control of the polynucleotide sequence control of the polynucleotide sequence the composition and control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the polynucleotide sequence control of the control of the control of the control of the control of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                            Human;
spinal
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                          Woolf C,
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(FARB )
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BAYER AG.
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The invention discloses a composition comprising two or more isolated or human polymucleotides or a polymucleotide which represents a fragmu derivative or allelic variation of the nucleic acid sequence. Also

fragment

rat

New composition comprising preparing a medicament for

two or more isolated polypeptides, useful treating pain in an animal.

for

Claim 1; Page; 1017pp;

English

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01-NOV-2001;
26-NOV-2001;
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(GEHO ) GEN HOSPITAL CORP
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ftp.wipo.int/pub/published_pct_sequences.
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2001US-0346382P.
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Pred. No. 0.87;
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RESULT 15
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Best Local :
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spinal
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                                                spared
                                                                                                                          Human Protein
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                                                  SNI; Chung.
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Pred. No. 0.8
                                                                     chronic constriction injury; CCI;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                   6 PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA 45
GPKQG 201
                                                                                SAPPGAPPPTPP----
                                                                                                                      SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
                                                                                                                                                                 PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D'urso D,
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                              13.4%;
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                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                Score 103.5; Di
Pred. No. 0.87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Costigan
                                                                                  -----SSGVPTTPPQAGGPPPPPAAVPGPGP 196
                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                               Indels 43;
                                                                                                                                                                                                                                                                                     Length 707;
                                                                                                                                                                                                                                             Gaps
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Search completed: April 14, 2006, 17:18:42 Job time : 55.857 secs

Sequence: Title: Perfect score: US-10-620-246-90 774 MRVNDPPAPGSDSARSRPAP....

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

.....RIDAIGSSFSKSVLTAVSAW 139

Searched:

Total number of hits satisfying chosen parameters:

283416

283416 seqs, 96216763 residues

Minimum Maximum 멂 seq length: seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su summaries

pir2:\*
pir3:\* pir1:

Database

PIR\_80:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Regult		Ouerv				
NO.	Score	Match	Length	B	ID	g g
1	103.5	13.4	707	N	A46302	PTB-associated spl
N	97.5	12.6	240	N	D70894	н
ω	93.5	12.1	365	N	A39481	serum response fac
4	92	•	419	N	G70602	hypothetical prote
ຫ	92	11.9	980	N	S54986	н
6	91.5	11.8	502	N	A55197	Wiskott-Aldrich sy
7	91.5	11.8	1446	Н	A45344	immediate-early pr
8	91		364	N	I48188	gene NKx6.1 protei
9	90.5	11.7	380	N	851797	vasodilator-stimul
10	10	11.6	924	N	F87103	initiation factor
11	89	•	403	N	S52796	prpL2 protein - hu
12	89	11.5	744	N	T35192	probable ABC trans
13	88.5	11.4	451	N	A41651	retinoic acid rece
14	œ	11.4	1460	Н	EDBEIF	immediate-early pr
15	87.5	•	625	N	S18420	regulatory protein
16	87.5	٠	817	N	S51342	verprolin - yeast
17	87	•	533	N	S37781	retinoid X recepto
18	87		1560	N	T00080	hypothetical prote
19	86.5	11.2	446	N	A34418	H-2 region II bind
20	86.5	11.2	448	N	D41727	retinoid X recepto
21	86.5	11.2	520	N	I84718	RXR-betal isoform
22	98		742	N	P84643	a
23	86	11.1	839	N	T04859	extensin homolog F
24	86	11.1	907	N	E96636	hypothetical prote
25	85.5	11.0	1058	N	T13286	cappuccino gene pr
26	85	11.0	211	N	B89716	protein F45B8.3 [i
27	85		241	N	T22216	
28	84.5	10.9	745	N	S13586	
29	84	10.9	721	N	B70766	hypothetical prote

RESULT D70894

45	44	43	42	41	40	9	38	37	36	35	34	ω ω	32	31	30
81.5	81.5	81.5	81.5	82	82	82.5	82.5	82.5	82.5	82.5	83	83	83.5	84	84
10.5	10.5	10.5	10.5	10.6	10.6	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.8	10.9	10.9
1820	373	319	133	1213	907	1278	1255	838	576	129	564	342	670	2357	846
N	N	N	ผ	N	N	N	N	۳	N	N	N	N	N	N	N
A55494	A47234	F75420	C86473	A41724	A45560	T27925	T31065	VGBEG1	T36729	T06174	H70804	S18649	F84540	A59249	H70599
latent transformin	homeobox protein H	hypothetical prote	arabinogalactan-pr	limb deformity (ld	sporozoite surface	hypothetical prote	diaphanous protein	glycoprotein H pre	probable serine/th	pZE40 protein - ba	hypothetical prote	homeotic protein H	hypothetical prote	class VII unconven	hypothetical prote

### ALIGNMENTS

밁 Ś 밁 δ 밁 8 A;Cross-references: GDB:138275
A;Map position: 4g-4g
G;Keywords: alternative splicing; pre-mRNA splicing; surface antigen
F;298-359/Domain: ribonucleoprotein repeat homology <RRM1>
F;372-438/Domain: ribonucleoprotein repeat homology <RRM2> A;Molecule type: mRNA
A;Residues: 1-707 <PAT:
A;Cross-references: UNIPROT:P23246; UNIPARC:UPI00001358B9; EMBL:X70944; NID:g38457; PID
A;Note: sequence extracted from NCBI backbone (NCBIP:127206)
R;Gower, H.J.; Moore, S.E.; Dickson, G.; Elsom, V.L.; Nayak, R.; Walsh, F.S.
Development 105, 723-731, 1989 R;Patton, J.G.; Porro, E.B.; Galceran, J.; Tempst, P.; Nadal-Ginard, B. Genes Dev. 7, 393-406, 1993
A;Title: Cloning and characterization of PSF, a novel pre-mRNA splicing factor. A;Reference number: A46302; MUID:93194059; PMID:8449401
A;Accession: A46302 PTB-associated splicing factor, long form - human

N;Alternate names: myoblast cell surface antigen 24.1D5; polypyrimidine tract-binding properties: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text\_change 31-Dec-2004

C;Accession: A46302; A43557; S29995 A;Status: preliminary A;Molecule type: mRNA A;Residues: 312-707 <GOW> A;Cross-references: UNIPARC:UPI000016A1B4; GB:X16850; NID:g23711; PIDN:CAA34747.1; PID: A;Title: Cloning and characterization of a myoblast cell surface antigen defined by A;Reference number: A43557; MUID:90091812; PMID:2480877 A;Accession: A43557 C;Genetics: A;Gene: GDB:SFPQ; PSF Query Match Best Local S Matches 35 106 197 GPKQG 201 159 SAPPGAPPPTPP 99 46 SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105 l Similarity 35; Conserv 6 PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA 45 -PKIG 109 PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT Conservative 13.4%; Score 103.5; DI Pred. No. 0.35; 6; Mismatches DB 2; Length 707; -SSGVPTTPPQAGGPPPPPAAVPGPGP 196 Indels 43; Gaps 158 24

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probable pra protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: D70894

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: D70894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serum response factor-related protein 2 - human N,Alternate names: myocyte-specific enhancer factor xmef2; RSRF2 C;Species: Homo sapiens (man) C;Pate: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change C;Accession: A39481; S25832; S24468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:053426; UNIPARC:UPI000013216B;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: pra
S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Human SRF-related proteins: DNA-binding properties A;Reference number: A39481; MUID:92084105; PMID:1748287 A;Accession: A39481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Pollock, R.; Treisman, R.
Genes Dev. 5, 2327-2341, 1991
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                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                             Genes Dev. 6, 1783-1798, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-365 < POL>
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Best Local S
Matches 36
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                                                                                                                                                                                                                                                                               Residues: 1-365 <YUY>
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                                            PPVGAEAWARRVPQPAAPPRRP------PQSASSLSASLRPPGAPATFLRPSP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSCVTSISEYDVGQFCVSQPSMIGQLVQWLLSVGGLAYLVWNYGYRQGTIGSSIGKSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPSAGGYAPPPPGPAIRTMPTESYTPWITRVLAAFIDWAPYVV--LVGIGWVIMLVTQT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPPGGGHEPPPAA---PPGG----SGYAPPPP---PSSGSGYPPPPPPPGGGAYPP
  TCCSG----WVSCC-IGPLISPSWPRVWVAAGGNWPT----GVELPGEGIPK 107
                                                                                   PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGL-PPPVPPTWLNNDV
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                                                                                                                             12.1%; Score 93.5; DB 2; llarity 32.7%; Pred. No. 1.3; Conservative 4; Mismatches 39;
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Pred. No. 0.
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                                                                                                                                                                                                                                                             PII
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Genetics 139, 537-547, 1995
A;Title: Identification of developmental regulatory genes
A;Reference number: S54986; MUID:95229045; PMID:7713416
A;Accession: S54986
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A; Residues: 1-980 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:005589;
A;Experimental source: strain H37Rv
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A; Residues: 1-419 < COL>
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                        114 WLAPGSRIDAIGSSFSKSVLTAVSAW
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Similarity 25.3%;
37; Conservative 1
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                                                                                                                                                      PPPPGAGAAPPPPPP---
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                                                                                                                                                                                                                                                           Score 92;
Pred. No.
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RESULT 4
G70602
hypothetical protein Rv1004c - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Species: 17-U1-1998 #sequence_revision 17-Ju1-1998 #text_change 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C;Accession: S54986
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A;Authors: Sqares, F. Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI00001688EC; EMBL:L36341; NID:g540283; PID:g540284
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RSTSAAAASYWWCICVPPPPPPPGTVIGGWRANYLASQG-----APSHAIP----VMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNNDV 64
                                                              LINDVTCCSGWVSCCIGPLISP-----SWPRVWVAAGGNWPTGVELPGEGIPKIGFVVL 113
                                                                                                                                                                                               PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGL---PPPPVPPT---W 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTATPSGPAAAEHAVPA--PFEPVADTIAPGLVPRPGVPAAAAVPRVGPPAVPGLPN---
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                                                                                                                                    -ĠĹGGPPÞLPSPŚŚTGWFWWTPAASPSTWWFW 532
                                                                                                                                                                                                                                                                                                 DB 2; Length 980;
                                                                                                                                                                                                                                                                     60; Indels
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SIRPKKKCLKAL--HWDKVDTPQVTVW

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A;Molecule type: mRNA
A;Residues: 1-424, 'PG', 427-502 <DER>
A;Cross-references: UNIPARC:UPI000017C422; GB:U12707; NID:g695150
A;Cross-references: UNIPARC:UPI000017C422; GB:U12707 (PIDN:AAA62663.1)
A;Note: the translated sequence in GenBank entry HSU12707 (PIDN:AAA62663.1)
R;Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, P.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 4706-4710, 1995
Proc. Identification of mutations in the Wiskott-Aldrich syndrome gene ar
A;Title: Identification of mutations in the Wiskott-Aldrich syndrome gene ar
A;Reference number: I38931; MUID:95273432; PMID:7753869
A;Accession: I38931
            A;Reference number: A45344; MUID:91021039; PMID:2171211
A;Accession: A45344
                                                                           immediate-early protein - suid herpesvirus 1 (strain Kaplan)
if;Species: suid herpesvirus 1
if;Species: suid herpesvirus 1
if;Cpate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
if;Accession: A45344
if;Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
if;Accession: A45344
if;Cipate: A;C; Baces, V; Schirm, S; Schwyzer, M.
virology 179, 365-377, 1990
A;Title: Pseudorables virus immediate-early gene overlaps with a
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A;Rosidues: 1-328, 'A',330-366,'LHHHPLQLLDVLDHCPLHPLELVGHPCHH','HRHHRHRRPAPGWDQPLPHSLILWC
A;Rcesidues: UNIPROT:P42768; UNIPARC:UPI000017C421; GB:U12707
A;Note: this sequence is corrected in reference A55197
A;Note: this sequence is corrected in reference A55197
A;Derry, J.M.J.; Ochs, H.D.; Francke, U.
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A;Map position: Xpl1.23-Xpl1.22
A;Note: defects in this gene may result in Wiskott-Aldrich syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-502 < KWA>
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A55197
Wiskott-Aldrich syndrome protein WASP -
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Status: translation
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Date: 23-Mar-1995 #sequence revision 24-Nov-1999

Accession: A54747; A55197; I38931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPIVGGNKGRSGPLPPVPLGIAPPPPTPRGPPPPGRGG-----PPPPPPPATGRSGPLPP 383
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not shown
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27.9%;
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PMID:8069912
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C;Date: 15-Jul-1995 #sequence_revision 09-Mar-1996 C;Accession: S51797; S55526 R;Haffner, C:; Jarchau, T.; Reinhard, M.; Hoppe, J. EMBO J. 14, 19-27, 1995 A;Title: Molecular cloning, structural analysis and A;Reference number: S51796; MUID:95129547; PMID:782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
I48188
A; Molecule type: mRNA
A; Residues: 1-380 < HAF1>
                                                                                                                                                                                 vasodilator-stimulated phosphoprotein - human
C;Species: Homo sapiens (man)
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;237-293/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Pancreatic beta cells express a diverse set of homeobox genes. A;Reference number: I48185; MUID:95083670; PMID:7991607 A;Accession: I48188 A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene NKx6.1 protein - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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                                         A; Accession: S51797
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Pred. No.
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Pred. No. 6.7;
1; Mismatches 35;
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                                                              PMID: 7828592
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                                                                                                                                                             #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----CAASSSAGL----
                                                                                                                        Lohmann, S.M.; Walter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1446;
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A;Cross-references:

UNIPROT: p50552; UNIPARC: UPI0000001C69; EMBL: Z46389; NID: g624963;

PI

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C;Accession: F87103

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R. R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holr eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R. A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: F87103

A;Residues: 1-924 <STO>
A;Cross-references: UNIPROT:Q9Z519; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g1309337

C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: $55240
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 11-32;87-96;140-154;255-282;297-303;305-322 <HAP2>
A;Residues: 11-32;87-96;140-154;255-282;297-303;305-322 <HAP2>
A;Cross-references: UNIPARC:UPI000017C415; UNIPARC:UPI000017C416; UNIPARC:UPI000017C417
C;Keywords: phosphoprotein
                                                                                                                                                                                                                         prpL2 protein - human (fragment)
c;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 10-Nov-1995
C;Accession: $52796
R;Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
F87103
                                                                                                                                                                A; Reference number: S52796
A; Accession: S52796
                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1995
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C;Date: 20-Apr-2001 #sequence_revision
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Query Match
Best Local S
Matches 26
                                                                           ;Molecule type: mRNA
;Residues: 1-403 <RUH>
;Cross-references: UNIPARC:UPI000017C32C; EMBL:X86019; NID:g762950;
                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT:Q9Z519; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g13093370;
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGWVSCCIGPLISPS--WPRVWVAAGGNWP----TGVELPGEGIPKIGFVVLWLAP-GS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHPG-----PAPKPGGRPPRVG-----NNPFSSAQSVA-RPIPRPP-----
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42.3%;
                 11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
Score 89; DB 2;
Pred. No. 3.3;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB 2;
Pred. No. 6.4;
4; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-Apr-2001 #text_change
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  20;
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                                         Length 403
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    Indels
  24;
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                                                                                  PID:g762951
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C;Accession: A41651
R;Yu, V.C.; Delsert, C.; Andersen, B.; Holloway, J.M.; Devary, O.V.; Naeaer, A.M.; Kim, Cell 67, 1251-1266, 1991
A;Title: RXRbeta: a coregulator that enhances binding of retinoic scid, thyroid hormone A;Reference number: A41651; MUID:92103690; PMID:1662118
A;Accession: A41651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
T35192
                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI0000170BFE; GB:M81766; NID:g206602; PIDN:AAA42025.1; C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                            retinoic acid receptor coregulator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Seeger, K.; Harris, D.; Parkhill, submitted to the EMBL Data Library, A;Reference number: Z21571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ABC transporter - Streptomyces coelicolor C;Specias: Streptomyces coelicolor C;Specias: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004 C;Accession: T35192
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A; Residues: 1-451 < YUA>
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A; Residues: 1-744 <SEE>
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                                                                                                                                                                                                             F,121-367/Domain: erbA transforming protein homology
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A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                      Similarity
VTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI--PKIGFVVLMLAP----
                                                          ÞÞSSÞÞGÞРHTPSAÞÞÞÞÞÞÞÞÞLGŠ-----ÞFPVÍSSSMGSÞĞLÞÞÞAÞÞGF----
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                                                                                                PPA--PGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNND 63
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                                                                                                                                    11.4%; Score 88.5; 1
27.7%; Pred. No. 4;
tive 12; Mismatches
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April 1998
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                                                                                                                                                                                                                   <ERBA>
                                                                                                                                                                         Length 451;
                                                                                                                                      Indels
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                                                                                                                                      39;
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RESULT 15
S18420
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C;Superfamily: response regulator (sigma54-dependent transcriptional activator), FhlA ty
C;Superfamily: nesponse regulator (sigma54-dependent transcriptional activator), FhlA ty
C;Keywords: DNA binding; P-loop; transcription regulation
C;Keywords: NA bolymerase sigma factor interaction domain homology <8FI>
F;205-426/Demain: RNA polymerase sigma factor interaction domain homology <8FI>
F;233-240/Region: nucleotide-binding motif A (P-loop) #status atypical
F;300-304/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S18420
R;Liang, Y.Y.; Kaminski, P.A.; Elmerich, C.
Mol. Microbiol. 5, 2735-2744, 1991
A;Title: Identification of a nifA-like regulatory gene of Azospirillum brasilense A;Reference number: S18420; MUID:92140038; PMID:1779783
A;Accession: S18420
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Nucleic Acids Res. 17, 4637-4646, 1989
A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vi A;Reference number: S04713; MUID:89315207; PMID:2546124
A;Accession: S04713
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A;Residues: 1-625 <LIA>
A;Cross-references: UNIPROT:P30667; UNIPARC:UPI000013007F; EMBL:X60714; NID:g38677; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory protein nifA - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
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A;Cross-references: UNIPROT:P11675; UNIPARC:UPI000017497B
A;Cross-references: UNIPROT:mmediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                श
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C;Species: suid herpesvirus 1
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Matches 26
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Matches 32; Conservat
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557 APP 559
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                                                 55 VPP 57
                                                                                                                                                   7 PAP----GSDSARSRPAPALGPDP-----PASGWFDSGLVPSRPICAASSSAGLPPP 54
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                                                                                                                                                                                                                                 Similarity
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                                                                                                       PAPVPEPAGAAAARGRPARRVVPRPLAGLRRRPAGG----SG--PPDPACPCPSRAPLPPQ 556
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Search completed: April 14, 2006, 17:34:33 Job time : 9.15065 secs

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Q5FIX1 HUMAN
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RESULT 2 Q86VG2_HUMAN Q86VG2_HUMAN PRELIMINARY, PRT; 707 AA.  ID Q86VG2; AC Q86VG2; DT 01-JUN-2003 (TrEMBLrel. 24, Created) DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) DT 01-JAR-2004 (TrEMBLrel. 26, Last annotation update) DE Splicing factor proline/glutamine rich (Polypyrimidine tract binding DE protein associated).	CHERY MACCH  13.87 SCORE 108.57 LENGTH 334;  Best Local Similarity 30.88; pred. No. 1.7;  Best Local Similarity 30.88; pred. No. 1.7;  Matches 49; Conservative 9; Mismatches 52; Indels 49; Gaps 9;  2 RVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGL 51  177 RVESPPERABPPASPTEPSPPPPPSPPASPSLPPAGAIDTRDTGSSEPQ 225  52 PPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGE 103	HUMAN PRELIMINARY; PRT; 334 AA.  -2002 (TrEMBLrel. 21, Created) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequence update) -2004 (TrEMBLrel. 21, Last sequences; Euteleo -2004 (TrEMBLrel. 21, Euseleo -2004 (TrEMBLrel) -2004 (TrEMBLrel. 21, Euseleo -2004 (TrEMBLrel) -2004 (TrEMBLE) -2004 (TrEMBLrel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrEMBLRel) -2004 (TrE	

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max. T.I., Schaetz T.E.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Stapleton M., Jouen B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Stapleton M., Jouen B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Usdin T.B., Toshiyki S., Carninci P., Prange C.,
RX Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RX RA S.S., Loquellano N.A., Peters G.J., Lu X., Glabs R.A.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RY Teneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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05VU37 HUMAN 1
Q5VU37;
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Pfam; PF08075; NOPS; 1.

Pfam; PF08075; RRM 1; 2.

Pfam; PF00076; RRM; 2.

SMART; SM00360; RRM; 2.

PROSITE; PS0102; RRM; 2.

ACTIVATOR: DNA damage; DNA repair; DNA-binding; Nuclear protein;

ACTIVATOR: DNA damage; DNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG00000116560; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0000398; F:nuclear mRNA splicing, via spliceosome;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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HSSP; O08583; 1NO8.
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TISSUB=Brain;
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                                                                                                                GPKQG
                                                                                                                                                     -PKIG 109
                                                                                                                                                                                          SAPPGAPPPTPP
                                                                                                                                                                                                                             SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105
                                                                                                                                                                                                                                                                 PPPPPQDSSKPVVAQGPGPAPGVGSTPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT
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                       PRELIMINARY;
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                       PRT;
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EMBL; AL646016; CAI17121.1; JOINED; G
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0016043; P:cell organization #
GO; GO:007242; P:intracellular sign#
InterPro; IPR000591; DEP.
InterPro; IPR009408; Drf FH1.
InterPro; IPR003104; FH2_actin_bd.
InterPro; IPR001120; Lectin_legB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2005) to the EMEL/GenBa
EMBL; AL590490; CAH70931.1; -; Genomic
EMBL; AL513142; CAH17121.1; -; Genomic
EMBL; AL646016; CAH17099.1; -; Genomic
EMBL; AL5359918; CAH70931.1; JOINED; Ge
EMBL; AL559918; CAH70931.1; JOINED; Ge
EMBL; AL513342; CAH70931.1; JOINED; Ge
EMBL; AL559918; CAH70931.1; JOINED; Ge
EMBL; AL5590490; CAH17121.1; JOINED; Ge
EMBL; AL590490; CAH17121.1; JOINED; Ge
EMBL; AL590490; CAH17099.1; JOINED; Ge
EMBL; AL590490; CAH17099.1; JOINED; Ge
EMBL; AL590490; CAH17955.1; JOINED; Ge
EMBL; AL590490; CAH17099.1; JOINED; Ge
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01-FEB-2005
13-SEP-2005
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PS00307; LECTIN LEGUME_BETA; UNKNOWN 1.
1865 AA; 194918 MW; 202D47DABE981F11
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nilarity 28.7%;
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Pred. No. 13;
8; Mismatches
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ng cascade;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local S
Matches 48
       Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFPQ protein (Fragment)
Name=SFPQ;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Complete
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STRAIN=IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino
Shiba T., Hattori M.;
                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6PIX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6PIX2_HUMAN
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OrderedLocusNames=nfa54870;
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
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HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genomic sequence of Nocardia farcinica . Natl. Acad. Sci. U.S.A. 101:14925-14930(2004). . , AP006618; BAD6039.1; -; Genomic_DNA. lete proteome; Hypothetical protein. ENCE 836 AA; 81926 MW; ACDF5523F8651CDD CRC64
4 C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWINNDVTCCSGWVSCCIGPLISPS--W---PRVWVAAGGNWPTGVBLPGEGIPKIGFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSTGSVDAAMTPDSSEDGTASPSGWAEQGAVPPRD----AAQRGVVPPSGRAEQGAVPPR
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ALGPD-----PPASGWPDSGLVPSRPICAASSSAGLPPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%;
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iaceae; Nocardia.
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Pred. No. 6.6;
L5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC027708; AAH27708.1; -; mRNA.
Ensembl; ENSG00000116560; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IE
InterPro; IPR012677; a b plait_nuc_bd.
InterPro; IPR012975; NOPS.
InterPro; IPR0012975; NOPS.
InterPro; IPR000764; RNP1_RNA_bd.
Pfam; PF08075; NOPS; 1.
Pfam; PF08075; NOPS; 1.
Pfam; PF08075; RRM 1; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
       TISSUE=Placenta;

MEDILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                          SFPQ protein Name=SFPQ;
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                                                                                                                                                                                                                                                                                                                                                                              Q9BSV4 HUMAN
Q9BSV4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA damage; DNA repair.
NON TER 525 525
SEQUENCE 525 AA; 55469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
   Fahey
                                                                                                                                                                                                         NUCLEOTIDE
                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                               Bukaryota;
                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                    TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106
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                                                                                                                                                                                                                                                                ; Metazoa;
Eutheria;
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Metazoa; Chordata; Crau...
Metazoa; Euarchontoglires; F
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Pred. No. 4.6;
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   Madan
                                                                                                                                                                                                                                                                 Primates;
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                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
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GO; GO:0003676; F:nucleic acid binding; IEGO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR012677; a b plait_nuc_bd.
InterPro; IPR012975; NOPS.
InterPro; IPR000504; RNP1_RNA_bd.
Pfam; PP00075; NOPS; 1.
Pfam; PP00076; RRM 1; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
  Patton J. "Cloning
                                                                                                                                                                                                                                                                                                                         P23246; P30808; 01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
splicing factor, proline-and glutamine-rich (binding protein-associated splicing factor) (factor) (PSP) (DNA-binding p52/p100 complex,
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                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
                                                                                               NUCLEOTIDE SEQUENCE (MI
SPLICING, AND FUNCTION
                                              TISSUE=Fetal brain;
MEDLINE=93194059; P
                                                                                                                                                                                                                                                                               DNA-pairing protein) (hPOMp100)
Name=SFPQ; Synonyms=PSF;
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L; BC004534; AAH04534.2;
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                                                PubMed=8449401;
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Euarchontoglires; Primates; Catarrhini;
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e-mRNA splicing
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         "The RNA-
by a dire
J. Biol.
                                                                                                                                                                                                                                        CHROMOSOMAL TRANSLOCATION WITH TFE3.

PubMed=939392; DOI=10.1038/8].onc.1201394;

Clark J. Lu Y.-J., Sidhar S.K., Parker C., Gill S.,

Clark J. Linehan W.M., Shipley J., Cooper C.S.;

"Fusion of splicing factor genes PSF and NonO (p54nrk
gene in papillary renal carcinoma.";

Oncogene 15:2233-2239(1997).
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EMBO J. 13:3356-3367(1994).
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TISSUE-Fetal skeletal muscle;
MEDLINE=90901812; Pubmde2480877;
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"The RNA-splicing factor PSF/p54 controls
by a direct interaction.";
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                                                                                                                          Straub
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MEDLINE=93176127; PubMed=8439294;
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SNRPA, AND
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                                                                                                                       PubMed=9756848; DOI=10.1074/jbc.273., Uhse A., Lisby M., Knudsen B.R.,
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"Transcriptional activation of human CYP17 in H295R adrenocortical cells depends on complex formation among p54(nrb)/Non0, protein-associated splicing factor, and SF-1, a complex that also participe in repression of transcription.";
Endocrinology 143:1280-1290(2002).
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Cell 106:
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MEDLINE=22290639; PubMed=12403470; DOI=10.1017/S1355838202022070;
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Mol. Endocrinol. 14:774-782(2000).
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                                                          DNA-BINDING, AND SUBUNIT.
Pubmed=15590677; DOI=10.1074/jbc.m412758200;
                                                                                                                                                                                                                                                                                                              Waterman M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                        *PSF is a novel corepressor that mediates the DNA binding domain of nuclear hormone
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*PSF is a novel corepres
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Pubmed=10858305; DOI=10.1021/bi992898e;
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rejoining
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                                                                                                                                                                                                                                                                                                                     polypyrimidine tracts. Interacts with U5 snRNA, probably by binding to a purine-rich sequence located on the 3' side of U5 snRNA stem 1b. May be involved in a pre-mRNA coupled splicing and polyadenylation process as component of a snRNP-free complex with SNRPA/U1A. The SPPQ-NONO heteromer associated with MATR3 may play a role in nuclear retention of defective RNAs. SPPQ may be involved in homologous DNA pairing; in vitro, promotes the invasion of ssDNA between a duplex DNA and produces a D-loop formation. The SPPQ-NONO heteromer may be involved in DNA unwinding by modulating the function of topoisomerase I/TOP1; in vitro, stimulates dissociation of TOP1 from DNA after cleavage and enhances its jumping between separate DNA helices. The SPPQ-NONO heteromer may be involved in DNA nonhomologous end joining (NHEJ) required for double-strand break repair and V(D) Trecombination and may stabilize paired DNA ends; in vitro, the complex strongly stimulates DNA end joining, binds directly to the DNA substrates and cooperates with the KN70/G22P1-KN80/XRCC5 (KN) dimer to
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                                                                                         establish a functional preligation complex. SPPQ is involved in transcriptional regulation. Transcriptional repression is probably mediated by an interaction of SPPQ with SIN3A and subsequent recruitment of histone deacatylases (HDACs). The SFPQ-NONO/SF-1 complex binds to the CYP17 promoter and regulates basal and cAMP-dependent transcriptional avtivity. SPPQ isoform Long binds to the DNA binding domains (DBD) of nuclear hormone receptors, like RXRA and probably THRA, and acts as transcriptional corepressor in absence of hormone ligands. Binds the DNA sequence 5'-CTGAGTC-3'
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(Polypyrimidine tract

\_TaxID=9606;

Mammalia;

Eutheria;

Chordata; Craniata; Vertebrata; Euarchontoglires; Primates; Cata

Catarrhini;

Hominidae

Euteleostomi;

Eukaryota; Metazoa;

NUCLEOTIDE SEQUENCE

Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AL590434; CAI12467.1; -; Genomic DNA. Ensembl; ENSG00000116560; Homo sapiens. GO; GO:0003676; F:nucleic acid binding; IEA. InterPro; IPR012677; a\_b\_plait\_nuc\_bd. Howden P.; Submitted

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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
M. Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
M. Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
M. Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
M. Anthouard V., Jubin C., Cattello L., Poulain J., De Berardinis V.,
M. Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
M. Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
M. Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
M. Cruaud C., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
M. Alindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
M. Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
M. Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
M. Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.,
Menome duplication in the teleost fish Tetraodon nigroviridis reveals
M. Mature 431:946-957(2004).
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Best Local Similarity
  NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.

-!- FUNCTION: Plays a key role in the control of the eukaryotic cell
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QAS986;
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13-SEP-2005 (TrEMBLrel. 31, Last
13-SEP-2005 (TrEMBLrel. 31, Last
Chromosome 3 SCAF14700, whole gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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InterPro; IPR000504;
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RESULT 11
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AC Q4S6R8;
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DT 13-SEP-2

Q4S6R8; Q4S6R8; 13-SEP-2005 (13-SEP-2005 (14)

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Created)
Last sequence update)

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PMART; SM00498;
                                                                                                                                                                                                                                                                     EMBL; AKI
SEQUENCE
                                                                                                                                                                                                                                                                          Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AK123968; BAC85736.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6ZVX4;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ41974.
Homo sapiens (Human)
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Mammalia; Eutheria;
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(4 HUMAN
QGZVX4 HUMAN PRELIMINARY;
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InterPro; IPR010473; Drf_GTPase bd
InterPro; IPR003104; FH2_actin_bd.
InterPro; IPR001265; Formin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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PR00828; FUN-
10498; FH2;
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                                                                                        PPTEG---
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                                            -TCCSGWVSCCIGPLISPSW-----PRVWVAAGGNWPTGVELPG 102
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33.7%;
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                                                                                                                                                                            Score 99; DB Pred. No. 2.8; 6; Mismatches
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Pred. No.
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Isogai T.;
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AM Marceli E., Bouneau L., Fischer C., Ozout-Costaz C., Bernot A.,
AM Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
AM Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
AM Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
AM Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
AM Houard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
AM Houard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
AM Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
AM Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
AM Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
AM Farra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
AM Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
AM Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
AM Lindblad-Toh K., Birren B.,
AM Lindblad-Toh K., Birren B.,
AM Lindblad-Toh K., Bircen B.,
AM Lindblad-Toh K., Bircen B.,
AM Lindblad-Toh K., Bircen B.,
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Best Local (
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   Sasaki T.,
Submitted
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QEZCX3;
Q5_UUL-2004 (TIEMBLIEL 27,
05_UUL-2004 (TIEMBLIEL 27,
01_FEB-2005 (TIEMBLIEL 29,
                                                                                                                       Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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Name=P0026A08.31-1; Synonyms=OJ1003_E05.5-1;
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; CAAB01014724; CAG03664.1; -; Genomic_DNA.
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                                                                    SEQUENCE.
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29.7%;
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SCAF14724, whole genome shotgun sequence.
Yamamoto K.; the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 ('
                                                                                                                                                                                                                                                                   MEDLINE-21429078; PubMed-11547680; DOI=10.1139/cjm-47-7-608; John T.R., Rice J.M., Johnson J.D.; "Analysis of pPG12, a 22.4-kb Frankia plasmid."; Can. J. Microbiol. 47:608-617(2001). EMBL; AV027524; AAK20154.1; -; Genomic DNA. GO; GO:0042242; F:cobyrinic acid a, c-dīamide synthase activi GO; GO:0042242; F:cobyrinic acid a, c-dīamide synthase activi GO; GO:0042242; F:cobyrinic acid a, c-dīamide synthase activi GO; GO:0009236; P:cobalamin biosynthesis; IEA. InterPro; IPR00256; CblA; 1. P. synth. Pfam; PF01656; CblA; 1. P. synth. Pfam; PF01656; CblA; 1. Hypothetical protein; Plasmid.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004556; BAC99532.1; -; Genomic DNA.
EMBL; AP003936; BAC99403.1; -; Genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0828; FORMIN SMART; SM00498; FH2; 1.
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InterPro; IPR001265; Formin.
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NUCLEOTIDE SEQUENCE.
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GO:0003779; F:actin binding; IEA
GO:0016043; F:cell organization
GO:0007275; P:development; IEA.
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                                                                                         RPARCCG---
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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.I

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
            TISSUE=Brain;
                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                  NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59GF6_HUMAN
Q59GF6;
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AE000516; AAK45283.1; -; Genomic_DNA.
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Similarity 29.3%;
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"None Title.";
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NON_TER 1
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                      P-----PPPLPGVGIPPPPPLPGAGIPPPPPLPGMGIPP----
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                                                                                                                                                         PPLPGAGIPPPPPLPGVGIPPPPPLPG---AGIPPPPPL----PGAGIPPPPPLPGVGIP
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Wagase T., Kikuno F.R.;
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             14,
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US-09-387-811-9
US-09-387-811-3169
US-09-49-016-9978
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US-09-252-991A-23769
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Sequence 90, Appl Sequence 278, App Sequence 933, App Sequence 28324, A Sequence 28328, A Sequence 28569, A Sequence 28669, A Sequence 21648, A Sequence 21648, A Sequence 21754, A Sequence 21754, A Sequence 21751, A Sequence 21751, A Sequence 214, Appl Sequence 4, Appli Sequence 4, Appli Sequence 7291, App Sequence 7291, App Sequence 9978, App Sequence 9978, App Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23769, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequence 23664, A Sequenc
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US-09-489-039A-12891 US-08-660-963-12 US-08-660-963-12 US-09-599-2877A-2 US-09-949-016-11282 US-09-949-016-11282 US-09-949-016-3131 US-09-527-991A-19331 US-09-680-897-2 US-09-188-914-2 US-09-188-914-2 US-09-525-991A-2485 US-09-525-991A-2485 US-09-525-991A-2485 US-09-525-991A-2485 US-09-525-991A-26613	N	N	N	N	N	N	N	N	۲	N	N	N	N	N	N	۲	N	N
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	20613, A	18097, A	30156, A	24927, A	32485, A	2, Appli	3, Appli	2, Appli	<ol><li>Appli</li></ol>	19331, A	24, Appl	24, Appl	11282, A	<ol><li>Appli</li></ol>	2, Appli	12, Appl	4, Appli	TERRIT

### ALIGNMENTS

US-09-050-739-90

Sequence 90, Application US/09050739
Patent No. 6641814

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, WILLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-18
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SCOTTMARE: Patentin Ver. 2.0
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; SOFTWARE: PatentIn Ver. 2.0
; SEG ID NO 90
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-90
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                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                               Matches 139;
121
                               121
                                                                       61
                                                                                                             61
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                                                                                                                                                                       1 MRVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWL
                                                                                                                                                                                                                                                 Similarity
                     IDAIGSSFSKSVLTAVSAW 139
                                                                       NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLWLAPGSR 120
                                                                                                                                                   MRVNDPPAPGSDSARSRPAPALGPDPPASGWPDSGLVPSRPICAASSSAGLPPPVPPTWL
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139
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Pred. No. 2.3e-66;
; Mismatches 0;
                                                                                                                                                                                                                                                               Length 139;
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                                                                                                                                                                                                                               0
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOPTWARE: CUREPATSeqPormatter Version 0.9
SEQ ID NO 993
LENGTH: 707
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US-09-538-092-993
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; OGRANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyce ID No.
US-09-919-039-278
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US-09-919-039-278
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APPLICANT: KABGY, MATCHEW R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT FILICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOPTWARE: PERL PROGRAM
1500 THE PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PR
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 278, Application US/09919039 Patent No. 6727066
                                                                                                          Matches
                                                                                                                                                                      Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P23246
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                          Local Similarity
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6 PPAPGSDSAR-----SRPAPALGPDPPASG----
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                                                                                                          Conservative
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                                                                                                                                          Score 103.5; D
Pred. No. 0.11;
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Pred. No. 0.11;
                                                                                                          Mismatches
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                                                                                                                                                                          DB 2;
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                                                                                                      Indels 43;
                                                                                                                                                                      Length
                                          ----WFDSGLVPSRPICAA 45
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CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28324
LENGTH. ...
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US-09-949-016-10120
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                               Sequence 28324, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10120, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                 APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                   LENGTH: 273
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 SAPPGAPPPTPP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 GPKQG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPPAVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 103.5; DE Pred. No. 0.12; 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGVPTTPPQAGGPPPPPAAVPGPGP 224
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US-09-252-991A-28328
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                                                                                                                                                                                                                                                                                                         RESULT 7
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                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28328
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28328, Application US/09252991A Patent No. 6551795
SEQ ID NO 30843
LENGTH: 663
                                                                                                                                                                                                                                                    Sequence 30843, Application US/09252991A Patent No. 6551795
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APPLICANT: Marc J.
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Best Local Similarity 29.6%;
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                              FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                66 CCSGWVSC---CIGPLISPS-WPRVW------VAAGGNWPTGVELP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGRVPAASASGSR 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNNDVT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
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US-09-252-991A-28569
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                                                                                                                                                                         Sequence 28569,
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30843
                                                                                                                                                                                                                              Patent No. 6551795
GENERAL INFORMATION:
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SEQ ID NO 21648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ASEMIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                           113 SÁSSPWP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 AAGGNWP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SCSSTSATPMPSSKACRESPPPAPP-----CSAGWTTCPRASSSCALCCTGWA---A 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 ICAASSSAGL-----PPPVPPTWLNNDVTCCSGWVSC----CIGPLISPSWPRVWV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 NVAGRSATDAWSSAPAPANCCCLFPAGP--SPASPAPAACRRWPRAACHWPAS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 12.4%;
l Similarity 27.8%;
37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DV---TCCSGWVS-----CCI---GPLISPSWP----RVWVAAGGNWPTGVELPGEG 104
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NUMBER: US 60/074,788

1998-02-18

1998-02-18
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Pred. No. 0.53;
9; Mismatches
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US-09-949-016-10372
Sequence 10372, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28569
                                                                                                                                                                                                                                  RESULT 11
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 43688
LENGTH: 313
TYPE: PRT
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Best Local S
Matches 44
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NUMBER OF SEQ ID NOS:
SEQ ID NO 28569
LENGTH: 794
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSAGLPPPVPPTWLNNDVTCCSGW-VSCCIGPLISPSWPRVWVAAGGNW-----P
                                                                                                                                                                                                                                                                                                                                                                                                       VPPTW-----LNNDVTCCSGWVSCCIGP--LISPSWPRVWVAAGGNW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTDRASVPG-----NYAMTWTS--ARSACLGSACMRCMPAAV 231
                                                                                                                                                                                                                                                                                         VQPQNPQQPQNPQQPGNSNPETAESVEQAAPVPPANVPASNENASV 182
                                                                                                                                                                                                                                                                                                                                                                    VPPTWRPLLPGQNGSGAPGSGLINGIVNPPQRPHPFWPN-WQSWVNSWRPTKPVPSTEAP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGGAPAGSNVPAGSSPGSSVLGPNPPA----GSVVPSIPVLPGGAGSWPWHPRPNIPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 95; DB 2; Length 313; Pred. No. 0.28;
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                                                                                                ASSOCIATED
OF DETECTION AND
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RESULT 13
US-09-199-637A-287
; Sequence 287, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
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US-09-252-991A-23285
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US-09-252-991A-23285
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 23285
LENGTH: 442
TYPE: PRT
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Best Local (
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 PPVGAEAWARRVPQPAAPPRRP------PQSASSLSASLRPPGAPATFLRPSP
                                                                                                                               196
                                                                                                                                                                  130 KSVLTAVSA 138
                                                                                                                                                                                                      138 WPARRGWRSAVRPSLARQDGPPACPRPRPCRTGAARRRTGPARAWFT--SPAPAQGASLA 195
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                                                                                                                                                                                                                                                                              85 --GTVSSCSRRSRDLPAGTRESRAHSFSGSAGRHAGARRRSRFAEPGW-----RPGRSPG 137
                                                                                                                                                                                                                                                                                                                   60 LNNDVTCCS-----
                                                                                                                                                                                                                                                                                                                                                       32 PPLAAGCAAPG--RAARYPPPATGRSRPAAGWSPPGCRSPRAVLQAIRSCPAPPP----
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                                                                                                                                                                                                                                                                                                                                                                                         PP-----APGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTW 59
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                                                                                                                                 204
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Pred. No. 0.65;
9; Mismatches
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Pred. No. 0.49
4; Mismatches
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                                                                                                                                                                                                                                            -GEGIPKIGFVVLWLAPGSRIDAIGSSFS 129
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US-09-252-991A-21454
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                                                                                                                                                                                                                                                                                          APPLICANT: MATC J. RUDENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUCINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21454
FENCENCE: 107
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                                                                                                                                         Query Match
Best Local Similarity
Matches 37; Conserv
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PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOPTWARE: FASTSEQ for Windows Version
SEQ ID NO 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21454, Application US/09252991A
Patent No. 6551795
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APPLICANT: Teongalis, John
TITLE OF INVENTION: VIRTLENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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APPLICANT:
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                    LENGTH: 187
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121 RPSAGCVPGPGWSGTGCAPCSRGRPCA-APPPSPAWPA--RSSAGSAPSPAPRP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RPSAGCVPGPGWSGTGCAPCSRGRPCA-APPPSPAWPA--RSSAGSAPSPAPRP 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                            6 PPAPGSDSARSRPAPALGPD---PPASG-----WFDSGLVPSR-PICAASSS----AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PPAPGSDSARSRPAPALGPD---PPASG-----WFDSGLVPSR-PICAASSS----AG
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Similarity 32.5%;
                                 LPPP--VP-PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELP 101
                                                                        PPRPGRSLADAAPAPCAAASRARPRASSTPGYRSTWKPLRRFPRRSPCCAATGSRSCRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPRPGRSLADAAPAPCAAASRARPRASSTPGYRSTWKPLRRPPRRSPCCAATGSRSCRAG
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Pred. No. 0.27;
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RESULT 15 US-09-252-991A-25096

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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25096
LENGTH: 414
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
Search completed: April 14, 2006, 17:37:59 Job time: 13.853 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Maximum Match 100%
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Maximum DB seq length: 200000000
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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5: /cgm2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*

6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
  Match
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US-10-437-963-169481
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Million cell updates/sec
            Sequence 90, Appl Sequence 90, Appl Sequence 90, Appl Sequence 90, Appl Sequence 278, Appl Sequence 278, Appl Sequence 169481, App Sequence 169481, App Sequence 741, App Sequence 16320, Sequence 163320, Sequence 14136, Sequence 14136, Sequence 14136, Sequence 15321, Sequence 15321, Sequence 15321, Sequence 15321, Sequence 15321, Sequence 292580, Sequence 152758, Sequence 152758, Sequence 152758, Sequence 36344, Appli Sequence 17, Appli Sequence 16, Appli Sequence 16, Appli Sequence 36344, Appli Sequence 36344, Appli Sequence 36344, Appli Sequence 36344, Appli Sequence 16, Appli Sequence 36344, Appli Sequence 36344, Appli Sequence 16, Appli Sequence 16, Appli Sequence 36344, Appli Sequence 36344, Appli Sequence 16, Appli Sequence 16, Appli Sequence 36344, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Se
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93.5	93.5	93.5	93.5	93.5	93.5	94	94	94	94	94	94	94	94.5	95	95	95	96
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
57757, A	16081, A	15, Appl	4, Appli	144769,	37061, A	3, Appli	51472, A	187947,	8672, Ap	58165, A	156311,	204838,	173295,	4, Appli	5022, Ap	283342,	151404,

### ALIGNMENTS

RESULT 1 US-09-791-171-90

Sequence 90, Application US/09791171 Patent No. US20020094336A1 GENERAL INFORMATION:

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APPLICANT: NIELSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: CETTINGER, Thomas
APPLICANT: RASMUSSER, Peter Birk
APPLICANT: RASMUSSER, Peter Birk
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Walter
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 05/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR APPLICATION NUMBER: 60/040,624
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTMARE: PATENTIN Ver. 2.0
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; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis US-09-791-171-90
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Best Local Sim
Matches 139;
121 IDAIGSSFSKSVLTAVSAW 139
121 IDAIGSSFSKSVLTAVSAW 139
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                                                                                                      NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLWLAPGSR
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Sequence 90, Application US/09804980
Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 139
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                      APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT APPLICATION NUMBER: US/50/50,739
PRIOR APPLICATION NUMBER: 09/05,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-01-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
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US-10-620-246-90
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ANDERSEN, Peter APPLICANT: NIBLSEN, Rikke APPLICANT: OBTTINGER, Tho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                    APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08 APPLICATION NUMBER: 60/116,673
                                                                                               APPLICATION NUMBER: 09/791,171 FILING DATE: 2001-02-20
                                                                                                                                             APPLICATION NUMBER: 10/138,473 FILING DATE: 2002-05-02
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RASMUSSEN, Peter Birk
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1999-01-21
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100.0%; Pred. No. 3.2e-55;
tive 0; Mismatches 0;
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US-10-437-963-133141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-90
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LENGTH: 139
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 133141
LENGTH: 377
                                                                                                                                         Matches
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APPLICANT:
APPLICANT:
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APPLICANT:
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Publication No. US20040123343A1
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La ROSA, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 37
                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(377
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                         Local
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77
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                                                                   17 APSSSPGGRRATPTSSPTPPASSGWATSSSSPSRPPARRPCSASSGCSAPPSLSSASSST
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                                                                                         8 APGSDSARSRPAPALGPDPPA-SGWPDSGLVPSRP----ICAASSSAGLPPPV-----
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Similarity 29.8%;
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RWPGVLPATARTPASSPPTWRP----
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                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yongwei
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                                --PPTWLNNDVTCCSGWVSCCIGPLISPSWPRV--WVAAG 91
                                                                                                                                       ω
                                                                                                                                                      Score 112; DB 4; Length 377; Pred. No. 0.46;
                                                                                                                                         Mismatches
                                                                                                                                         33; Indels
 PPPSPPTWPAPPRWSGAG 116
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                                                                                                                                         44;
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RESULT 5 US-10-767-701-53499

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; ORGANIAM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 2457215CD1
US-09-919-039-278
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US-09-919-039-278
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                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 278, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kaser, Matthew R. TITLE OF INVENTION: GENES EX PILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kovalic, Davi
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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LOCATION: (1)..(123
OTHER INFORMATION:
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 46
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SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105
                                     PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWLAPGSR 120
                                                                           PPAPGSDSAR-----SRPAPALGPDPPASG-----WPDSGLVPSRPICAA 45
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p. US20030108871A1
                                                                                                                Conservative
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US20040172684A1
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29.7%;
                                                                                                                                13.4%;
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Pred. No. 0.22;
7; Mismatches
                                                                                                              Score 103.5; | Pred. No. 4.2; | 6; Mismatches
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                                                                                                                                                    DB 3;
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                                                                                                                                                  Length 707;
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                                                                                                                Indels
                                                                                                              43;
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                                                                                                                                                                                                                                                                                                         SEQ ID NO 33360
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-9-27
PRIOR PILING DATE: 2000-9-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
OTHER INFORMATION: MAP TO ACOO6111.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER,
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL
OTHER INFORMATION: EXPRESSED IN BONE MARROW,
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
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PREPLICATION NUMBER: US 60/236,359

DR FILING DATE: 2000-09-27

DR APPLICATION NUMBER: PCT/US01/00666

DR FILING DATE: 2001-01-30

DR PILING DATE: 2001-01-30

PREPLICATION UNBER: PCT/US01/00667

DR APPLICATION UNBER: PCT/US01/00667

DR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
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US20020048763A1
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       BONE MARROW, SIGNAL
                                                     SIGNAL =
                                 SIGNAL
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= 17
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                                                                                                                                                     RESULT 9
                                                                                                                                US-10-437-963-169481
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Matches
                                                                           Sequence 169481, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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SEQ ID NO 185237
LENGTH: 285
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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-10-437-963-185237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(285)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                            120 ------RGCC-----APTWRRTWPSAS---PSSV 139
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                                                                                                                                                                                                                                                                                                                       PPA--PGSD-SARSRPAPALGPDP---PASGWFDSGLVPSRPICAASSSAGLPPPVPPTW 59
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Li, Ping
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EXPRESSED IN BT474, SIGNAL = 13
EXPRESSED IN HBL100, SIGNAL = 18
SWISSPROT HIT: Q01705, EVALUE 9.30e-02
EST_HUMAN HIT: AW003023.1, EVALUE 2.00e-06
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Pred. No. 2.5;
8; Mismatches
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LENGTH: 199
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Best Local Similarity
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169481
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                                                                                        Query Match
Best Local
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APPLICANT: Penn, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OP INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Barbazuk, Brad Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221) B
                                                                                                                                                            ORGANISM: Homo sapiens

PEATURE:

OTHER INFORMATION: MAP TO AL049853.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

OTHER INFORMATION: SWISSPROT HIT: P23206, EVALUE 3.00e-08
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                  Similarity 26.6
37; Conservative
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PGSDSARSRPAPA----LGPD-----PPASGWFDSGLVPSRPICAAS-----SSAGLPP 53
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                                                                  Score 99.5; DB
Pred. No. 2.5;
15; Mismatches
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Pred. No. 2.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-741
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US-09-925-302-741
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US-09-925-302-741
                                                                                                           NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 741
                                                                                                                                                                                                                                                                                                                                      Sequence 741, Applic Publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 741
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GENERAL INFORMATION:
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Best Local :
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Query Match
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                                                                                                                                                            APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
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                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                          Application US/09925302 to. US20030064072A9
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ilarity 29.7%;
Conservative
 12.9%;
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 Score 99.5;
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 Length 212;
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RESULT 14
US-10-437-963-114935
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US-10-437-963-163320
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Sequence 114935, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 163320
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Best Local :
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APPLICANT:
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                                                                                               273 GGGDGAR 279
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                                                                                                                                                                                                                                                                                                                                      160 HWCSSSSAAGLCTPRFAWIDASFPATSSRRRRAAPQPTPRATPAPSWAAPPSPPRRRRCS
                                                                                                                                                                                                                                                                                                                                                                                                           102 RRRPPPAPA--PARSGPAPAPAGQCRLPPPPPPPAASDSPPLPPHAPAAASACAASASIR 159
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                                                                                                                                                                                                                                                                                                 61 ---NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWP----TGVELPGEGIPKIGFVVL 113
                                                                                                                                                                                                                                                                                                                                                                        41 PICAASSSAGL-----PPPVP----PTWL---
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47; Conserv
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Barbazuk, Brad
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25.1%; Pred. No. 3.8;
tive 13; Mismatches
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CRCANISM: Sorghum bicolor
FERTURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C80510_1.pep
US-10-767-701-40674
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US-10-767-701-40674
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US-10-437-963-114935
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114935
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40674
LENGTH: 155
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Best Local Similarity 22.8%;
Matches 31; Conservative
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Publication No. US20040172684A1
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ORGANISM: Oryza sativa
FEATURE:
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86 AVVSSARGSTFAKSTLT 102
143
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R-----RWPTSVPL 151
                                                                                                                                                                                                                                    PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLN----
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                                            RVWVAAGGNWPTGVEL 100
                                                                                                                                                                                         PPAPPPPPRAPPPPPLAPPAPRGARRPRGRPPAAP--PAGRAAAPAPPVRPPWAGGRPG 82
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                                                                                         PGAAPEPPPSRAAPTRRPRAPPAPPPPTAPRGRCGGVSPGSCQRSALGSCFSPGFFWAWP 142
                                                                                                                                                                                                                                                                                   Score 98; DB 4; Length 155; Pred. No. 2.6; 7; Mismatches 48; Indels
                                                                                                                                          ----NDVTCCSGWVSCCIGPLISPSWP 84
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Search completed: April 14, 2006, 18:40:39 Job time : 49.8785 secs

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Minimum
Maximum
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Maximum Match 100%
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Perfect score:
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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991.565 Million cell update
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-043-806-368
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US-11-150-487-10
US-11-150-487-1
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7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11 7 US-11	10.5	10.5	10.6	10.7	10.7	10.7	11.0	11.0	11.1	11.1	11.2	11.2	11.3	11.3	11.4	11.7	11.7	11.7	11.7
7 US-11-149-945-2 7 US-11-150-487-24 7 US-11-150-487-24 7 US-11-150-487-24 7 US-11-087-099-9879 7 US-11-096-568A-27199 7 US-11-096-568A-27199 7 US-11-096-568A-21231 7 US-11-124-368A-335 7 US-11-150-487-16 7 US-11-150-487-16 7 US-11-150-487-16 7 US-11-150-487-16 7 US-11-196-568A-2123 6 US-10-644-807-349 7 US-11-096-568A-2123 7 US-11-188-299-17645 7 US-11-196-568A-24535 7 US-11-096-568A-24535	273	319	1870	761	283	137	716	716	315	229	533	412	277	277	667	638	638	505	505
US-11-150-845-2 US-11-150-845-24 US-11-150-845-24 US-11-150-487-24 US-11-160-487-24 US-11-096-568A-1871 US-11-096-568A-27199 US-11-096-568A-27199 US-11-096-568A-27199 US-11-096-568A-27199 US-11-1096-568A-21231 US-11-1072-512-3048 US-11-072-512-3048 US-11-150-845-16 US-11-150-845-16 US-11-150-487-16 US-11-160-487-16 US-11-160-4887-16 US-11-160-568A-21223 US-11-096-568A-24535 US-11-096-568A-24535	7	7	7	σ	7	σ	7	7	7	7	7	7	7	7	7	7	7	7	7
	US-11-096-568A-22109	US-11-096-568A-24535	US-11-188-298-17645	US-10-204-639-19	US-11-096-568A-21223	US-10-644-807-349	US-11-150-487-16	US-11-150-845-16	US-11-072-512-3207	US-11-072-512-3048	US-11-124-368A-335	US-11-096-568A-21231	US-11-096-568A-27199	US-11-096-568A-1871	US-11-087-099-9879	US-11-150-487-24	US-11-150-845-24	US-11-150-487-4	US-11-149-945-2
	22109, A	24535, A	17645, A	19, Appl	21223, A		16, Appl	16, Appl	3207, Ap	3048, Ap	335, App	21231, A	27199, A	1871, Ap	9879, Ap	24, Appl	24, Appl	4, Appli	2, Appli

## ALIGNMENTS

AND ASSAYS AND METHOL

RESULT 1 US-11-051-720-324

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Sequence 324, Application US/11051720

Publication No. US20060046257A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER, AND

TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 1847.1002

CURRENT APPLICATION NUMBER: US/11/051,720

CURRENT APPLICATION NUMBER: US/11/051,720

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 1780

SEQ ID NO 324

LENGTH: 584

TYPE: PRT

ORGANISM: Homo sapiens

US-11-051-720-324
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                  Sequence 368, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Movel Nucleotide and Amino Acid Sequences,
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.1%; Score 101.5; DI Best Local Similarity 26.3%; Pred. No. 0.13; Matches 41; Conservative 16; Mismatches
SEQ ID NO 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 PDPPPGPGVPPTGW--GPTLPSRAVLARSSAEGGQPRGTVSTAPGMGLGCSPG---LCVG
                                                                                                                                                                                                                                                                                                                                                                                   486 CTPAPAPPLPGHRPPGTARDRSGDKDLPS-LAALSA 520
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US-11-087-099-11981
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US-11-043-806-368
                                                                                                                                                                                                                                                   US-10-979-095-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Triticum aestivum 
US-11-087-099-11981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 41
                                                                                                                          GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YANG, Junming
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BURFORD, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11981, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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Best Local (
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Publication No. US20060068481A1
TITLE
                 APPLICANT:
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 OF INVENTION: HUMAN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 PDPPPGPGVPPTGW--GPTLPSRAVLARSSAEGGQPRGTVSTAPGMGLGCSPG---LCVG 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 13.0%;
Similarity 28.8%;
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                                                                             AU-YOUNG, Janice
LU, Dyung Aina M.
REDDY, Roopa
                                              YME, Henry
YAO, Monique G.
                                LAL, Preeti
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ilarity 26.3%;
Conservative 1
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                 Farrah A.
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Pred. No. 0.13;
.6; Mismatches
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RESULT 5
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PRIOR PILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGram
SEQ ID NO 7
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/11150845 Publication No. US20060003399A1 GENERAL INFORMATION:
                                                                           Matches
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                                                                                                               Query Match
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/979,095
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/10/168,582
PRIOR FILING DATE: 2002-06-20
PRIOR FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 020552-007720US
CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/673,444
PRIOR PLING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/578,949
PRIOR PILING DATE: 2004-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cytokinetics, Inc.
APPLICANT: Tomasevic, Nenad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pierce, Daniel
APPLICANT: Finer, Jeffrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION
                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (1). (398)
OTHER INFORMATION: 105WASP
                                                                                                                                                                                                                              LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 PAEAAAQGYPAP-----PPAPAW-----PSRPVPRSGAHWSHGPPPPGMPPPAWRQPSL
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                                     6 PPAPGSDSARSRPAPAL------GPDPPASGWFDSGLVPSRPICAASSSAGLPP
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 PPIVGGNKGRSGPLPPVPLGIAPPPPTPRGPPPPGRGG-----PPPPPPPATGRSGPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jia, Zhiheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakowicz, Roman
                                                                             Conservative
                                                                                             11.8%;
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Pred. No. 0.64;
10; Mismatches
                                                                           5; Mismatches
                                                                                             Score 91.5; DB Pred. No. 0.68;
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                                                                                                               DB 7;
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                                                                                                                 Length 398;
                                                                               Indels
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                                                                               Gaps
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1). (398)
; OTHER INFORMATION: 105WASP
US-11-150-487-10
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US-11-150-487-10
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                                                                                                                                                                                                          Sequence 14, Application US/11122795 Publication No. US20050287518A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn version 3.3 SEQ ID NO 10 LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
FILE REFERENCE: 020552-007910US
CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT APPLICATION NUMBER: US 60/578,913
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR PILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 70
SOFTMANDE OF SEQ ID NOS: 70
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APPLICANT:
              APPLICANT: Burton, Dennis R.
APPLICANT: Chamberlain, Chester
APPLICANT: The Scripps Research Institute et al.
TITLE OP INVENTION: Labeled Peptides, Proteins and
TITLE OP INVENTION: Useful for their Preparation
FILE REFERENCE: 1361.007US3
                                                                                                                               APPLICANT: Hahn, Klaus M.
APPLICANT: Toutchkine, Alexei
APPLICANT: Muthyala, Rajeev
APPLICANT: Kraynov, Vadim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cytokinetics, Inc
APPLICANT: Tomasevic, Nenad
CURRENT APPLICATION NUMBER: US/11/122,795
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                                                                                                                             Muthyala, Rajeev
Kraynov, Vadim
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Russell, Alan
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Pred. No. 0.68;
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                                                      Antibodies and Processes
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US-11-150-845-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-795-14
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Best Local S
Matches 36
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                IENGTH: 502
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1).-(502)
OTHER INFORMATION: FL-WASP
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APPLICANT: Tomasevic, Nenad
APPLICANT: Jia, Zhiheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/578,949
PRIOR FILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/673,444
PRIOR FILING DATE: 2005-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sakowicz, Roman
APPLICANT: Pierce, Daniel
APPLICANT: Pierce, Dafrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION
FILE REPERENCE: 020552-00772005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 11.8%;
Local Similarity 27.9%;
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                                                                                                                                 54 PVP----PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIG 109
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                                                      FVVLWLAPG 118
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r Windows Version
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Pred. No. 0.85;
5; Mismatches 43;
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FILE REFERENCE: 020552-007910US
CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR FILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
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US-11-149-945-1
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US-11-150-487-2
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                                                            US-11-150-487-2
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Publication No. US20060014266A1
Query Match
Best Local Similarity
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Best Local (
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APPLICANT: Tomasevic, Nenad
APPLICANT: Tomasevic, Nenad
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: PURIFICATION OF ARP2/3 COMPLEX AND COMPOSITIONS CONTAINING
TITLE OF INVENTION: PURIFIED ARP2/3 COMPLEX
FILE REFERENCE: 020552-007810US
CURRENT APPLICATION NUMBER: US/11/149,945
CURRENT FILING DATE: 2005-66-10
PRIOR APPLICATION NUMBER: US 60/578,969
PRIOR FILING DATE: 2004-06-10
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Manping
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cytokinetics, Inc
APPLICANT: Tomasevic, Nenad
APPLICANT: Russell, Alan
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ORGANISM: Homo sapiens
                                                                             NAME/KEY: misc_feature
LOCATION: (1). (502)
OTHER INFORMATION: FL-WASP
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                           ENGTH: 502
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11.8%;
27.9%;
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Pred. No. 0.85;
5; Mismatches
Score 91.5; DB Pred. No. 0.85;
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                       Length 502;
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RESULT 12
US-11-150-845-20
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US-11-079-907-28
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Publication No. US20060003399A1
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SEQ ID NO 28
LENGTH: 502
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Publication No.
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                 FILE REFERENCE: 020552-007720US
CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/673,444
PRIOR FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/578,949
PRIOR FILING DATE: 2004-06-10
                                                                                                                                              APPLICANT: Pierce, Daniel
APPLICANT: Finer, Jeffrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION ASSAY
                                                                                                                                                                                                    APPLICANT: Cytokinetics, Inc.
APPLICANT: Tomasevic, Nenad
APPLICANT: Jia, Zhiheng
APPLICANT: Sakowicz, Roman
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CURRENT APPLICATION NUMBER: US/11/079,907
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/552,663
PRIOR FILING DATE: 2004-03-12
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APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Live Cell Biosensors
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NUMBER OF SEQ ID NOS:
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36; Conserv
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27.9%;
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Pred. No. 0.85;
5; Mismatches 43;
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FILE REFERENCE: 020552-007910US
CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR FILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 70
SOPTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 609
RESULT 14
US-11-087-099-7887
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Best Local
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Best Local Similarity 27.9%;
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SEQ ID NO 20
LENGTH: 609
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APPLICANT: Tomasevic, Nenad
APPLICANT: Russell, Alan
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Local Similarity 27.9%; Pred. No. 1;
hes 36; Conservative 5; Mismatches
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                                                                       -----LAPG 346
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Pred. No. 1;
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 18316
LENGTH: 647
TYPE: PAT
ORGANISM: Brassica napus
US-11-188-298-18316
Search completed: April 14, 2006, 18:42:16 Job time : 6.95625 secs
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Publication No. US20060075522A1
GENERAL INFORMATION:
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SEQ ID NO 7887
SEQ ID NO 7887
TYPE: PRT
TYPE: PRT
ORGANISM: Brassica napus
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Matches 22; Conserv
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Best Local Similarity 40.0%;
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(5345)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
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                                                                                12 PPSPPSNSTTTTPPPASAPPPTTPSSPPPPS-TIPTSPPPSSRSTPSAPPPSPPT
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nilarity 40.0%;
Conservative
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Pred. No. 1.1;
9; Mismatches
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Abu47535	Abu14715	Abu47382	Abu31901	Aau77662	Abb07334	Abb07346	Aae08868	Aab15971	Aaw60665	Aaw46473	Aar06609	Adf91417	Adv83185	Adv81046	Adv89793	Abp27074	Adc96608	Adw11153	Abp27075	Abu29407
-	Protein e	Protein e	Protein e	E. coli C	Cold-shoc	Cold-shoc	Escherich	E. coli p	E.coli co	Amino aci	Cold shoc	E. coli c	Streptoco	Streptoco	Streptoco	Streptoco	B. faeciu	Cold shoc	Streptoco	Protein e

# ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                             08-OCT-1998
                                                                                                                                                  01-APR-1998;
                                                                                                                                                                        WO9844119-A1
                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                         21-JAN-1999
                                                                                                                                                                                                                                    AAW72934;
                                                                                                                                                                                                                                               AAW72934 standard; protein; 67
                                                                                                                                                                                              infection.
                                                                                                                                                                                                              Mycobacterium tuberculosis antigen CFP7B.
                                                                                                                                                                                                                         (first entry)
                                                                                                                     97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                                                   tuberculosis.
                                                                                                                                                                                                   tuberculosis; antigen; vaccine;
                                                                                                                                                  98WO-DK000132
                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                   immunological; immunogen;
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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 222; 163pp;

English.

N-PSDB;

AAV63944.

WPI; 1998-542705/46.

Andersen P, Oettinger T,

Nielsen , Florio

Ξ, Z

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

(STAT-)

STATENS SERUM INST.

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fregment (1) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion to evoke a polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cepitoge from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or tuberculosis complex. The induction of a strong immune crepsonse in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 67
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05-JAN-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic; Mycobacterium tuberculosia; immune response; infection; tuberculosia; fusion polypeptide; T-cell pplicope; ESAT-6, MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP3OA; CFP7B; CFP1B; CFP27; CFP3OA; RD1-ORF; CFP1OA; CFP16; CFP19; CFP23;
                                                                                                                                                                                                                                               Example 3;
                                                                                                                                                                                                                                                                        New immunogenic fragment of Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
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                                                                                                                                                                                                                                               Page 81; 265pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of antigen CFP7B.
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Best Local :
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08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
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01-JUL-1999;
01-JUL-1999;
                                                                                                                                                           WPI; 200
N-PSDB;
                                                                                                                                                                                                                            Pompejus
Lee H, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; discount carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope of for diagnosis of TB in a mammal by performing a DTH type test; use of CPP27, CPP30A, RD1-ORF2, RD1-ORF3, RD1-ORF5, MPT59-ESAT6 ESAT6-MPT59, CPP10A, CPP16, CPP19, CPP23, CPP25A, CPP30B, CPP7B or a cell epitope of for the preparation of an immunological composition;
                                                              New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of tine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; stress; resistance; fine chemical production; organic acid; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000;
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                                            carbohydrates,
                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1999;
27-AUG-1999;
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DB; AAF71025.
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                   Kroeger
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99DB-01030429.
99US-0142632P.
99DB-01031413.
99DB-01031457.
99DB-01032239.
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99DB-01032314.
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                                                or
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                                              enzymes.
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Pred. No. 2.4
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                                                                                                                                                                                                                                                   Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jstance; tolerance; SRT;
proteinogenic amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                     Haberhauer
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MPT59-ESAT6,
CPP7B or a T-
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Claim 20; Page 231-232; 526pp; English

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RESULT 4
AAB78911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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25-JUN-1999;
01-JUL-1999;
01-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2001
                                                                                                                                                                                                                            23-JUN-2000;
                                                                                                                                                                                                                                                                                          04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evolutionary study; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carbohydrate; aromatic compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                               2000WO-IB000922
99US-0141031P.
99DE-01030429.
99US-0142692P.
99US-01031413.
99DE-01031457.
99DE-01031541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRT protein sequence SEQ ID NO:82
                                                                                                                                                                                                                                                                                                                                                                                                                    glutamicum.
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77.6%;
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Pred. No. 7.5e-27;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vitamin; cofactor; polyketide; enzyme;
l hazard; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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26-SEP-2001

(first entry)

AAG89941 standard; protein;

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.

C glutamicum protein fragment SEQ ID NO: 3695.

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RESULT 5
                                                                                                                                                                                                                                                                                                                                                   cc expression in host cells and production of fine chemicals, such as, an corganic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine chemical production can be modulated. The presence of [I] or the SRT compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine cc proteins [III] encoded by them are used for diagnosing the presence or containing them can be used to map the genomes of organisms related to C. containing them can be used to map the genomes of organisms related to C. cc quitamicum, to identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein regions required compound of an environment that is normally environmentally or chemically hazardous to it. [I] and protein molecules encoded by it increase the survival of C. glutamicum to conditions. By increasing the growth rate or maintaining a normal growth rate in poor or toxic conditions, the yield, condition and/or efficiency or production of fine chemicals from a cc culture may be increased.
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Matches
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14-JUL-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70984 to AAP71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) poteins given in AAB78871 to AAB7 The C. gluttamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
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Lee H, K
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N-PSDB; AAF71024.
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 230-231; 526pp; English
                                                                                                                                                                                                                                                                                                                                             culture may be increased
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                                                                                                                                                     1 MAQGTVKWFNGEKGFGFIAPNDGSADLFVHYSEIQGSGFRNLEENQPVEFEVGEGAKGPQ 60
                                                                                                                                                                                1 MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
                                                                                                                                                                                                                               52;
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                                                                            AQQVRAL 67
                                                                                                             ATGVRSL
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99DE-01032914.
99DE-01040764.
99US-0151214P.
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77.6%;
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                                                                                                                                                                                                                               Score 282; DB
Pred. No. 7.5e
5; Mismatches
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ADZ21478
ID ADZ2
XX
AC ADZ2
XX
OT 30-J
DE COTY
XX
KW Abic
KW heat
KW col(
XX
COS)
XX
W COS
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homelogue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino particularly L-lysine. The present sequence and organic acids, pattern to the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                     Abiotic stress tolerance; transgenic plant; crop improvement; heat tolerance; cold tolerance; salt tolerance; drought tolerance;
                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                         ADZ21478 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
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Tateishi N,
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07-APR-2000;
                                          Corynebacterium glutamicum
                                                                                                                                                                30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
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DB; AAH65160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             point of a gene, measuring expression of a gene, analyzing on profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                               AQQVRAL 67
                                                                                                                                                                                                                                                                                                                           ATGVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3695; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2000JP-00159162.
2000JP-00280988.
                                                                                                                                                               (first entry)
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Senoh A, Ikeda
                                                                                                                                  glutamicum cold shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                               78.6%;
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da M,
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Ozaki A;
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.5e-27;
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RESULT 7
AAD78917
ID AAB78917
XX AAB8
AC AAB7
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DT 30-A
DT C. 9
XX COry
KW Cory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of a Corynebacterium CC glutamicum cold shock protein (sep). The invention provides a plant that CC shows improved abiotic stress tolerance as a result of the expression of a Csp in its cells. In one embodiment, a polynucleotide encoding a Csp is CC operably linked to a plant promoter and plant terminator. The polynucleotide preferably encodes a protein comprising a specified Csp conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 or its homologues, Escherichia coli CspA ADZ21428 or its homologues, a Csp is CC its homologues, Escherichia coli CspA ADZ21429 or its homologues, a csp is constitutive, temporally-regulated, developmentally-regulated, tissue-constitutive, temporally-regulated, developmentally-regulated, tissue-specific, of constitutive, temporally-regulated, developmentally-regulated, tissue-specific, and abiotic stress-tolerant transgenic plant that has been cransformed with a DNA molecule that expresses a Csp is claimed. The plant may be a crop plant, a monocot or dicot, and is especially selected from soybean, corn, canola, rice, cotton, barley, oat, turf grass, cotton cand wheat. The transgenic plant thougheat plant tolerance, cold colerance, salt tolerance, drought tolerance and survival after cold colerance, salt tolerance, drought tolerance and survival after cold shock than the corresponding non-transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 52
                  nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleoside; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA molecule comprising a DNA polynucleotide promoter and a DNA that encodes a cold shock protein, useful producing plants with increased tolerance to abiotic stress.
                                                                                                Corynebacterium glutamicum; stress; resistance; tolerance; SRT fine chemical production; organic acid; proteinogenic amino aci
                                                                                                                                                          C. glutamicum SRT protein sequence SEQ ID NO:88
                                                                                                                                                                                                                                                                               AAB78914 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67 AA;
                                                                                                                                                                                                     30-APR-2001
                                                                                                                                                                                                                                          AAB78914;
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DB; ADZ21477.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                               AQQVRAL
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2003US-0530453P.
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 282; DB
Pred. No. 7.5e
5; Mismatches
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No. 7.5e-27;
                                                                         proteinogenic amino acid;
e; pyrimidine base; nucleo
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AQAVRAI 67

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CC AAP70984 to AAP71133 encode the Corynebacterium glutamicum stress, CC rhe C: glutamicum SRT genes (I) can be used in vectors (II) for C: cxpression in host cells and production of fine chemicals, such as, an CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC compound, a votamic can be modulated. The presence of (I) or the SRT CC containing them can be used to map the genomes of organisms related to C. glutamicum, to identify and localise C. glutamicum sequences of interest, CC containing them can be used to map the genomes of organisms related to C. CC glutamicum, in modulating the SRT protein activity, and in modulating the sequences of interest, CC containing a nenvironment that is normally environmentally or chemically hazardous to it. (I) and protein molecules encoded by it increase the CC survival of C. glutamicum to chemical and environmental hazards and CC survival of C. glutamicum to chemical and multiplication in large scale containing a normal growth rate in poor or toxic conditions, the yield, containing a hard protein continued growth and multiplication, the yield, and protein and hor conditions of fine chemicals from a content on and/or efficiency or production of fine chemicals from a
                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                      Sequence 67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061972/07.
N-PSDB; AAF71027.
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27-AUG-1999;
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09-JUL-1999;
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08-JUL-1999;
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01-JUL-1999;
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ATGVRSL
                                                          MAQGTVKWFNPEKGFGFIAPSDGSADVFVHYSEIEGNGFRTLEENQLVEFEIGEGAKGLQ 60
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99DB-01031413,
99DB-01031457.
99DB-01031541.
99DB-01032209.
99DB-01032230.
99DB-01032914.
99DB-01032914.
99US-0151214P.
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99DE-01030429.
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4; Mismatches
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                                                                                                                                                                                                                           Length 67;
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RESULT 9 ABU34189 ID ABU3

ABU34189 standard; protein;

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                                                                                                                Matches
                                                                                                                                         Query Match
                                                                                                                             Best Local
                                                                                                                                                                                             sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides dermutation point of a gene, expression profile or patt
                                                                                                                                                                       Sequence 67
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N-PSDB; AAH65310.
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; SBQ ID NO 3845; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
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acid synthesis.
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AQAVRAI 67
                            ATGVRSL
                                                        MAQGTVKWFNPEKGFGFIAPSDGSADVFVHYSBIEGNGFRTLEENQLVEFBIGEGAKGLQ
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                                                                                                                Conservative
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda M,
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                            63
                                                                                                                            76.6%;
77.6%;
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                                                                                                             Score 275; DB 4;
Pred. No. 5.5e-26;
4; Mismatches 11
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Ozaki A;
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ABU34189;

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the 6213 antibense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting by the creation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation of the biological pathway in which a proliferation-required gene or a gene on which the test compound that inhibits proliferation of a gene on which the test compound that inhibits proliferation of a gene on which the test compound that inhibits proliferation of a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the contiferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational for a content and the content of a condidate molecules for rational care acids are useful.
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 62113; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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Forsyth
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Xu HH;
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Query Match Best Local Similarity

71.3%; 64.2%;

Score Pred.

256; DB 6; No. 1.2e-23;

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                                                                                                                                                                                                                                                                                                                 polypeptides. The invention also relates to a recombinant expression vector comprising a polymucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polymucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid comprising a sequence encoding an Enterococcus polypeptide, useful for preparing a composition for diagnosing treating E. fecalis infection.
                                                                                                                                                                                                                                                                         Sequence
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N-PSDB; ADH82881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Enterococcus faecalis polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4171; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOUC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6617156-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-1997;
                                                                                                                                                                      44;
                61
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                                                                                                1 MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTBIQGTGFRTLEENQKVEFEIGHSPKGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOUCETTE-STAMM L A. BUSH D.
                                                                                                                                                                                                 Similarity
                  ATGV
                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVGVSTV 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAQGTVKWFNGEKGFGFITPDDGTKDLFVHYSEIQGSGYRSLDENQRVQFDVEQGAKGFQ
                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 88 AA.
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                                                                                                                                                                                              63.4%;
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                                                                                                                                                                                              Score 227.5; DB 7
Pred. No. 5.6e-20;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                         12;
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                                                                                                                                                                         Indels
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RESULT 11
ABM78962
ID ABM78
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                                                                                                                                                                                            CC and 5' untranslated region (UTR) from a cold shock inducible gene, such cases, which directs its expression. An AT-rich sequence that enhances translation under cold shock inducible conditions is present either in the coding sequence of the heterologous polypeptide or in an additional celement inserted between the coding sequence and the cold shock inducible conditions is present either in the coding sequence and the cold shock inducible compacter and 5' UTR. The DNA molecule preferably also includes the cepa CC promoter and 5' UTR. The DNA molecule preferably also includes the need CC for chemical induction, and under cold conditions all ribosomes in the CC host are forced to express the single trarget protein, which simplifies CC purification. When used to prepare isotopically labelled proteins; the CC ulture size, and thus amount of expensive labelled reagent, can be CC reduced. The method can also be used to produce proteins native to cold-cx colimate organisms at high yield
                                                                                                                                           Query Match
Best Local
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence of Escherichia coli cold shock protein CspG. The invention provides a DNA molecule or vector at host cell containing the DNA molecule or vector for use in the product of a heterologous polypeptide under conditions that elicit a cold show response in the host cells. The DNA molecule and vector include a
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding heterologous protein, useful particularly for producing isotopically labeled proteins, includes a cold-shock inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002; 2002US-0361069P
14-AUG-2002; 2002US-0402921P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 73; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cold shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAKA-)
                                                                                                                            Local Similarity
les 42; Conserv
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67
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                              VRSL 67
                                                                               GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG 63
                                                                                                                                                                                            70
                                                              GLVKWFNADKGFGFITPDDGSKDVFVHFTAIQSNEFRTLNENQKVEFSIEQGQRGPAAAN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phadtare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cape.
                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli cold shock protein CspG.
                                                                                                                            Conservative
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                                                                                                                                         62.1%;
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                                                                                                                            5;
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                                                                                                                          Score 223; DB 7; 1
Pred. No. 1.5e-19;
5; Mismatches 17;
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                                                                                                                                                         Length 70;
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RESULT 12
ADZ21446
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                                                                                                                                                                                                                                            The present sequence is the protein sequence of a cold shock protein CC (Csp) from Escherichia coli. The invention provides a plant that shows comproved abiotic stress tolerance as a result of the expression of a Csp is in its cells. In one embodiment, a polynucleotide encoding a Csp is CC operably linked to a plant promoter and plant terminator. The CC polynucleotide preferably encodes a protein comprising a specified Csp CC conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 or its homologues, Escherichia coli CspA ADZ21428 or its homologues, a Csp CC from Agrobacterium tumefaciens or other Csp protein of the invention, CC such as the present Csp. The promoter is selected from an inducible, constitutive, temporally-regulated, developmentally-regulated, tissue-cc preferred, cold enhanced, cold-specific, stress enhanced, stress-cc predific, drought inducible, water deficit inducible or tissue-specific promoter. An abiotic stress-tolerant transgenic plant that has been CC transformed with a DNA molecule that expresses a Csp is claimed. The CC plant may be a crop plant, a monocot or dicot, and is especially selected from soybean, corn, cancia, rice, cotton, barley, oat, turf grass, cotton and and selected confidence of the transgenic plant that has been confidence of the promoter of the confidence of the corn, cancia, rice, cotton, barley, oat, turf grass, cotton and shear the transgenic plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a crop plant may be a cro
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA molecule comprising a DNA polynucleotide promoter and a DNA that encodes a cold shock protein, useful producing plants with increased tolerance to abiotic stress.
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                     and wheat. The transgenic plant shows improved heat tolerance, ctolerance, salt tolerance, drought tolerance and survival after shock than the corresponding non-transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 19; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-285434/29.
N-PSDB; ADZ21445.
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17-DEC-2003; 2003US-0530453P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abiotic stress tolerance; transgenic plant; crop improvement; heat tolerance; cold tolerance; salt tolerance; drought tolerance; cold shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MONS ) MONSANTO TECHNOLOGY LLC.
            64 VRSL
                                                         7
                                                                                                                                                  1 Similarity 65.6
42; Conservative
                                                       GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRILEENQKVEFEIGHSPKGPQATG 63
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            67
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                                                                                                                                                                      62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shock protein.
                                                                                                                                                Score 223; DB 9;
Pred. No. 1.5e-19;
5; Mismatches 17;
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RESULT 14
ADH54477
ID ADH54
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AC ADH54
XC ADH54
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DT 25-MJ
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ABO66959
ID ABO66
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                        The invention describes a new isolated nucleic acid encoding a Klebsiel pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
           Escherichia coli
                                              Escherichia
                                                                                 ADH54477;
                                                                                                                                                                                                                                                         Sequence 131
                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 13476; 932pp;
                                                                                                                                                                                                                                                                                                                                                                  New nucleic
preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-2003
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                            Cold shock inducible
                                                               25-MAR-2004
                                                                                                  ADH54477 standard; protein; 70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6610836-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004
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                                                                                                                                               127
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                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                 NVIAL 131
                                                                                                                                                                 GVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                        Osborne
                                                                                                                                                                                                                                                                                                                                                                  acid encoding a Klebsiella pneumoniae polypeptide, useful vaccine composition against Klebsiella pneumoniae.
                                             coli cspG
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                         A
A
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0117747P
                                                                                                                                                                                                                              61.8%;
                          gene; physiological
                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide
                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                      Score 222; DB 7;
Pred. No. 4.4e-19;
7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription regulatory element; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              веqid 13476
                                                                                                                                                                                                                                                                                                                                                 English.
                            stress;
                                                                                                                                                                                                                                       Length 131;
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RESULT 15
ABB07338
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Best Local :
                                                                     13-FEB-1989;
09-MAR-1992;
01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid molecule which prolongs the expression of cold shock inducible genes under conditions that elicit the cold shock (cs) response in a bacterium, comprises the 5-UTR of cspI operably linked to a non-native promoter. The nucleic acid is useful for regulating expression of cold shock inducible genes to elicit the cold shock response in bacterium under conditions of physiological stress. The present sequence is Escherichia coli cspG protein used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid comprising the 5-UTR of cspI operably linked to a native promoter, useful for regulating expression of cold shock inc genes to elicit the cold shock response in bacterium under condition
Inouye M, Jo
Goldstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                             03-FEB-1998;
                                                                                                                                                                                                                Streptomyces
                                                                                                                                                                                                                                            Cold-shock induced protein;

    clavuligerus CspA-like protein SC7.0.

                                                                                                                                                                                                                                                                                                    09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    physiological stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000; 2000US-00516667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2003.
                                                                                                                                                                                   US6333191-B1
                                                                                                                                                                                                                                                                                                                                ABB07338;
                                                                                                                                                                                                                                                                                                                                                       ABB07338 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inouye M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2000; 2000US-00516667
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                                          (UYNE-) UNIV NEW JERSEY MEDICINE &
                                                                                                                                                       25-DEC-2001.
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                Jones
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                                                                     89US-00310332.
92US-00852013.
94US-00203806.
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              Etchegaray J,
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                                                                                                                                                                                                                                            Cap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 221; DB 7;
Pred. No. 2.6e-19;
6; Mismatches 17
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                                                                                                                                                                                                                                            prokaryotic;
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                                            DENTISTRY.
                Jiang
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                Pollitt
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Search completed: April 14, 2006, 17:18:45
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                                                                                                                                                                                                                                                                                                               The invention relates to a family of stimuli-induced in particular stress cc or cold-shock induced genes and proteins. An isolated DNA molecule (I) is provided that comprises a prokaryotic promoter that is induced under conditions eliciting a cold shock response (Csp), or the promoter that is comprise a cc decrease in temperature below the normal physiological growth temperature of the prokaryotic cell, preferably bacterium. (I) is useful for encoding proteins under stimuli-induced, particularly stress or cold-shock induced conditions. The encoded proteins are useful in staining DNA and in the c stabilization of DNA and RNA, and thus increasing the efficiency of DNA cand RNA in various in vitro reactions. The encoded protein is also useful as desaturase to denature DNA irrespective of temperature. The proteins care also useful for commercial purposes. The present sequence represents
                                                                                                                                                                                                                               Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA molecules useful for encoding proteins under stress or cold-induced conditions, comprising a prokaryotic promoter that is induced under conditions eliciting a cold shock response.
                                                                                                                                                                                                                                                                                                               Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 10; 33pp; English.
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                                                                                                                                                                                                                             y Match 60.9%;
Local Similarity 65.6%;
les 42; Conservative
                                                                           60 AENV 63
                                                                                                               61 ATGV 64
                                                                                                                                                    Score 218.5; DB 5;
Pred. No. 4.9e-19;
6; Mismatches 15;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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                                                      Database
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                              seq length: 0
seq length: 2000000000
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359
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                                                                                                                                                                                                                                                                                                                                             1 MPQGTVKWFNAEKGFGFIAP.....VEFEIGHSPKGPQATGVRSL
                                                                                                                                                                                                                                                     283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                           Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       April 14,
                                                      PIR_80:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd
pir1:*
pir2:*
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                                                                                                                                                                                                                                                                                                                                                                                                                  Search time 3.92873 Seconds (without alignments) 1640.866 Million cell updates/sec
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score and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

#### SUMMARIES

29	28		26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	0	s	4	ω	2	_	No.	Result
207	207.5	207.5	209.5	210	211	211	211	211	215	216	216	216	216	217	217	218.5	219	220	220	220	221	221	222	222	223	223	352	359	Score	
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67	66	66	65	70	70	70	70	70	69	69	69	69	69	70	69	66	70	69	69	69	70	69	69	69	70	70	67	67	Length	
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G82568	AH1607	AD1245	H86645	D70412	器86030	A91184	AG0981	OCECJ	AG0316	H85793	S43618	E90945	AB0727	C64910	AI0212	S26378	AD0755	F90711	849050	B85562	E85634	F84967	AH0579	A84987	D64840	A90772	F86933	A70564	ID	
	cold shock protein	shock	Bhock		shock	shock	Bhock	major cold shock p	probable cold shoc	cold shock protein	shock	cold shock protein	<b>shock</b>	shock	shock	cold shock protein	shock	Bhock		cold shock protein		shock-like	shock-like	cold shock-like pr		<b>shock</b>	cold	ğ	Description	

A;Status: preliminary

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45	44	43	42	41	40	39	38	37	36	35	<b>3</b>	33	32	<u>3</u> 1	30
199	199.5	199.5	199.5	200	200.5	200.5	201	201	202.5	202.5	204	206	206.5	206.5	206.5
55.4	55.6	55.6	55.6	55.7	55.8	55.8	56.0	56.0	56.4	56.4	56.8	57.4	57.5	57.5	57.5
67	67	66	66	70	69	66	70	67	66	65	70	70	66	66	66
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
T42055	A45723	B89917	A89853	AD0443	A82489	图69608	AE0443	T34593	I40390	B84101	AC0324	AB0202	140158	AB1698	AH1326
cold shock protein		major cold shock p										cold shock protein	major cold shock p	major cold-shock p	major cold-shock p

#### ALIGNMENTS

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probable cold shock protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2004 C;Accession: F86933

R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroy eam, M.A.; Rutherford, X.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86933
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Comoor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P;4-64/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:006360; UNIPARC:UPI000012856D; GB:Z95436; GB:AL123456; NID:
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-67 <COL>
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;Gene: cspA
;Superfamily: cold shock protein, CspA type; cold shock domain homology
;Superfamil: cold shock domain homology <CSD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 359; DB 2; Similarity 100.0%; Pred. No. 3.7e-35; 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ 60
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Holroyd
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C;Species: Escneriuma vol.
C;Date: 12-Sep-1997 #sequence_revision
C;Accession: D64840
R;Blattner, F.R.; Plunkett III, G.; Blc
.A.; Rose, D.J.; Mau, B.; Shao, Y.
.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species Becherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C;Accession: A90772
C;Accession: A90772
C;Accession: A90772
C;Accession: A90772
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C;Accession: A90772
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-70 <HAY>
A;Cross-references: UNIPROT:Q47130; UNIPARC:UPI000012858A; GB:BA000007; PIDN:BAB34568.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A; Residues: 1-67 <STO>
A; Cross-references: UNIPROT: 069550;
C; Genetics:
A; Gene: cspA
C; Superfamily: cold shock protein, C
                                                     A;Status: nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-70 <BLAT>
                                                                                                             Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
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                           Cross-references: UNIPROT:Q47130; Experimental source: strain K-12,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene:
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Best Local
               Genetics:
                                                                                                  Accession: D64840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily:
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capG; capI
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                                                                                                                                                                                                                                                                                                           VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cold shock protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                          62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.1%;
97.0%;
                                                                                      not
                                                                                                                                                            G.; Bloch,
Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 223; DB 2; Length 70
Pred. No. 3.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 352; DB 2;
Pred. No. 2.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CspA type; cold shock domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CspA type;
                           UNIPARC:UPI000012858A;
substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIPARC:UPI00000D434B; GB:AL450380; NID:g13092550;
                                                                                   shown;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M1smatches
                                                                                                                                                                                                    17-Sep-1997 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli (strain 0157:H7,
                                                                                                                                                                          C.A.;
                                                                                      translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cold shock domain
                                                                                                                                                                          Perna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 67
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                      not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                           Z.T.;
                                            GB:AE000201;
                                                                                      ahown
                                                                                                                                                                           Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                          V.; Riley,
                                            GB:U00096;
                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         substrain
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                                                                                                                                                                           :
                                             NID
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                A;Gene:
C;Superf
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                                                         A; Cross-references: UNIPARC: UPI000005A176;
                                                                                                                                                                                                                                                                                                                                                                       밁
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C; Superfamily:
C; Keywords: DNA
F; 7-67/Domain:
Superfamily: cold shock protein, CspA type; cold shock domain; Keywords: DNA binding; stress-induced protein; transcription; 7-67/Domain: cold shock domain homology <CSD>
                                     n homology
regulation
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Matches
                                                                                              Query Match
Best Local :
 67
                    64 VRSL 67
                                                                                   l Similarity
42; Conserv
                                          7
                                                              4
TIVV
                                         GLVKWFNADKGFGFTTPDDGSKDVFVHFTATQSNEFRTLNENQKVBFSTEQGQRGPAAAN
                                                      GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSFKGPQATG
                                                                                    Conservative
 70
                                                                                             62.1%;
                                                                                    5
                                                                                   Score 223; DB 2;
Pred. No. 3.3e-19;
5; Mismatches 17
                                                                                                       Length 70
                                                                                     Indels
                                                                                    0
                                                                                   Gape
                                            66
                                                                 63
                                                                                     0
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision
C;Accession: A84987
R;Shigenobu, S.; Watanabe, H.; Hattori,
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of A;Reference number: A84930; A;Accession: A84987
                                                                                                                                                                A; Gene: cspE; 1
C; Superfamily:
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-69 <STO>
                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI000005E5D4; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                 cold shock-like
                                                                                                  Matches
                                                                                                                Query Match
Best Local (
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                                                                                                                Local Similarity
                                                                                                                                                                               серв; ви489
63
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                                                                w
                                                                                                 42;
 GVRSL 67
                                                           QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQAT
                                  KGNVKWFNESKGFGFITPEDGSKDVFVHFSAIQSNGFKTLAEGQSVEFEITEGAKGPSAA
                                                                                                                                                                 cold shock
                                                                                                                                                                                                                                                                                                                                                                                                                              protein capE [imported] - Buchnera
                                                                                                  Conservative
                                                                                                                61.8%;
                                                                                                                                                                protein,
                                                                                                                                                                                                                                                                                                                 the endocellular bacterial symbiont of aphids Buchnera MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                Hattori,
                                                                                                  4.
                                                                                                 Pred. No. 4.36
4; Mismatches
                                                                                                                Score 222; DB 2;
Pred. No. 4.3e-19
                                                                                                                                                              CspA type; cold shock domain
                                                                                                                                                                                                                                                                                                                                                                                                 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                M.; Sakaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ·ds
                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 31-Dec-2004
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                                                                                                                                 Length
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain
                                                                                                                                                                                                                                                                                                                                                                  Ishikawa, H.
                                                                                                                                   69
                                                                                                                                                                   homology
                                                                                                    0
                                                                                                 Gaps
                                                                    62
                                       64
                                                                                                    0
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cold shock-like protein cspE [imported] - Salmonella enterica subsp. enterica (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 31-Dec-2004 C;Accession: AH0579 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-69 <PAR> A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608 , S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 R; Parkhill, J.; Dougan, G.; James, th, T.; Connerton, P.; Cronin, A.; A; Accession: AH0579 K.D.; Thomson, N.R.; , P.; Davies, R. Pickard, I Skelton, J.; Stevens, Salmonella enterica so D.; Wain, J.; Churcher , L.; White, N.; Farrar gerovar gero.

~

7

65

NVISL

;Supertamily:

cold

**shock** 

protein,

CspA type;

cold

shock domain homology

GB:AL513382; PIDN:CAD05106.1; PID:g16501881;

STY0678

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C;Species: buchar:
C;Date: 02-Mar-2001 #sequence__tc.__
C;Date: 02-Mar-2001 #sequence__tc.__
C;Accession: P84967
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, M.; Watanabe, H.; Hattori, M.; Sakaki,
R;Shigenobu, M.; Sakaki, M.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watanabe, H.; Watana
                             S
                                                                                                                                                                                                                                                           A;Experimental source: strain C;Genetics:
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-70 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homolog of Salmonella cold shock protein [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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A; Residues: 1-69 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: E85634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cold shock-like protein cspC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                Cross-references: UNIPARC:UPI0000165753; GB:AE005174; NID:g12514257; PIDN:AAG55537.1; Rxperimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: E85634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: cspC; BU322; Superfamily: cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPARC:UPI000005E539; Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                        Matches
                                                                                                                                                                                                      Superfamily: cold shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                        41;
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                                                                                                                   Similarity
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GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGFQATG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGFQAT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVTAL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGQVKWFNESKGFGFITPSDGSKDVFVHFSSIQGNGFKTLTEGQNVEFEIQDGQKGPAAV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGTVKWFNAEKGFGFIAPEDGSADVFVHYTBIQGTGFRTLEENQKVEFBIGHSPKGPQAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cold shock protein, CspA type;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                61.6%;
                                                                                                                                                                                                protein, CspA type; cold shock domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [imported] -
                                                                                        4
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                                                                                                                Score 221; DB 2;
Pred. No. 5.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 221; DB 2;
Pred. No. 5.6e-19;
4; Mismatches 19
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Pred. No. 4.3e-19;
7; Mismatches 17
                                                                                        Mismatches
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                                                                                        16;
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                                                                                                                                        Length 70
                                                                                        Indels
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C;Genetics: msmC; gicA
A;Gene: cspE; msmC; gicA
C;Superfamily: cold shock protein, CspA type; cold
C;Keywords: DNA binding; transcription regulation
C;Keywords: DNA binding; transcription cSD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Yamanaka, K.; Mitani, T.; Ogura, T.; Niki, H.; Hiraga, S. Mol. Microbiol. 13, 301-312, 1994
A;Title: Cloning, sequencing, and characterization of multicopy A;Reference number: $49048; MUID:95075315; PMID:7984109
A;Accession: $49050
                                                                                                                                                            A;Cross-references: UNIPARC:UPI000000023B; GB:AE000167; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-69 < BLAT>
                                                                                                                                                                                                                                                                                                                      Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                        R; Blattner, F.R.; Plunkett III, G.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S49050; E64796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cold shock protein homolog cspE - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cold shock protein [imported] - Bscherichia coli (strain 0157:H7, substrain C;Species: Bscherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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A;Experimental source: strain K-12
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A; Residues: 1-69 < YAM>
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A; Residues: 1-69 <STO>
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Pred. No. 7.4e-19;
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                                                                                                                                                                                                                                                                       shown; translation not
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                                                                                                                                                                                                                                                                                                                                                        K-12
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K.; Apodaca
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RiHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Reference number: A99829; MUID:21156231; PMID:11258796
A;Accession: P90711
A;Status: preliminary
A;Molecule type: DNA
A;Residuse; 1-69 <- CHAY>
A;Cross-references: UNIPROT:P36997; UNIPARC:UPI00000023B; GB:BA000007; PIDN:BAB34085.1; C;Genetics: G-C;Genetics: Strain O157:H7, substrain RIMD 0509952
C;Genetics: Ecs0662
C;Superfamily: cold shock protein, CspA type; cold shock domain homology
                                                                                                                                                                                                                                                                                                                                                                                 , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cold shock protein [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 31-Dec-2004 C;Accession: AD0755 C;Accession: AD0755 A; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chu R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Dickard, L.; White, N.; Fickard, D.; Wain, J.; Chu R;Parkhill, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fickard, D.; Wain, N.; Fi
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A; Residues: 1-70 < PAR>
                                                                                                                                                                                                                                                                                                                   A;Accession: AD0755
A;Status: prelimina
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Best Local S
Matches 41
Query Match
Best Local Similarity
                                                                                                          Superfamily:
                                                                                                                                                                                                            Cross-references: UNIPARC:UPI0000059C99; GB:AL513382; PIDN:CAD05743.1; PID:g16503235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
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Pred. No. 7.4e-19;
7; Mismatches 17
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Pred. No. 7.4e-19;
Score 219; DB 2;
Pred. No. 9.8e-19;
                                                                                                      CapA type;
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cold shock protein 7K homolog [similarity] - Streptomyces clavuligerus (;Species: Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004 C;Accession: S26378; S25584 R;Av-Gay, Y.; Aharonowitz, Y.; Cohen, G. Nucleic Acids Res. 20, 5478, 1992 Nucleic Acids Res. 20, 5478, 1992 A;Title: Streptomyces contain a 7.0 kDa cold shock like protein. A;Reference number: S26378; MUID:93065223; PMID:1437568
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S26378
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C;Accession: AI0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: cold shock protein, CspA type; cold C;Keywords: DNA binding; transcription regulation F;4-63/Domain: cold shock domain homology <CSD>
                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <KUR>
                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tragg, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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A; Residues: 1-66 < AVG>
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A;Status: nucleic acid sequence not
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A; Experimental source:
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                                                                                                                                             Superfamily:
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3 QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQAT
                                                                Similarity
40; Conserv
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                                                                                   60.4%;
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                                                                                                                                             protein, CspA type; cold shock domain
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                                                                                     Score 217; DB 2;
Pred. No. 1.7e-18;
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RESULT 15
(C64910
Cold shock protein homolog cspI - Escherichia coli (strain K-12)
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C;Superfamily: cold shock protein, CspA type; cold shock domain homology
C;Keywords: DNA binding; transcription regulation
F;7-67/Domain: cold shock domain homology <CSD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P77605; UNIPARC:UPI000012858D; GB:AB000252; GB:U00096; NID:
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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Query Match Best Local S Matches 67

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Conservative

100.0%; Score 359; DB 1; Length 100.0%; Pred. No. 8.2e-34; tive 0; Mismatches 0; Indels

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Transcription;	; 1. ; DNA-binding;	<pre>52; COLD_SHOCK; plete proteome;</pre>	COM	PROSITE; PS Activator;	A PR
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Q7w2i2 bordetella	Q7W2I2_BORPA	œ a	20.	223	44
	CSPE BUCBP	, ,,	ง	223	4.2
Q8nkz7 xanthomonas Q5h1p7 xanthomonas	Q8NKZ7_XANAC Q5H1P7_XANOR	55 B 50 S	NN	22 <b>4</b> 22 <b>4</b>	41 42
	Q7CLT8_XANCP	20.00	201	224	40
	CSPA_BORPE	0 7 ·	יאי	224	38
POa353 bordetella POa354 bordetella	CSPA BORBA	772	200	224	36
Q872x2 enterococcu Q8r985 thermoanaer	Q82ZXZ_ENTFA Q8R985_THETN	2 2 2	63.1	227.5	υ ω u u 4. n
ralstonia	Q8XTV2_RALSO	2	i w	•	32

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RESULT 2
CSPA MYCTU
ID GSPA MYCTU
ID GSPA MYCTU
ID GSPA M
AC P63848
DT 10-MAY
DE P70bab
GN Name=c
OC Mycoba
OC Bacter
OC CYCTIE
OC MYCODA
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RA COLE S
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HSSP; P41016; 1HZC.

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InterPro; IPR012156; Cold_shock_CspA.

InterPro; IPR012129; CSP_DNA bd.

InterPro; IPR012340; OB_NA_bd_sub.

Pfam; PF00313; CSD; 1.

PIRSF; PIRSF002599; Cold_shock_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-98295987; PubMed=9634230; DOI=10.1038/31159; MEDINES-8295987; PubMed=9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544(1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Peterson J.D., DeBoy R.T., Dodson W.C., Umayam L.A., Ermolaeva M.D., Sinlzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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01-NOV-1997 (Rel. 35, Created)
25-OCT-2004 (Rel. 45, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
Probable cold shock protein A.
Name-cepA; OrderedLocusMames=Rv3648c,
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae; Mycobacteriaceae; Mycobacterium tuberculosis complex. MCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collabor between the Swiss Institute of Bioinformatics and the EMBL outstet the European Bioinformatics Institute. There are no restrictions cuse as long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENO
STRAIN-CDC 1551 / OBIACOB;
MEDILINE-22206494; PubMed=12218036;
DOI-10.1128/JB.184.19.5479-5490.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
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Corynebacterineae; Mycobacteriaceae; Mycobacterium;

    -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarit:
    -!- SIMILARITY: Contains 1 CSD (cold-shock) domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome comparison of Mycobacterium tuberculosis clinical and
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RESULT 3
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DT 05-UUL-2004 (TrEMBLrel. 27,
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DE CEPA.1. Actinobacteria; Av
OC Corynebacterium paratuberculo.
OC Mycobacterium avium complex
CC Mycobacterium avium complex
CX NCBI_TaxID=1770;
RP NUCLEOTIDE SEQUENCE.
STRAIN=kl0;
RP NUCLEOTIDE SEQUENCE.
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InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
Pfam; PF00313; CSD; 1.
PIRSP; PIRSP002599; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
PRODOM; PD000621; Cold_shock; 1.
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PRODOM; PD000621; Cold shock; 1
SWART; SW00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1
Activator; Complete proteome; DX
Transcription regulation.
DOMAIN
4 64 CSI
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PROSITE; PS00352; COLD_SHOCK;
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67 AA; 7370 MW; F87506E09EE87C82 CRC64;
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Pred. No. 8.2
0; Mismatches
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Pred. No. 8.2e-34;
Mismatches 0;
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Best Local :
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GO; GO:0006355; P:regulation of transcription, DN
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold shock.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR012129; CSP.
InterPro; IPR012129; CSP.
InterPro; IPR012340; NA-bind_OB_sub.
Pfam; PF00313; CSD; 1.
PIRSF; PIRSF002599; Cold_shock_A; 1.
PIRSF; PIRSF002599; Cold_shock_N; 1.
PRINTS; PR000621; Cold_shock; 1.
SNART; SM00357; CSP; 1.
                                           Matches
                                                                                        Proupom; FULL CSP; 1.

SMART; SM00357; CSP; 1.

PROSITE; PS00352; COLD SHOCK; 1.

Activator; Complete proteome; D:

Transcription regulation.

CROCIENCE 67 AA; 7342 MW; AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Wingall K.L., Basham D., Brown D., Chillingworth T., Connor R., Puries R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandram M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.,
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MEDLINE-93188700; PubMed=8446027;

Biglmeier K., Honore N., Woods S.A.,

"Use of an ordered cosmid library to

of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).
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01-AUG-1998 (TERMBLrel. 07, Last sequence up
01-FBB-2005 (TERMBLrel. 29, Last annotation
Small cold-shock protein (Putative cold shoo
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Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                        Similarity
MPQGTVXWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSFKGPQ
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(APR-1998)
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                                           Conservative
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ProDom; PD000621; COSP, 1.

SMART; SM00357; CSP, 1.

PROSITE; PS00352; COLD SHOCK; 1.

Activator; DNA-binding; Transcription; Transcription; SEQUENCE 67 AA; 7347 MW; 56C116E09EF746EA CRC64;
                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Putative cold shock protein. OrderedLocusNames=nfa3660;
                                                                                                                                                                                                                                                                                                                                                                                              Q5Z2Y3_NOCFA
Q5Z2Y3;
   NUCLEOTIDE SEQUENCE
STRAIN=IFM 10152;
                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Nocardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE:.
Shires K.I., Powles R., Steyn L.;
Shires K.I., Powles R., Steyn L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                                                                                            NCBI_TaxID=37329;
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Pred. No. 1e-31;
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RESULT 7
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DT 05-JUL-2004 (TrEMBLrel. 27,
DE Cold-shock protein
GN Name=csph; OrderedLocusName
OS Actinobacterium diphtheriae
OS Corynebacterium diphtheriae
OC Corynebacterium diphtheriae
OX NCBI TaxID=1717;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=BLOtype gravis / NCTI
RR NUCLEOTIDE SEQUENCE.
RC STRAIN=BLOtype gravis / NCTI
RA Cerdeno-Tarraga A.-M. Efst.
RA Cerdeno-Tarraga A.-M. Efst.
RA Pallen M., Holroyd S., Jaget
RA Pallen M., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
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Best Local S
Matches 59
L Nucleic Acids Res. 31:6516-6523(2003).

C -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

C -!- SIMILARITY: Contains 1 CSD (cold-shock) domain.

R EMBL; BX248354; CAR48825.1; -; Genomic_DNA.

R GO; GO:000357; F:DNA binding; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-depend GO; GO:0006350; P:transcription; IEA.

R InterPro; IPR002059; COld_shock.

R InterPro; IPR012156; Cold_shock.

R InterPro; IPR012156; CSP.

R Ffam; PF00313; CSD; 1.
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GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold_shock.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
Pfam; PP00313; CSD; 1.
Pfs; PIRSP00259; COld_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
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Cold-shock protein.
Cold-shock protein.
Name=cspA; OrderedLocusNames=DIP0320;
Name=cspA; OrderedLocusNames=DIP0320;
Corynebacterium diphtheriae.
Corynebacterides; Corynebacterides; Corynebacterium.
                                                                                                                                                                                                                                                                               Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.( Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K. De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhi, Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhi, Thomson N.R., digital Post of Corynebacterium diphtheriae NCTC13129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Biotype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nax/gkg874;
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Activator; Complete proteome; DNA-binding; Transcription;
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Pred. No. 3.6e-29;
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RESULT 8
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Q4JSS1;
Q4JSS1;
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative cold shock protein.
Name=cspA; ORFNames=jk1955;
Corynebacterium jelkelum (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Parmebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K411;
PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
Tauch A., Kaiser O., Hain T., Goesmann A., Weisshaar B.,
Tauch A., Kaiser O., Hain T., Goesmann A., Weisshaar B.,
Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty
Albersmeier A., Meyer F., Rupp O., Schneiker S., Viehoever P.,
                                                                                                                                                                                                                                                                                                           Linke B., Tauch A.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR931997; CAIJ8B136.1; -; Genomic DNA.
SEQUENCE 67 AA; 7267 MW; D60BAE570600DJA3 CRC64;
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PROSITE; PS00352; COLD SHOCK;
Activator; Complete proteome;
Transcription regulation.
SEQUENCE 67 AA; 7347 MW; E
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PRODORS; PD000621; Cold_shock; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K411
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AQNVTAL
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    DNA-binding; Transcription;

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1. No. 3.3e-27;
                                                                                                                                                                                                                               296; DB 2;
No. 1.7e-26;
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RESULT 9
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ID Q8FLY0\_C
AC Q8FLY0;
DT 01-MAR-2

QBFLYO COREF QBFLYO; 01-MAR-2003 (

(TrEMBLrel.

23,

PRELIMINARY;

PRT;

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RESULT 10

OBNTX7_CORGL PRELIMINARY; PRT; 67 AA.

ID QBNTX7_CORGL PRELIMINARY; PRT; 67 AA.

AC QBNTX7; Q6M813;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 13-SEP-2005 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cold shock proteins (COLD-SHOCK PROTEIN CSPA).

GN Name=cspA; OrderedLocusNames=cgl0114, cg0215;
GN Name=cspA; OrderedLocusNames=cgl0114, cg0215;
GN Name=cspA; OrderedLocusNames=cgl0114, cg0215;
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InterPro; IPR011129; CSP.
InterPro; IPR0112340; NA-bind_OB_sub.
Pfam; PP00313; CSD; 1.
Pfam; PP000350; COLDSHOCK.
PRINTS; PR00050; COLDSHOCK.
PRODOM; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
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GO; G
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Activator; Complete proteome, Da-binding; Hypothetical Transcription; Transcription regulation.
SEQUENCE 251 AA; 27583 MW; OCA3D167507D8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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OrderedLocusNames=CE2729;
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-!- SIMILARITY: Contains 1 CSD (cold-shock)
EMBL; BA000035; BAC19539.1; -; Genomic_DNA.
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STRAIN=YS-314 / AJ 1
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GO:0003677; F:DNA binding; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO:0006350; P:transcription; IEA.
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InterPro; IPR012156; Cold_Shock_CspA.
InterPro; IPR011129; CSP.
InterPro; IPR011129; CSP.
InterPro; IPR0112340; NA-bind_OB_sub.
Pfam; PF00313; CSD; 1.
PIRST; PIRST002599; Cold_Shock_A; 1.
PRINTS; PR00505; COLDSHOCK.
ProDom; PD000621; Cold_Shock; 1.
SMART; SM00357; CSP; 1.
                                   STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLING=22830012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Kallnowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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QBNTJ9; Q6M854;
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QBNTJ9; Q6M854;
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                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=ATCC 13032 /
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GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of trans

GO; GO:0006350; P:transcription; IEA.
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"Complete ger
                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
STRAIN=ATCC 13032 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and its impact
and vitamins.";
                                                                                                                                                                                                                                                                                                        Submitted
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       McHardy A.C.,
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-!- SIMILARITY: Contains 1 CSD (cold-shock)

EMBL; BA000036; BAB97567.1; -; Genomic_DNA.

EMBL; BX927148; CAF18741.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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       Meyer F.,
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                                                                                                                                                                                                                                                                                                        sequence of Corynebacterium
02) to the EMBL/GenBank/DDBJ
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       Moeckel B.,
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Pred. No. 7e-25;
5; Mismatches
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    DNA-binding; Transcription;

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   Kraemer R.,
ferle W., Pu
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GO; GO:000357; F:DNA binding; IRA.
GO; GO:0006355; P:regulation of transcr
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold shock.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
InterPro; IPR01312340; NA-bind_OB_sub.
Pfam; PF00313; CSD; 1.
PRINTS; PINSF000559; COLDSHOCK_A; 1.
PRNITS; PR000501; COLDSHOCK_Frober; PR00051; Cold_shock_1.
SMART; SN00357; CSP; 1.
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GO; GO
GO; GO
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
MEDLINE=27723752; PubMed=12840036; DOI=10.1101/gr.1285603;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Putative cold shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and its impact
and vitamins."
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The complete Corynebacterium
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-|- SIMILARITY: Contains 1 CSD (cold-shock) domain.
EMBL; BA00035; BAC17116.1; -; Genomic_DNA.
HSSP; P32081; 1CSP.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-deg
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold_shock.
                                                                                                                                                                                                                                                                                      replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                         Nishio Y., Nakamura Y.,
Sugimoto S., Matsui K.,
Gojobori T.;
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Activator; Complete proteome; DNA-binding; Transcription;
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-!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
EMBL; BA00036; BAB97701.1; -; Genomic DNA.
EMBL; BX927148; CAF18878.1; -; Genomic DNA.
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J. Biotechnol. 104:5-25(2003).
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COREF
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R InterPro; IPR011340; NA-bind_OB_sub.
R Pfam; pP00313; CSD; 1.
R PIRSF; PIRSF002599; Cold_shock_A; 1.
R PIRSF; PR00050; COLDSHOCK.
R PRINTS; PR000521; Cold_shock; 1.
R PROSTITE; PS00357; CSP; 1.
R PROSTITE; PS00357; CSD_SHOCK; 1.
R PROSTITE; PS00357; COLD_SHOCK; 1.
R PROSTITE; PS00352; COLD_SHOCK; 1.
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Best Local S
Matches 52
                                                             PIRSF; PIRSF002599; Cold shock A; PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
                                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Actinobacteria;
Micrococcineae; Micrococca
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat)
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat)
Cold-shock protein, DNA-binding.
ORFNamessArthDBAFT 1862;
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Q4NFR7;
      SEQUENCE
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   S00352; CÓLD_SHOCK; 1.
DNA-binding; Transcription;
67 AA; 7267 MW; 850595CD01
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nilarity 77.6%;
Conservative
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      scription; Transcription regulation.
850595CD0EC77CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Query Match

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Score

266;

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Length

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CSP ARTGO
ID — (SSP ARTGO STANDARD; PRT; 67 AA.
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DT 01-OCT-1996 (Rel. 48, Last sequence update)
DT 01-OCT-1996 (Rel. 48, Last sequence update)
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Best Local S
Matches 47
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berger F., Morellet N., Menu F., Potier P.; "Cold shock and cold accilmation proteins in the bacterium Arthrobacter globiformis SI55."; J. Bacteriol. 178:2999-3007(1996).
                                                                                                                                                                                                                                                                                                                                                Activator; DNA-binding; Transcription; Transcription regulation.

    -i- SUBCELLULAR LOCATION: Cytoplasmic.
    -i- INDUCTION: In response to low temperature.
    -i- SIMILARITY: Contains 1 CSD (cold-shock) domain.

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Micrococcineae; Micrococcaceae; Arthrobacter.
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                                                    ATGV 64
                                                                                                                                  MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
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                                                                                                         MAQGTVKWFNAEKGFGFITPDDSDGDVFVHYSEIQTGGFKTLDENARVQFEIGQGAKGPQ
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73.4%;
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                                                                                                                                                                                                           Score 260; DB 1; 1
Pred. No. 2.5e-22;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                       850595CD0EDACBF4 CRC64;
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RESULT

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Search completed: April 14, 2006, 17:32:30 Job time: 26.7208 secs

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AC Q4NLE1;
AC Q4NLE1;
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Q4NLE1;
13-SEP-2005 (113-SEP-2005)
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00313; CSD; 1.

PIRSF; PIRSF002599; Cold shock A;

PRINTS; PR00050; CCLDSHOCK.

ProDom; PD000621; Cold shock; 1.

SMART; SM00357; CSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lariner F., Land M.;
"Annotation of the draft genome assembly of Arthrobacter Submitted (JUN-2005) to the RMBL/GenBank/DDBJ databases.
-I- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TYENBLYel. 31, Last sequence update)
13-SEP-2005 (TYENBLYel. 31, Last annotation update)
Cold-shock protein, DNA-binding.
ORFNames=ArthDRAFT_4299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FB24; US DOE Joint Genome Institute (PGF-ORNL);
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Bacteria, Actinobacteria, Actino
Micrococcineae, Micrococcaceae,
                                                                                                                                                                                                                                                                                                                         PROSITE; PS00352; COLD_SHOCK; 1.
Activator; DNA-binding; Transcription; Transcription regulation
SEQUENCE 67 AA; 7250 MW; 8173679D2C37B1D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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5
                                                  13
                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                Similarity
  ABNIRPL
                                                     ATGVRSL
                                                                                                           MATGTVKWFNAEKGFGFIAPDDGSADVFAHYSAIATSGYRSLDENQKVEFDVTQGPKGPQ
                                                                                                                                       MPQGTVKWFNAEKGFGF1APEDGSADVFVHYTE1QGTGFRTLBENQKVEFE1GHSPKGPQ
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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Sequence 147, App
Sequence 82, Appl
Sequence 84, Appl
Sequence 8171, Ap
Sequence 1171, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12349, A
Sequence 9, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 1235, Appl
Sequence 7, Appli
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Sequence 14126, A
Sequence 17, Appli
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Qy 61 ATGVRSL 67           Db 61 ATGVRSL 67	Qy 1 MPQGTVKWFNABKGPGFIAPEDGSADVFVHYTBIQGTGFRTLEENQKVBFBIGHSPKGPQ	Query Match 100.0%; Score 359; DB 2; Length Best Local Similarity 100.0%; Pred. No. 3.5e-40; Matches 67; Conservative 0; Mismatches 0; Indel	US-09-050-739-147  US-09-050-739-147  Sequence 147, Application US/09050739  Patent No. 6641814  GENERAL INFORMATION: APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: NIELSEN, Rikke APPLICANT: ROSENTRINGER, Thomas APPLICANT: ROSENTRANDS, Ida APPLICANT: ROSENTRANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin CURRENT APPLICATION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FILER EFFERENCE: 670001-2002.1  CURRENT APPLICATION NUMBER: US/09/050,739  CURRENT APPLICATION NUMBER: 03-6/97  EARLIER APPLICATION NUMBER: 1277/97  EARLIER FILING DATE: 1997-04-02  EARLIER APPLICATION NUMBER: 60/044,624  EARLIER APPLICATION NUMBER: 60/070,488  EARLIER FILING DATE: 1997-04-18  EARLIER FILING DATE: 1998-01-05  NUMBER: 0F SEQ ID NOS: 173  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 147  TYPE: PRT  GORGANISM: Mycobacterium tuberculosis  US-09-050-739-147	ALIGNMENTS	28 205 57.1 67 2 US-09-902-540-16294 29 205 57.1 70 2 US-09-93-427-2 30 205 57.1 85 2 US-09-93-427-2 31 204 56.8 68 2 US-09-902-540-16803 32 201.5 56.1 66 2 US-09-002-76-2 33 201.5 55.8 79 2 US-09-013-001C-3081 35 199.5 55.6 67 1 US-08-203-806B-12 36 199.5 55.4 71 1 US-08-203-806B-2 37 199 55.4 71 1 US-08-203-806B-2 39 199 55.4 71 1 US-08-203-806B-2 40 199 55.4 71 2 US-09-17-754A-8 41 199 55.4 71 2 US-09-17-754A-8 42 199 55.4 71 2 US-09-17-754A-8 43 199 55.4 71 2 US-09-23-427-4 44 198.5 55.3 66 2 US-09-923-550-14444 45 196.5 54.7 70 2 US-09-134-000C-5696
	NQKVEFEIGHSPKGPQ 60	th 67; els 0; Gaps 0;	TIDE FRAGMENTS		Sequence 16294, A Sequence 2549, Appli Sequence 2549, Appli Sequence 16803, A Sequence 7943, Appli Sequence 3081, Ap Sequence 112, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, Appli Sequence 14, Appli Sequence 9, Appli Sequence 17, Appli Sequence 17, Appli Sequence 372, Appli Sequence 372, Appli Sequence 14444, A Sequence 14444, A

US-09-603-208A-82 US-09-603-208A-82 ; Sequence 82, Application US/09603208A ; Patent No. 6822084

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; ORGANISM: Corynebacterium glutamicum
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Matches 52
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SEQ ID NO 82
LENGTH: 67
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APPLICANT: Lee, Heung-Shick
APPLICANT: Lie, Heung-Shick
APPLICANT: Kim, Hyung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
CURRENT APPLICATION NUMBER: US/09/603,208A
CURRENT FILING DATE: 2000-06-23
CURRENT APPLICATION NUMBER: US/09/603,208A
                 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS FILE REFERENCE: BGI-124CP
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PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/:
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PRIOR APPLICATION NUMBER: 60/:
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FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19932209.0
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Lee, Heung-Shick
Kim, Hyung-Joon
                                                                                                                Schroder, Hartwig
Zelder, Oskar
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Kroger, Burkhard
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77.6%;
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CURRENT APPLICATION NUMBER: US/09/603,208A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142692
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 1930429.7
PRIOR APPLICATION NUMBER: DE 1930429.7
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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US-09-603-208A-84
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SEQ ID NO 84
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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PRIOR FILING DATE:
PRIOR APPLICATION NI
PRIOR FILING DATE:
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Lee, Heung-Shick
APPLICANT: Lee, Heung-Shick
TITLE OF INVENTION: CORYNEBACTERIUM GLUTANICUM GENES E
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REPERENCE: BGI-124CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE
PRIOR FILING DATE: 1999-08-31
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APPLICATION NUMBER:
FILING DATE: 1999-
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FILING DATE: 1999-06-25
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l Similarity 77.6%;
52; Conservative
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                                                                                                                                                                                                            Schroder, Harung Schroder, Harung Schroder, Oskar Zelder, Oskar Zelder, Oskar Haberhauer, Gregor Haberhauer, Gregor Lee, Heung-Shick Kim, Hyung-Goon GLUTAMICUM GENES ENCODING STRESS, CONTRON: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, CONTRONS CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
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TUMBER: DE 19941382.7
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Pred. No. 5.8e-30;
5; Mismatches 10
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60

APPLICATION NUMBER: DE 19932209.0

1999-07-08

1999-07-08 IMBER: DE 19931541.8

FILING DATE: APPLICATION NUMBER:

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RESULT 6
US-09-489-039A-13476
US-09-489-039A-13476
; Sequence 13476, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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US-09-134-000C-4171
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PRIOR APPLICATION NUMBER: DE 1993230.9
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
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Best Local S
Matches 44
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APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICATION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

PRIOR FILING DATE: 1997-08-15
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4171
LENGTH: 88
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Best Local (
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    APPLICANT:
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ORGANISM: Corynebacterium glutamicum
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44; Conservative
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Gary Breton et. al
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                                                                                                                                                                                                                                                                                                                  Score 227.5; DB 2;
Pred. No. 1.4e-22;
7; Mismatches 12;
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Pred. No. 4.9e-29;
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FILE REFERENCE: 2709.2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION UNMEER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13476

LENGTH: 131

TYPE: PRT
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US-08-203-806B-11
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Patent No. 6610533
GENERRAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Wang, Nan
APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
CURRENT FILING DATE: 2001-08-01
CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
                                                                                                                                              Sequence 11, Application US/08203806B Patent No. 5714575
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 70
TYPE: PRT
                                                     APPLICANT:
APPLICANT:
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                    APPLICANT:
                                                                                                         APPLICANT:
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GVRSL 67
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                                                                                                                                                                                                                                                                                                                         7 GLVKWENADKGFGFITPDDGSKDVFVHFTALQSNEFRTLNENQKVEFSIEQGQRGFAAAN 66
                                                                                                                                                                                                                                                                                                                                                   4 GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG 63
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                                                                    Jones, Pamela
Etchegaray, Jean-Pierre
              Weining, Jian
Pollitt, N. Stephen
Goldstein, Joel
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ilarity 64.1%;
Conservative
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                                                                                                         Inouye,
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                                                                                                         Masayori
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63.1%;
Nucleic Acid Sequences, Stress-induced
                                                                                                                                                                                                                                                                                                                                                                                              Score 221; DB 2; Pred. No. 7.7e-22; 6; Mismatches 17;
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Pred. No. 1.3e-21;
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Query Match
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Thehes 42; Conserv
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                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09017754A Patent No. 6333191 GENERAL INFORMATION:
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5998P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8393
TELEPHONE: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acide
TYPE: amino acide
TOPOLOGY: linn
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Proteins and Uses
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welser & Associates
STREET: 230 South Fifteenth Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/203,806B FILING DATE: 01-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces clavuligerus
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                   WEINING, JIANG
POLITT, N. STEPHEN
GOLDSTEIN, JOEL
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
PROTEINS AND USES THEREOF
                                                                                                                                                  NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      APPLICANT: INOUYE, MASAYORI
                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATGV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
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                                                                                                 ADDRESSEE: SCHNADER,
STREET: 1600 Market (
CITY: Philadelphia
                                                                   STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            AENV 63
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                                                     ZIP: 19103
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Pred. No. 1.5e-21;
6; Mismatches 15;
                                                                                                                    Street,
                                                                                                                      HARRISON, SEGAL & LEWIS,
Street, Suite 3600
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GENERAL INFORMATION:

APPLICANT: INGUYE, MASSYORI

APPLICANT: Wang, Nan

APPLICANT: Wang, Nan

APPLICANT: Yamanaka, Kunitoshi

TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: 1053-00

CURRENT APPLICATION NUMBER: US/09/516,667

CURRENT FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 87

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 79

LENGTH: 70

CORGANISM: E. Coli

US-09-516-667-79
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HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-017-754A-11
RESULT 11
US-09-902-540-12349
; Sequence 12349, Application US/09902540
; Patent No. 6833447
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
TELEPAX: 215-751-2658
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Matches
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                    Local
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SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                 67 VVAL 70
                                                                                                                                                   64 VRSL 67
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                                                                                                                                                                                                                                                                                      Similarity
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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llarity 64.1%;
Conservative
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Pred. No. 1.5e-21;
6; Mismatches 15;
                                                                                                                                                                                                                                                                Score 217; DB 2; Length 70; Pred. No. 2.6e-21; 7; Mismatches 16; Indels
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US-08-203-806B-4
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US-09-902-540-12349
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/99/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12349
IELEX: 834809 WEISTAK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino
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                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REGISTRATION NUMBER: 377.5998P
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSES: Weiser & Associates
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goldstein, Joel
TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced
TITLE OF INVENTION: Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                 REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
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Local Similarity 62.1%;
hes 41; Conservative
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/203,806B FILING DATE: 01-MAR-1994 CLASSIFICATION: 435
                                                                                               TELEPHONE: 215-875-8383
TELEPAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                             19102
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Goldstein, Joel
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Etchegaray, Jean-Pierre
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Pred. No. 3.3e-21;
6; Mismatches 19
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US-08-203-806B-9
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; MOLECULE TYPE: protein
US-08-203-806B-4
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                                                                                    Best Local
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Patent No. 5714575
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                                                                                                                                                                                                                                   TELEX: 834809 WEISTAK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                 MOLECULE TYPE: F
ORIGINAL SOURCE:
ORGANISM: Esch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced TITLE OF INVENTION: Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pollitt, N. Stephen
APPLICANT: Goldstein, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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SOFTWARE: Patentin Polaria
                                                                                                                                                                                                                                                                                          TELEPHONE: 215-875-8394
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Local Similarity 61.5%;
hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/203,806B FILING DATE: 01-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19102
                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                    Similarity
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GY: linear
KGQVKWFNESKGFGFITPADGSKDVFVHFSAIQGNGFKTLAEGQNVEFEIQDGQKGPAAV
                          QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQAT 62
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230 South Fifteenth Street, Suite 500
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Etchegaray, Jean-Pierre
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                                                                                                                                                      Escherichia coli
                                                                                                                                                                                    protein
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                                                                  60.2%; Score 216; DB 1; Length 69; 61.5%; Pred. No. 3.5e-21; tive 6; Mismatches 19; Indels
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Pred. No. 3.5e-21;
6; Mismatches 19
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RESULT 14
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Sequence 9, Application US/09017754A
PATENT NO. 6333191
GENERAL INFORMATION:
APPLICANT: INOUTE, MASAYORI
JONES, PAMELA
ETCHEGARAY, JEAN-PIERRE
WEINING, JIANG
POLITT, N. STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 40; Conservat
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SEQUENCE CHARACTENISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-BASE #1.0, VE
SOFTWARE: PATENTIN RE-BASE #1.0, VE
CURRENT APPLICATION NUMBER: US/09/017,754A
FILING DATE: 03-Feb-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHNADER, HARRISON, SEGAL & LEWIS, LLP
STREET: 1600 Market Street, Suite 3600
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WEINING, JIANG
WEINING, JIANG
POLITT, N. STEPHEN
GOLDSTEIN, JOEL
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
PROTEINS AND USES THEREOF
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61.5%;
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Search completed: April 14, 2006, 17:37:59 Job time: 6.19531 secs
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Best Local Similarity 61.5%;
Matches 40; Conservative
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/017,754A
PPLICATION NUMBER: US/09/017,754A
PILLING DATE: 03-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 113-cip2-div-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHNADER, HARRISON, SEGAL & LEWIS, LLP
STREET: 1600 Market Street, Suite 3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOLDSTEIN, JOEL
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                          65 NVTAI 69
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                                                                                                                                                 LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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ZIP: 19103
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Pred. No. 3.5e-21;
6; Mismatches 19
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Maximum
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Maximum Match 100%
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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US-09-804-980-147
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US-09-804-980-147
US-09-738-626-3695
US-10-953-856-51
US-09-738-626-313
US-10-156-761-12354
US-10-156-761-1354
US-10-156-761-1366
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US-10-282-122A-57331
US-09-912-020-328
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Sequence 3845, Ap
Sequence 62113, A
Sequence 11466, A
Sequence 11, Appl
Sequence 19, Appl
Sequence 5731, Appl
Sequence 5731, Appl
Sequence 57316, A
Sequence 57316, A
Sequence 59825, A
Sequence 73106, A
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Sequence 75459, A
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Sequence 53, Appl
Sequence 54, Appl
Sequence 57, Appl
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Sequence 55, Appl
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		Query Ma Best Loo Matches	RESULT 1  US-09-791-171-  SEQUENCE 14/ PATENT NO. I  GENERAL INFE  APPLICANT: APPLICA OF IN  FILE REFERE CURRENT FILE CURRENT FILE FRIOR APPLI PRIOR APPLI PRIOR FILLI PRIO		22222222222222222222222222222222222222
. 61 A	3-3	atch cal	BSULT 1 S-09-791-171-147 Sequence 147, Ap Patent No. US200 GENERAL INFORMAT APPLICANT: ANDE APPLICANT: RAS APPLICANT: RAS APPLICANT: FLO APPLICANT: FLO TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT FILING DA PRIOR FILING DA PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR APPLICATI PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR PILING DA PRIOR APPLICATI PRIOR TILING DA PRIOR APPLICATI PRIOR PILING DA PRIOR APPLICATI PRIOR PILING DA PRIOR PILING PRI		200 200 200 200 200 200 200 201 201 201
ATGVRSL 6	mpQGTVKWFNAEKGF           mpQGTVKWFNAEKGF	Similarity 7; Conser	SULT 1 -09-791-171-147 Sequence 147, Application Batent No. US20020094336A1 GENERAL INFORMATION: APPLICANT: ANDERSEN, Pete APPLICANT: NIELSEN, Rikk APPLICANT: RASMUSSEN, Pete APPLICANT: RESMUSSEN, Pete APPLICANT: RESMUSSEN, Pete APPLICANT: RESMUSSEN, Pete APPLICANT: FICHIO, Walte TITLE OF INVENTION: NUCLE TITLE OF INVENTION: UNCLE TITLE OF INVENTION: UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE OF INVENTION UNCLE FILIE DATE: 1997-0 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION UNCLE FILIE DATE: 1997-0 PRIOR APPLICATION UNCLE FILIE DATE: 1998-0 PRIOR APPLICATION UNCLE PRIOR FILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR APPLICATION UNCLE PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR APPLICATION UNCLE PRIOR PILLING DATE: 1997-0 PRIOR PILLING DATE: 1997-0 PRIOR PILLING DATE: 1997-0 PRIOR PILLING DATE: 1997-0 PRIOR PILLING DATE: 1997-0 PRIOR PILLING DATE: 1997-0 PRIOR PILLING		55.55.66.00.00.00.00.00.00.00.00.00.00.00.00.
67 67	NAEKGFG        NAEKGFG	100. 100. vative	-171-147  NO. US20020094336A1  NO. US20020094336A1  NINFORMATION: ANT: ANDERSEN, Peter ANT: NIELSEN, Rikke ANT: NIELSEN, Rikke ANT: RASMUSSEN, Peter Birk ANT: ROSENKRANDS, Ida ANT: FLORIO, Walter OF INVENTION: NUCLEIC ACIDS FRA OF INVENTION: NUCLEIC ACIDS FRA DEFICATION NUMBER: US/09/791 TT APPLICATION NUMBER: 03/05/07 TT APPLICATION NUMBER: 03/6/97 FILING DATE: 1997-01-02 APPLICATION NUMBER: 1277/97 APPLICATION NUMBER: 1277/97 FILING DATE: 1997-01-02 APPLICATION NUMBER: 00/044,624 APPLICATION NUMBER: 60/044,624 FILING DATE: 1997-04-08 APPLICATION NUMBER: 60/070,488 FILING DATE: 1998-01-05 OF SEG ID NOS: 173 RE: PatentIn Ver. 2.0 NO 147 PRT PRT PRT 1SM: Mycobacterium tuberculosis		799
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	MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ 	Score 359; D Pred. No. 1.6 0; Mismatches	171 ; FRAGMENTS ; FRAGMENTS ; TUBERCU //791,171 739 624 488	ALIGNMENTS	US-10-156-761-11981 US-10-282-122A-56326 US-10-282-122A-57510 US-10-282-122A-60873 US-10-282-122A-60873 US-10-194-438-4 US-10-156-761-12310 US-10-156-761-18431 US-10-953-856-95 US-10-953-856-95 US-10-282-122A-45991 US-10-282-122A-68525 US-10-953-856-65 US-10-953-856-65 US-10-953-856-65 US-10-953-856-61 US-10-953-856-61 US-10-953-856-61 US-10-953-856-61 US-10-953-856-61 US-10-953-856-61
	QGTGFRTLEE          QGTGFRTLEE	DB 3; Length 6e-38; 0; Indel	AND POLYPEPTIDE		22-56326 22-57510 22-57510 23-60873 23-60873 23-45991 23-45991 23-45991 23-45991 23-45991 23-45991 23-45991 23-45991 24-45991 24-45991 25-659
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RESULT 2 US-09-804-980-147

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GENERAL INFORMATION:

APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DAYE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOPTWARE: Patentin version 3.0
SEQ ID NO 147
LENGTH: 67
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 147, Application US/10620246 Publication No. US20040115211A1 GENERAL INFORMATION:
                                                          SOPTWARE: PatentIn
SEQ ID NO 147
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WELDINGH, KARIN
APPLICANT: FLORIO, WALTER
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REPERENCE: 670001-2002.1A
                                                                                                                       PRIOR APPLICATION NUMBER: 1281/98 PRIOR FILING DATE: 1998-10-08
                                                                                                          NUMBER OF SEQ ID NOS: 173
ORGANISM: Mycobacterium tuberculosis
                                             LENGTH: 67
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                                                                                                                                                                                                           APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/070,488
                                                                                                                                                                    FILING DATE: 1999-01-21
                                                                                                                                                                                        APPLICATION NUMBER: 60/116,673
                                                                                                                                                                                                                                                      FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/791,171
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 10/138,473
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-01-05
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RASMUSSEN, Peter Birk
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Pred. No. 1.6e-38;
; Mismatches 0;
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 3695
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US-10-953-856-51
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Sequence 51, Application US/10953856
Publication No. US20050097640A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology
TITLE OF INVENTION: Methods for enhancing abiotic stress tolerance in plants of INVENTION: compositions thereof
FILE REFERENCE: Docket number (39-21)51768C
CURRENT APPLICATION NUMBER: US/10/953,856
CURRENT FILING DATE: 2004-09-29
NUMBER OF SEQ ID NOS: 95
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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RESULT 7
US-10-282-122A-62113
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APPLICANT: SENCH, MACHIKO
APPLICANT: SENCH, MACHIRO
APPLICANT: SENCH, MACATO
APPLICANT: SENCH, MACATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOTTWARE: PATENTIN YET. 3.0
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Matches
Sequence 62113, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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SEQ ID NO 51
LENGTH: 67
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Best Local (
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LENGTH: 67
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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ANDO, SBIKO
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Sequence 12354, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SHEA, TADAYOSHI
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US-10-156-761-12354
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62113
LENGTH: 67
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Matches
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FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
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PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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Foreyth, R.
Xu, H.
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Trawick, John
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Zyskind, Judith
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Haselbeck, Robert
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US-10-953-856-19
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Sequence 19, Application US/10953856
Publication No. US20050097640A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology
TITLE OF INVENTION: Methods for enhancing abiotic
TITLE OF INVENTION: compositions thereof
FILE REFERENCE: Docket number (38-21)51768C
CURRENT APPLICATION NUMBER: US/10/953,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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SEQ ID NO 11466
LENGTH: 68
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Best Local :
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SEQ ID NO 12354
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Best Local
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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TYPE: PRT
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nes 44; Conservative
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Pred. No. 6.8e-22;
Midmatches 13;
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Pred. No. 1.7e-22;
5; Mismatches 18;
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                                                          stress tolerance
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APPLICANT: IKEBA, HARNO
APPLICANT: IKEBA, HARNO
APPLICANT: IKEBA, HARNO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8364
LENGTH: 67
TYPE: PRT
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US-10-156-761-8364
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; CROANISM: Escherichia coli
; ORGANISM: Escherichia coli
US-10-953-856-19
                                                                                                                                                                                     US-10-953-856-13
                                                                                                                                                                                                        RESULT 12
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Sequence 13, Application US/10953856
Publication No. US20050097640A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology
TITLE OF INVENTION: Methods for enhancing abiotic stress tolerance in plants
TITLE OF INVENTION: compositions thereof
FILE REFERENCE: Docket number (38-21)51768C
CURRENT APPLICATION NUMBER: US/10/953,856
CURRENT FILING DATE: 2004-09-29
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NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
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Best Local Similarity 65.6%;
Matches 42; Conservative
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Pred. No. 1.1e-20;
4; Mismatches 19
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Pred. No. 6.6e-21;
5; Mismatches 17
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PatentIn version 3.2

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                                                   ; ORGANISM: Enterococcus faecalis
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SOPTWARE: PatentIn versions of ID NO 13
 Best Local Similarity
                   Query Match
                                                                                                                            SEQ ID NO 57331
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APPLICANT:
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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ORGANISM: Escherichia coli
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                                                                                                                                                                                                                     APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                             FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/253,625
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Zyskind, Jud
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Haselbeck, Robert
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Pred. No. 1e-19;
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Pred. No. 5.2e-20;
6; Mismatches 19
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RESULT 15
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US-09-912-020-328
                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio,
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 485

SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 328

LENGTH: 70

TYPE: PRT

ORGANISM: E. Coli
                                                                                                                                                                                                                                                        GENERAL INFORMATION
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                                                                                                                                                                                                                                                                        Sequence 42639, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR PILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
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APPLICANT:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John
TITLE OF INVENTION: Identification FILE REFERENCE: ELITRA.034A
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG 63
                                                 Yamamoto, R. Forsyth, R.
                                                                                     Trawick, John
Carr, Grant
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Pred. No. 2.3e-19;
8; Mismatches 17
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

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Best Local Similarity 60.9%;
Matches 39; Conservative
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Maximum Match 100%
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ALLIGNMENTS 56192	US-11-188-298-16630	US-11-188-298-16521	US-11-188-298-10981	US-11-188-298-5412	US-11-096-568A-27878	US-11-096-568A-27879	US-11-096-568A-27880	US-11-096-568A-30604	US-11-082-389-26	US-11-098-686-10907	US-11-188-298-1224	US-11-188-298-15364	US-11-188-298-13172	US-11-188-298-10851	US-11-188-298-4166	US-11-188-298-17481	US-11-188-298-11910	US-11-188-298-10200	US-11-188-298-6359	US-11-188-298-7875
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APPLICANT: INCUTE, MASSAYOTI
APPLICANT: PHADTARE, Sangita
APPLICANT: Qing, Guoliang
APPLICANT: Qing, Guoliang
APPLICANT: KE, Haiping
TITLE OF INVENTION: COLD SHOCK INDUCIBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
FILE REFERENCE: INCOVER 2.1 PCT
CURRENT FILING DATE: 2004-09-01
PRIOR PHILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/402,921
PRIOR PHILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 50
SOPTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 70
TYPE: PRT
ORGANISH: Escherichia coli
PEATURES:
OTHER INFORMATION: Symthetic
US-10-506-192-6
RESULT 2
US-10-506-192-2
; Sequence 2, Application US/10506192
; Publication No. US20050272924A1
; GENERAL INFORMATION:
; APPLICANT: INOUYE, Masayori
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Matches 42
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Pred. No. 5e-21;
5; Mismatches
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CURRENT APPLICATION NUMBER: US/10/506,192
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR FILING DATE: 2002-03-01
PRIOR PRILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 70
TYPE: PRT
ORGANISM: Escherichia coli
US-10-506-192-2
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APPLICANT: Hecker, Michael
APPLICANT: Hecker, Michael
APPLICANT: Juergen, Britta
APPLICANT: Voigt, Britta
APPLICANT: Voigt, Britta
FILLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REPERENCE: HENK-0122 / H5692
FULE REPERENCE: HENK-0122 / H5692
CURRENT APPLICATION UNMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP2003/009979
PRIOR APPLICATION NUMBER: DE 10242433.0
PRIOR APPLICATION NUMBER: DE 10242433.0
PRIOR FILING DATE: 2002-9-11
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Best Local Similarity 60.9
Conservative
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APPLICANT: Feesche, JOETS
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Breves, Roland
APPLICANT: Schweder, Thomas
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Publication No. US20060040279A1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 130
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      67 VISL 70
                                           64 VRSL 67
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                                                                                                        4 GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG 63
                                                                                   7 GIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGN 66
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APPLICANT: Feesche, Joerg
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Breves, Roland
APPLICANT: Breves, Roland
APPLICANT: Schweder, Thomas
APPLICANT: Hecker, Michael
APPLICANT: Hecker, Michael
APPLICANT: Voigt, Britta
APPLICANT: Voigt, Brigit
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5692
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT APPLICATION NUMBER: PCT/EP2003/009979
PRIOR APPLICATION NUMBER: PCT/EP2003/009979
PRIOR APPLICATION NUMBER: DE 10242433.0
PRIOR APPLICATION NUMBER: DE 10242433.0
PRIOR APPLICATION NUMBER: DS 10242433.0
PRIOR FILING DATE: 2003-09-01
I NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 67
                                        TYPE: PRT; ORGANISM: Bacillus US-11-077-619-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Escherichia coli; FEATURE: ; OTHER INFORMATION: Synthetic US-10-506-192-8
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APPLICANT: KE, Haiping
APPLICANT: KE, Haiping
TITLE OF INVENTION: COLD SHOCK INDUCIBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION INVEST: 1004-09-01
CURRENT APPLICATION NUMBER: 60/361,069
PRIOR PILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/402,921
PRIOR FILING DATE: 2002-08-14
NUMBER: OF SEQ ID NOS: 50
SOCTWARE: PATENTIN VETSION 3.3
SEQ ID NO 8
LENGTH: 70
TYPER: PET
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APPLICANT: INOUYE, MABBAYORI
APPLICANT: XIA, Bing
APPLICANT: PHADTARE, Sangi
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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PHADTARE, Sangita
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Pred. No. 2.1e-18;
9; Mismatches 17
Score 199.5;
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Length 67;
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US-11-077-619-22
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Best Local Similarity
Matches 38; Conserv
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SEQ ID NO 22
LENGTH: 71
TYPE: PRT
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              APPLICANT: Qing, Guoliang
APPLICANT: KE, Halping
TITLE OF INVENTION: COLD SHOCK INDUCIBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES
TILE REPERENCE: INOUYSE-2.1 PCT
CURRENT APPLICATION NUMBER: US/10/506,192
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
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APPLICANT: Voigt, Birgit
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5692
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/SP2003/009979
PRIOR APPLICATION NUMBER: DE 10242433.0
PRIOR FILING DATE: 2002-09-01
PRIOR PPLICATION NUMBER: DE 10242433.0
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 130
                                                                                                                                                                                                                                    APPLICANT: INOUYE, Masayori
APPLICANT: XIA, Bing
APPLICANT: PHADTARE, Sangi
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APPLICANT: Maurer, Karl-
NUMBER OF
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  SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maurer, Karl-Heinz
Breves, Roland
Schweder, Thomas
Hecker, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                             V 67
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                                                                                                                                                                                                                                      XIA, Bing
PHADTARE, Sangita
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APPLICANT: Schweder, Thomas

APPLICANT: Hecker, Michael

APPLICANT: Hecker, Michael

APPLICANT: Voigt, Biritta

APPLICANT: Voigt, Birgit

TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL

FILE REFERENCES: HENK-0.122 / H5692

CURRENT APPLICATION NUMBER: US/11/077,619

CURRENT FILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: PCT/EP2003/00979

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-09-11

NUMBER OF SEQ ID NOS: 130

SECTIVARE: PatentIn version 3.3
                                                         RESULT 9
US-10-467-657-3284
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                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 98
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-11-077-619-98
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US-11-077-619-98
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; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-506-192-4
Sequence 3284, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 72
TYPE: PRT
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Best Local Similarity
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APPLICANT: Maurer, Karl-Heinz
APPLICANT: Breves, Roland
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es 38; Conservative
                                                                                                                                                                                                                                                                                 40; Conservative
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                                                                                                                                                                                                        MLEGKVKWFNSEKGFGFIEVE-GQDDVFVHFCAIQGEGFKTLEEGQSVSFEIVEGNRGPQ 59
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                                                                                                                                                                                                                                                                                                  55.3%; Score 198.5; DB 7; 62.5%; Pred. No. 5.5e-18;
                                                                                                                                                                                                                                                                                 5; Mismatches
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Pred. No. 5.3e-18;
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APPLICANT: CHIRON SPA APPLICANT: FONTANA MARIA Rita APPLICANT: PIZZA MARIAGIRAZI APPLICANT: MASIGNANI Vega APPLICANT: MONACI Blisabetta

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Sequence 302, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Russell, William M.
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
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US-11-169-041-216
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Publication No. US20060019284A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER

TITLE OF INVENTION: CELLS

FILE REFERENCE: 10001 NP

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT FILING DATE: 2005-06-28

CURRENT FILING DATE: 2005-06-28
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SEQ ID NO 3284
LENGTH: 80
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SEQ ID NO 216
LENGTH: 364
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1369
LENGTH: 147
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 302
LENGTH: 67
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
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Sequence 7806, Application US/11079463

Publication No. US20060073161A1

GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRATITIE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHO0-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1369, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
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TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
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Similarity 44.1%;
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Pred. No. 0.00045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00045;
                                                                                                                                                                                                                                                                                                                                                 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6490
SEQ ID NO 6490
CRANISM: Staphylococcus aureus subsp. aureus Mu50
US-11-087-099-6490
                                                                                                                                                                                                                                                                  RESULT 15
US-11-087-099-6490
; Sequence 6490, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-821-234-1048
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US-10-821-234-1048
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; ORGANISM: B.fragilis
US-11-079-463-7806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1048
LENGTH: 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1048, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 21; Conserv
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
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ilarity 37.5%;
Conservative
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18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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Pred. No. 0.14;
7; Mismatches 27;
Score 65; DB 7; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                    Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 826;
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Matches 16; Conservative 3; Mismatches 20; Indels

Oy 20 PEDGSADVFVHYTEIOGTGFRTLEENOKVEFEI--GHSPKG 58
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Gaps

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24 PLDDKVKIKVHYAGICGTDIHTYEGHYKVNFPVTLGHEFSG 64

Search completed: April 14, 2006, 18:42:17 Job time : 3.871 secs

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